Access DB# 98886

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner # : _____ Date: _____
Art Unit: _____ Phone Number 30_____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

BEST AVAILABLE COPY

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 – 703-308-4498
jan.delaval@uspto.gov

****

STAFF USE ONLY		Type of Search		Vendors and cost where applicable	
Searcher:	Jan	NA Sequence (#)	✓	STN	
Searcher Phone #:	4498	AA Sequence (#)		Dialog	
Searcher Location:		Structure (#)		Questel/Orbit	
Date Searcher Picked Up:	7/15/03	Bibliographic		Dr.Link	
Date Completed:	7/19/03	Litigation		Lexis/Nexis	
Searcher Prep & Review Time:		Fulltext		Sequence Systems	✓
Clerical Prep Time:	15	Patent Family		WWW/Internet	
Online Time:	+10	Other		Other (specify)	

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:46:48 ; Search time 5485.97 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1512.6	77.2	68790	9	AF017732	AF017732 Homo sapi
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ALIGNMENTS

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DEFINITION Sequence 6 from patent US 6312693.
ACCESSION AR176315
VERSION AR176315.1 GI:17918670
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 8858)
AUTHORS Aruffo,A.A., Hollenbaugh,D., Siadak,A.W., Berry,K.K., Harris,L., Thorne,B.A., Bajorath,J., Huse,W.D., Wu,H. and Watkins,J.D.
TITLE Antibodies against human CD40
JOURNAL Patent: US 6312693-A 6 06-NOV-2001;

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ORIGIN

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  Best Local Similarity   90.6%;  Pred. No. 0;
  Matches 1783;  Conservative    0;  Mismatches  137;  Indels   49;  Gaps    4;

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Qy        367 -ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGT---------- 414
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Qy        415 ------------AGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGGGGGTCGGATGACG 462
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shimizu,N. and Kawasaki,K.
  TITLE     Homo sapiens genomic DNA, chromosome 2p11.2, clone:cos141
  JOURNAL   Published Only in Database (2000)
REFERENCE   2  (bases 1 to 37201)
  AUTHORS   Shimizu,N. and Kawasaki,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2000) Nobuyoshi Shimizu, Keio University, School
            of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
            160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp,
            Tel:81-3-3351-2370, Fax:81-3-3351-2370)
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                     /evidence=not_experimental
                     /rpt_family="L2"
     repeat_region   34233. .34258
                     /evidence=not_experimental
                     /rpt_family="(TA)n"
     repeat_region   complement(35506. .35799)
                     /evidence=not_experimental
                     /rpt_family="AluJo"
     repeat_region   complement(36550. .36800)
                     /evidence=not_experimental
                     /rpt_family="MER82"
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                     /rpt_family="AluJb"
BASE COUNT    11316 a    7697 c    7764 g   10424 t
ORIGIN

  Query Match             77.4%;  Score 1517.4;  DB 9;  Length 37201;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1518;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 166276)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-DEC-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT
            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            Contact: submissions@watson.wustl.edu
            ---------------- Project Information -----------------
            Center project name: H_NH1435C03
            ------------------------------------------------------
            ------------- Summary Statistics --------------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 164631 bases at least Q40
            Consensus quality: 165062 bases at least Q30
            Consensus quality: 165346 bases at least Q20
            Insert size: 166000; agarose-fp
            Insert size: 165976; sum-of-contigs
            Quality coverage: 6.84 in Q20 bases; agarose-fp
            Quality coverage: 6.81 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 4 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    21011: contig of 21011 bp in length
            *    21012    21111: gap of unknown length
            *    21112    63536: contig of 42425 bp in length
            *    63537    63636: gap of unknown length
            *    63637   152378: contig of 88742 bp in length
            *   152379   152478: gap of unknown length
            *   152479   166276: contig of 13798 bp in length.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /clone="RP11-1435C3"
     misc_feature    1. .21011
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                     clone_end:T7
                     vector_side:left"
     misc_feature    21112. .63536
                     /note="assembly_name:Contig11"
     misc_feature    63637. .152378
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                     clone_end:SP6
                     vector_side:right"
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                     /note="assembly_name:Contig9"
BASE COUNT    51344 a  32704 c  32660 g  49267 t    301 others
ORIGIN

  Query Match             77.4%;  Score 1517.4;  DB 2;  Length 166276;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1518;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     144744 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 144803

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     144804 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 144863

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     144864 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 144923

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     144924 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 144983

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     144984 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 145043

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Db     145044 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 145103

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
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Db     145104 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 145163

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Db     145164 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 145223

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Db     145224 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 145283

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Db     145284 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 145343

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db     145344 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 145403

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db     145404 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 145463

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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Db     145464 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 145523

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
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Db     145524 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 145583

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 1332
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Db     145584 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 145643

Qy       1333 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 1392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     145644 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 145703

Qy       1393 CCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCT 1452
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Db     145704 CCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCT 145763

Qy       1453 CCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTG 1512
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Qy       1513 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
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Db     145824 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 145883
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Qy       1573 ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 1632
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Db     145884 ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 145943

Qy       1633 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1692
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Db     145944 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 146003

Qy       1693 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
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Db     146004 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 146063

Qy       1753 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 1812
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Db     146064 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 146123

Qy       1813 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
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Db     146124 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 146183

Qy       1873 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1932
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Db     146184 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 146243

Qy       1933 TCAGCAATCCCACTTCTAG 1951
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Db     146244 TCAGCAATCCCACTTCTAG 146262
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RESULT 4
AC096579/c
LOCUS       AC096579               176555 bp    DNA     linear   PRI 01-MAR-2002
DEFINITION  Homo sapiens BAC clone RP11-601N4 from 2, complete sequence.
ACCESSION   AC096579 AC023416
VERSION     AC096579.1  GI:15638889
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 176555)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
  PUBMED    9847074
REFERENCE   2  (bases 1 to 176555)
  AUTHORS   Grewal,N. and Abbott,A.
  TITLE     The sequence of Homo sapiens BAC clone RP11-601N4
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 176555)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-SEP-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 176555)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Sep 18, 2001 this sequence version replaced gi:7705152.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0601N04
                Drafting Center: WIBR
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO. For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-450E9; the clone sequenced
            to the right is RP11-685N3.  Actual start of this clone is at base
            position 1 of RP11-601N4; actual end is at base position 176555 of
            RP11-601N4.

            Data from AC062029 and AC060807 was used to finish this clone,
            AC023416.  Polymorphisms have been identified between AC023416 and
            AC062029.

            The sequence of AC023416 has been incorporated into AC096579.
FEATURES             Location/Qualifiers
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     repeat_region   305. .507
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     misc_feature    2755. .2937
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     misc_feature    3289. .3365
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                /rpt_family="MIR"
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misc_feature    9706. .9764
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                (NID:g13520858)"
misc_feature    9744. .9764
                /note="match to EST BG571262 (NID:g13578915)"
misc_feature    10484
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misc_feature    10562. .10703
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                /note="similar to Mus musculus EST AA547167 (NID:g2308458)
                vk81a10.s1"
misc_feature    10630. .10703
                /note="similar to Homo sapiens EST AI587263 (NID:g4573704)
                tq04a07.x1"
misc_feature    10668. .10703
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misc_feature    11302. .11806

  Query Match             77.4%;  Score 1517.4;  DB 9;  Length 176555;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1518;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132041 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 131982

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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Db     131981 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 131922

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
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Db     131921 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 131862

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
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Db     131861 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 131802

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
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Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
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Db     131681 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 131622

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Db     131621 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 131562

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Db     131501 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 131442

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db     131441 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 131382

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db     131381 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 131322

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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Db     131321 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 131262

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131261 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 131202
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Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 1332
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Qy       1333 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 1392
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Qy       1393 CCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCT 1452
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Db     131081 CCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCT 131022

Qy       1453 CCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTG 1512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     131021 CCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTG 130962

Qy       1513 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130961 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 130902

Qy       1573 ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 1632
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     130901 ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 130842

Qy       1633 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130841 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 130782

Qy       1693 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
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Db     130781 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 130722

Qy       1753 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 1812
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Db     130721 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 130662

Qy       1813 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130661 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 130602

Qy       1873 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1932
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     130601 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 130542

Qy       1933 TCAGCAATCCCACTTCTAG 1951
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Db     130541 TCAGCAATCCCACTTCTAG 130523
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RESULT 5
HSU72063
LOCUS       HSU72063                2737 bp    DNA     linear   PRI 14-OCT-1996
DEFINITION  Human immunoglobulin kappa chain constant region gene, partial cds.
ACCESSION   U72063
VERSION     U72063.1  GI:1619959
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2737)
  AUTHORS   Hu,W.X., Cao,Y., Li,X.Y., Lee,L.M. and Yao,K.T.
  TITLE     Comparison of NPC Transforming Gene Tx to Ig Kappa Constant Region
            Gene and Their Expression in Different Cell Lines (Chinese with
            English Abstract)
  JOURNAL   Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 27, 215-221 (1995)
REFERENCE   2  (bases 1 to 2737)
  AUTHORS   Hu,W.X.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-SEP-1996) Medicine/Hematology, UTHSCSA, 7703 Floyd
            Curl Drive, San Antonio, TX 78284, USA
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                     /cell_type="epithelial"
                     /tissue_type="nasopharyngeal carcinoma"
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                     RGEC"
BASE COUNT      820 a    645 c    536 g    736 t
ORIGIN
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  Best Local Similarity   99.8%;  Pred. No. 0;
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Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 61

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 121

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 181

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 241

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 301

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 361

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 421

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 481

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 541

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 601

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 661

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 721

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 781
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Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
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Db        782 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 841

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 1332
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 901

Qy       1333 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 1392
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Db        902 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 961

Qy       1393 CCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCT 1452
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Db        962 CCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCT 1021

Qy       1453 CCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTG 1512
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 CCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTG 1081

Qy       1513 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
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Db       1082 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1141

Qy       1573 ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 1632
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1142 ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 1201

Qy       1633 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1692
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1261

Qy       1693 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
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Db       1262 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1321

Qy       1753 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 1812
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Db       1322 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTCGCA 1381

Qy       1813 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
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Db       1382 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1441

Qy       1873 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1932
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Db       1442 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1501

Qy       1933 TCAGCAATCCCACTTCTAG 1951
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Db       1502 TCAGCAATCCCACTTCTAG 1520


RESULT 6
AF178581
LOCUS       AF178581               7810 bp    DNA     linear   PRI 26-JUN-2002
DEFINITION  Homo sapiens nasopharyngeal carcinoma gene sequence.
ACCESSION   AF178581 AF276073 AF500623
VERSION     AF178581.3  GI:21592476
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 7810)
  AUTHORS   Ming,L., Wei,R., Xinxian,W., Linqing,X., Wei,L. and Ya,C.
  TITLE     Nucleotide sequence analysis of a transforming gene isolated from
            nasopharyngeal carcinoma cell line CNE2: an aberrant human
            immunoglobulin kappa light chain which lacks variable region
  JOURNAL   DNA Seq. 15, 1-5 (2002)
REFERENCE   2  (bases 1 to 7810)
  AUTHORS   Ming,L., Wei,R., Wei,L., Xinxian,W., Lingqin,X. and Ya,C.
  TITLE     An analysis of EcoRI/XhoI 3 kb fragment sequence of Nasopharyngeal
            carcinoma transforming gene
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 7810)
  AUTHORS   Wei,R., Ming,L., Linqing,X., Xinxian,W., Wei,L. and Ya,C.
  TITLE     Nucleotide sequence analysis of Tx, a transforming gene isolated
            From a nasopharyngeal carcinoma cell line CNE2
  JOURNAL   Unpublished
REFERENCE   4  (bases 1 to 7810)
  AUTHORS   Xinxian,W.
  TITLE     An analysis of the full sequence of Nasopharyngeal carcinoma
            transforming gene
  JOURNAL   Unpublished
REFERENCE   5  (bases 1 to 7810)
  AUTHORS   Ming,L., Wei,R., Wei,L., Xinxian,W., Lingqin,X. and Ya,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-1999) Molecular Biology Laboratory, Cancer
            Research Institute of Hunan Medical University, 88 Xiangya Road,
            Changsha, Hunan 410078, People's Republic of China
REFERENCE   6  (bases 1 to 7810)
  AUTHORS   Wei,L., Ming,L., Wei,R., Xinxian,W., Lingqin,X. and Ya,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-OCT-2000) Molecular Biology Laboratory, Cancer
            Research Institute of Hunan Medical University, 88 Xiangya Road,
            Changsha, Hunan 410078, People's Republic of China
  REMARK    Sequence update by submitter
REFERENCE   7  (bases 1 to 7810)
  AUTHORS   Wei,L., Ming,L., Wei,L. and Ya,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2002) Molecular Biology, Cancer Research
            Institute, Xiangya Medical School of Central South University, 88
            Xiangya Road, Changsha, Hunan 410078, People's Republic of China
  REMARK    Sequence update by submitter
COMMENT     On Jun 26, 2002 this sequence version replaced gi:10800410.
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Qy       853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Qy       913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Qy       973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Qy      1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Qy      1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Qy      1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
Db      5795 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 5854

Qy      1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
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Qy      1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 1332
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Qy      1513 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
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Qy      1573 ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 1632
Db      6215 ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 6274

Qy      1633 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1692
Db      6275 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 6334

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Qy      1753 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCA 1812
Db      6395 AATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTCGCA 6454

Qy      1813 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 1872
Db      6455 AGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAA 6514

Qy      1873 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 1932
Db      6515 AACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAAC 6574

Qy      1933 TCAGCAATCCCACTTCTAG 1951
Db      6575 TCAGCAATCCCACTTCTAG 6593
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RESULT 7
AF017732

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LOCUS       AF017732               68790 bp    DNA     linear   PRI 24-OCT-1997
DEFINITION  Homo sapiens chromosome 2 cosmids cos111 and cos 607/6 containing
            immunoglobulin Vk-JkCk region, complete sequence.
ACCESSION   AF017732
VERSION     AF017732.1  GI:2558844
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 68790)
  AUTHORS   Brandt,P., Jaerke,D., Scharfe,M., Dose,S., Schoen,O. and
            Bloecker,H.
  TITLE     Human DNA sequence from cosmids cos111 and cos607/6 on chromosome
            II contains ESTs
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 68790)
  AUTHORS   Brandt,P., Jaerke,D., Scharfe,M., Dose,S., Schoen,O. and
            Bloecker,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-AUG-1997) Genomanalyse, Genomanalyse Gesellschaft
            fuer Biotechnologische Forschung mbH, Mascheroder Weg 1, 38124
            Braunschweig, Germany
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                     /clone="cos111, cos 607/6"
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     repeat_region   complement(741. .802)
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repeat_region        complement(28816. .28910)
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repeat_region        42422. .42521
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repeat_region        42885. .43707
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repeat_region        complement(44658. .44759)
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repeat_region        complement(47358. .47473)
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repeat_region        complement(47951. .48304)
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repeat_region        complement(48376. .48503)
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  Matches 1515;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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Db      62126 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 62185

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62186 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 62245

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
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Db      62246 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 62305

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
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Db      62306 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 62365

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
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Db      62366 TCTGTCCCTTACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 62425

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Db      62426 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 62485

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
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Db      62486 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 62545

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Db      62546 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 62605

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Db      62606 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 62665

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Db      62666 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGT 62725

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db      62786 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 62845

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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Db      62846 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 62905

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Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 1332
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Db      62966 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTT 63025

Qy       1333 TACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAA 1392
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Qy       1513 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 1572
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Db      63206 CTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTT 63265

Qy       1573 ACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAG 1632
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Db      63266 ACAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAG 63325

Qy       1633 AAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATA 1692
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Qy       1693 AAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTT 1752
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Qy       1933 TCAGCAATCCCACTTCTAG 1951
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Db      63626 TCAGCAATCCCACTTCTAG 63644

RESULT 8
AR035237
LOCUS       AR035237                1701 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 54 from patent US 5871732.
ACCESSION   AR035237
VERSION     AR035237.1  GI:5951905
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1701)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE     Anti-CD4 antibody homologs useful in prophylaxis and treatment of
            AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 54 16-FEB-1999;
FEATURES             Location/Qualifiers
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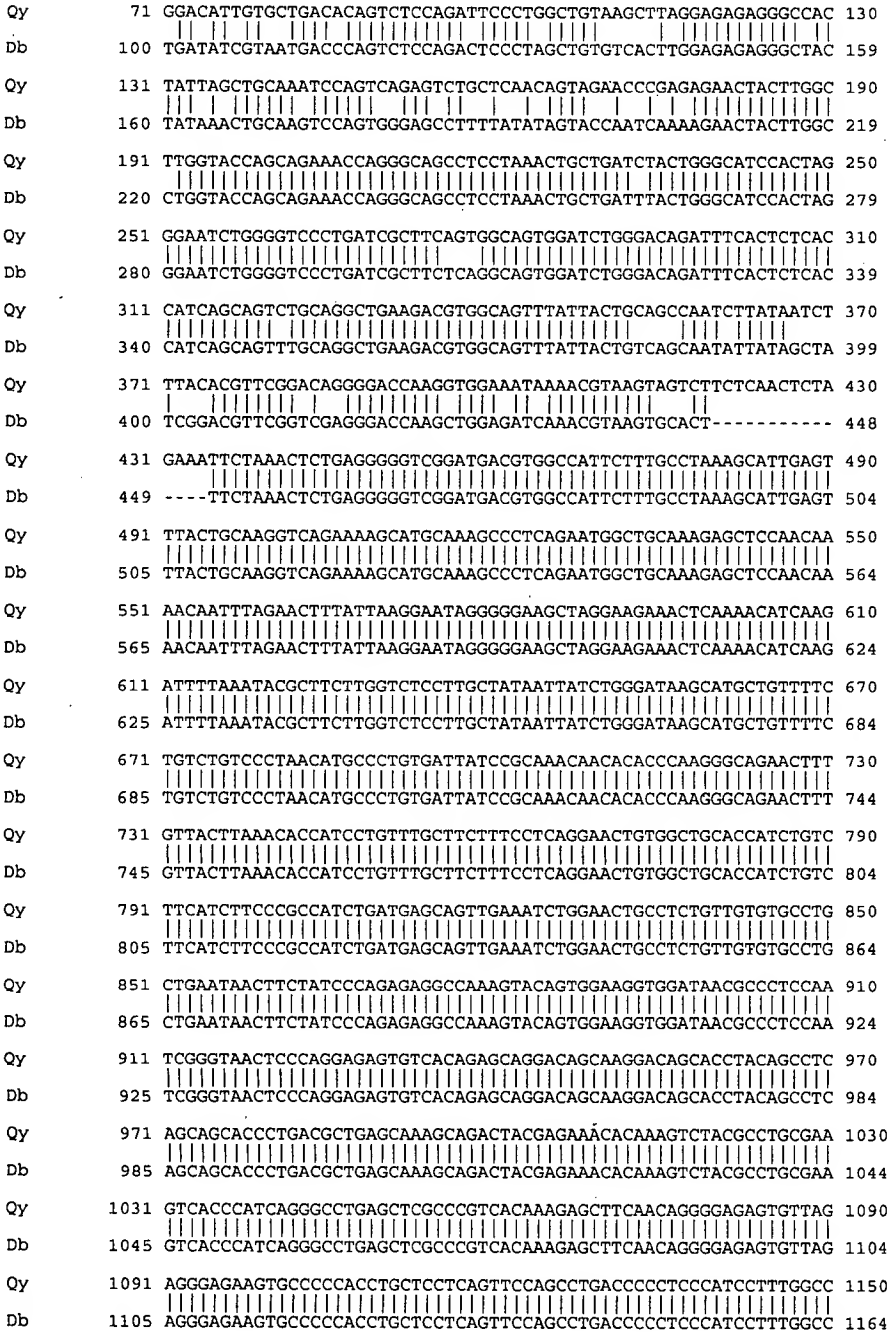

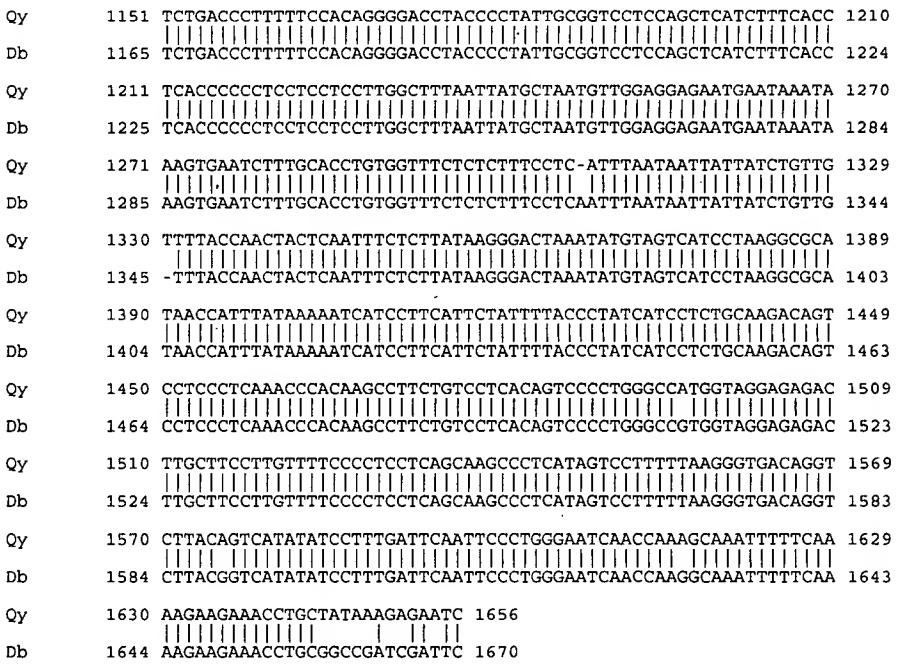

RESULT 9
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DEFINITION Sequence 55 from patent US 5871732.
ACCESSION AR035238
VERSION AR035238.1 GI:5951906
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1701)
AUTHORS Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
TITLE Anti-CD4 antibody homologs useful in prophylaxis and treatment of AIDS, ARC and HIV infection
JOURNAL Patent: US 5871732-A 55 16-FEB-1999;
FEATURES Location/Qualifiers
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Query Match 72.9%; Score 1429.4; DB 6; Length 1701;
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Qy       311 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCT 370
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Qy       371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTA 430
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Qy       431 GAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 490
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Qy       551 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAG 610
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Qy       611 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 670
Db       625 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 684

Qy       671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 730
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Qy       731 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 790
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Qy       971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1030
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Qy      1091 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1150
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Qy      1151 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1210
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Qy      1330 TTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1389
Db      1345 -TTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1403

Qy      1390 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1449
Db      1404 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1463

Qy      1450 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGAC 1509
Db      1464 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGAC 1523

Qy      1510 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1569
Db      1524 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1583

Qy      1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
Db      1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA 1643

Qy      1630 AAGAAGAAACCTGCTATAAAGAGAATC 1656
Db      1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670
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RESULT 10
HSIGKA.
LOCUS       HSIGKA                  5364 bp    DNA     linear   PRI 16-OCT-1992
DEFINITION  H.sapiens DNA for IG kappa JC region.
ACCESSION   X67858
VERSION     X67858.1  GI:33217
KEYWORDS    Ig kappa light chain.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5364)
  AUTHORS   Garrard,W.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1992) W.T. Garrard, UT Southwestern Medical
            Centre, Department of Biochemistry, 5323 Harry Hines Blvd., Dallas
            TX 75235, USA
REFERENCE   2  (bases 1 to 5364)
  AUTHORS   Whitehurst,C., Henney,H.R., Max,E.E., Schroeder,H.W. Jr.,
            Stuber,F., Siminovitch,K.A. and Garrard,W.T.
  TITLE     Nucleotide sequence of the intron of the germline human kappa
            immunoglobulin gene connecting the J and C regions reveals a matrix
            association region (MAR) next to the enhancer
  JOURNAL   Nucleic Acids Res. 20 (18), 4929-4930 (1992)
  MEDLINE   93027217
   PUBMED   1408808
FEATURES             Location/Qualifiers
     source          1. .5364
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /germline
     misc_feature    252. .290
                     /note="J1 region"
     misc_feature    613. .651
                     /note="J2 region"
     misc_feature    917. .955
                     /note="J3 region"
     misc_feature    1252. .1290
                     /note="J4 region"
     misc_feature    1570. .1608
                     /note="J5 region"
     misc_feature    2661. .3661
                     /note="matrix association region (MAR)"
     enhancer        3742. .3866
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     misc_feature    4491. .4993
                     /note="constant region"
BASE COUNT     1623 a   1035 c   1114 g   1592 t
ORIGIN

  Query Match           60.4%;  Score 1183.2;  DB 9;  Length 5364;
  Best Local Similarity   99.6%;  Pred. No. 2.8e-270;
  Matches 1207;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4154 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 4213

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4214 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 4273

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4274 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 4333

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4334 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 4393

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4394 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 4453

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4454 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 4513

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4514 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 4573

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4574 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 4633

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4634 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 4693

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4694 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 4753

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4754 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 4813

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4814 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 4873

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4874 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 4933

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4934 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 4993

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db       4994 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 5052

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5053 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 5112

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5113 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 5172

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTT 1511
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       5173 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTT 5232

Qy       1512 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 1571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5233 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 5292

Qy       1572 TACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAA 1631
              ||| |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       5293 TACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAA 5352

Qy       1632 GAAGAAACCTGC 1643
              ||||||||||||
Db       5353 GAAGAAACCTGC 5364


RESULT 11
AR035236
LOCUS       AR035236               1276 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 53 from patent US 5871732.
ACCESSION   AR035236
VERSION     AR035236.1  GI:5951904
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1276)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE     Anti-CD4 antibody homologs useful in prophylaxis and treatment of
            AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 53 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1276
                     /organism="unknown"
BASE COUNT      340 a    352 c    244 g    340 t
ORIGIN

  Query Match           60.3%;  Score 1181.4;  DB 6;  Length 1276;
  Best Local Similarity   98.9%;  Pred. No. 6.4e-270;
  Matches 1210;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    2;

Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 203

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443
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Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 563

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 683

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 743

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 803

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTGTTTT 923

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
              |||||||||||||||||||||||||||||||||||||||  |||||||||| |||||
Db        924 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTACTCCTAAGGCG-ATAAC 982

Qy       1394 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
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Db        983 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1043 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1102

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1103 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162

Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        1163 CAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGA 1222

Qy       1634 AGAAACCTGCTATAAAGAGAATC 1656
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Db        1223 AGAAACCTGCGGCCGATCGATTC 1245
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RESULT 12
HSIGK1
LOCUS       HSIGK1                  1209 bp    DNA     linear   PRI 07-JAN-1995
DEFINITION  C-terminal part of human kappa-immunoglobulin gene coding for amino
            acids 109 to 214.
ACCESSION   V00557 J00241
VERSION     V00557.1  GI:33140
KEYWORDS    germ line; Ig kappa light chain; immunoglobulin.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Hieter,P.A., Max,E.E., Seidman,J.G., Maizel,J.V. Jr. and Leder,P.
  TITLE     Cloned human and mouse kappa immunoglobulin constant and J region
            genes conserve homology in functional segments
  JOURNAL   Cell 22 (1 Pt 1), 197-207 (1980)
  MEDLINE   81042304
   PUBMED   6775818
FEATURES             Location/Qualifiers
     source          1. .1209
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             336. .653
                     /note="reading frame; Protein sequence is in conflict with
                     the conceptual translation"
                     /codon_start=1
                     /protein_id="CAA23823.1"
                     /db_xref="GI:1335148"
                     /db_xref="SWISS-PROT:P01834"
                     /translation="TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
                     ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
                     RGEC"
     polyA_site      833
                     /note="poly adenylation site"
BASE COUNT      320 a    330 c    234 g    325 t
ORIGIN
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Query Match 60.3%; Score 1181.2; DB 9; Length 1209;
Best Local Similarity 99.6%; Pred. No. 7.1e-270;
Matches 1205; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 60

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 120

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 180

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 240

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 300

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 360

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 420

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 480

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 540

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 600

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 660

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        661 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 720

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 780

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 840

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db        841 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-TTT 899

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 959

Qy       1394 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1019

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1020 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTTGC 1079

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1080 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1139

Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
              | ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1140 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1199

Qy       1634 AGAAACCTGC 1643
              ||||||||||
Db       1200 AGAAACCTGC 1209
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RESULT 13
HUMIGKC3
LOCUS       HUMIGKC3                1209 bp    DNA     linear   PRI 05-JAN-1995
DEFINITION  Human Ig germline kappa-L chain, C region (inv3 allele).
ACCESSION   J00241
VERSION     J00241.1  GI:185938
KEYWORDS    C-region; germline; immunoglobulin light chain;
            immunoglobulin-kappa.
SEGMENT     3 of 3
SOURCE      Homo sapiens placenta DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Hieter,P.A., Max,E.E., Seidman,J.G., Maizel,J.V. Jr. and Leder,P.
  TITLE     Cloned human and mouse kappa immunoglobulin constant and J region
            genes conserve homology in functional segments
  JOURNAL   Cell 22 (1 Pt 1), 197-207 (1980)
  MEDLINE   81042304
   PUBMED   6775818
REFERENCE   2  (bases 1 to 1209)
  AUTHORS   Hieter,P.A., Maizel,J.V. Jr. and Leder,P.
  TITLE     Evolution of human immunoglobulin kappa J region genes
  JOURNAL   J. Biol. Chem. 257 (3), 1516-1522 (1982)
  MEDLINE   82120090
   PUBMED   6276389
COMMENT     Compared in [1] with the mouse C-kappa gene. There is a short
            stretch containing a highly conserved, repeated pentanucleotide
            sequence 'cagca' (bases 511-550). The authors [1] show that there
            is probably only one C-kappa locus in the human genome, instead of
            three as was previously assumed. They also present a physical map
            of the J-C region. [1] also reported the sequences for the active
            V-J1 region and the germline J4 gene. [1] compared with NBRF data.
               EMBL features not translated to GenBank features:
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```
                key         from     to        description
                POLYA       833      833       poly adenylation site
                CDS         336      653       reading frame.
FEATURES              Location/Qualifiers
     source           1. .1209
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /map="2p12"
                      /tissue_type="placenta"
                      /germline
     gene             join(K01325.1:1. .199,1. .656)
                      /gene="IGKC"
     intron           <1. .333
                      /gene="IGKC"
                      /note="kappa intron J-C"
     CDS              <334. .656
                      /gene="IGKC"
                      /note="C region"
                      /codon_start=3
                      /product="immunoglobulin kappa chain"
                      /protein_id="AAA58989.1"
                      /db_xref="GI:185945"
                      /db_xref="GDB:G00-120-088"
                      /translation="TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
                      ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
                      RGEC"
BASE COUNT      320 a    330 c    234 g    325 t
ORIGIN      Chromosome 2p12; about 700 bp after <humigkc2>.
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  Query Match             60.3%;  Score 1181.2;  DB 9;  Length 1209;
  Best Local Similarity   99.6%;  Pred. No. 7.1e-270;
  Matches 1205;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 60

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 120

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 180

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 240

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 300

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 360

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 420

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 480

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 540

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 600
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Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 660

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 720

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 780

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 840

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db        841 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-TTT 899

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        900 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 959

Qy       1394 CATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        960 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1019

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        1020 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTTGC 1079

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1080 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1139

Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
             | ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        1140 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1199

Qy       1634 AGAAACCTGC 1643
             ||||||||||
Db        1200 AGAAACCTGC 1209


RESULT 14
AR035234
LOCUS       AR035234               1241 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 51 from patent US 5871732.
ACCESSION   AR035234
VERSION     AR035234.1  GI:5951902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1241)
  AUTHORS   Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
  TITLE     Anti-CD4 antibody homologs useful in prophylaxis and treatment of
            AIDS, ARC and HIV infection
  JOURNAL   Patent: US 5871732-A 51 16-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .1241
                     /organism="unknown"
BASE COUNT      329 a    340 c    242 g    330 t
ORIGIN

  Query Match           60.3%;  Score 1181.2;  DB 6;  Length 1241;
  Best Local Similarity   99.6%;  Pred. No. 7.1e-270;
  Matches 1205;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 203

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 563

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 683

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
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Db        684 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 743

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
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Db        744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 803

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
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Db        804 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db        864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-TTT 922

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
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Db        923 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 982

Qy       1394 CATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
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Db        983 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
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Db        1043 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTTGC 1102

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1103 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162
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Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
             | |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1163 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1222

Qy       1634 AGAAACCTGC 1643
              ||||||||||
Db       1223 AGAAACCTGC 1232


RESULT 15
HSKAPPALC
LOCUS       HSKAPPALC               1075 bp    mRNA    linear   PRI 09-MAY-1996
DEFINITION  H.sapiens gene encoding kappa light chain constant region.
ACCESSION   X96754
VERSION     X96754.1  GI:1237214
KEYWORDS    constant region; immunoglobulin; immunoglobulin kappa chain;
            immunoglobulin light chain; immunoglobulin superfamily.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1075)
  AUTHORS   Hilger,C., Grigioni,F. and Hentges,F.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1075)
  AUTHORS   Hilger,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-1996) C. Hilger, Centre Hospitalier, 4 Rue
            Barble, L-1210 Luxembourg, LUXEMBOURG
COMMENT     Related sequences V00557 and J00241.
FEATURES             Location/Qualifiers
     source          1. .1075
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                     /db_xref="taxon:9606"
                     /clone="pBkappa5"
                     /cell_type="peripheral blood lymphocytes"
                     /dev_stage="adult"
     C_region        291. .611
                     /product="kappa light chain constant region"
                     /note="C-terminal"
BASE COUNT      282 a    301 c    204 g    288 t
ORIGIN

  Query Match             54.7%;  Score 1071.8;  DB 9;  Length 1075;
  Best Local Similarity   99.8%;  Pred. No. 7e-244;
  Matches 1073;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        480 AAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAG 539
              |||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||
Db          1 AAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTTAGAGTGGCTGCAAAG 60

Qy        540 AGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTC 599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTC 120

Qy        600 AAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGC 659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGC 180

Qy        660 ATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAG 719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAG 240

Qy        720 GGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTG 779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTG 300

Qy        780 CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTG 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTG 360

Qy        840 TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATA 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        361 TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATA 420

Qy        900 ACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCA 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCA 480

Qy        960 CCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCT 540

Qy       1020 ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG 600

Qy       1080 GAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCC 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCC 660

Qy       1140 ATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCT 1199
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Db        661 ATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCT 720

Qy       1200 CATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGA 1259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGA 780

Qy       1260 ATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTA 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTA 840

Qy       1320 TTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATC 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATC 900

Qy       1380 CTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCT 1439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCT 960

Qy       1440 GCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1020

Qy       1500 TAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTT 1554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTT 1075

Search completed: July 18, 2003, 13:47:24
Job time : 5490.97 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:16:54 ; Search time 3396.49 Seconds
(without alignments)
9345.860 Million cell updates/sec

Title: US-09-627-896B-21
Perfect score: 1960
Sequence: 1 tctagaccaccatggattca.....cccacttctaggatcaattc 1960

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	672	34.3	672	14	BM788938	BM788938 K-EST0068
	2	553.8	28.3	656	14	BM819800	BM819800 K-EST0087
c	3	523.4	26.7	552	13	BM510472	BM510472 ij46b02.x
	4	521.8	26.6	557	14	BM768769	BM768769 K-EST0051
	5	521.8	26.6	610	14	BQ049622	BQ049622 AGENCOURT
	6	521.8	26.6	643	14	BQ712156	BQ712156 AGENCOURT
c	7	521.4	26.6	648	14	BM974791	BM974791 UI-CF-EC1
c	8	520.4	26.6	544	10	AW575364	AW575364 UI-HF-BL0
	9	520.2	26.5	641	14	BQ062789	BQ062789 AGENCOURT
c	10	520.2	26.5	927	14	BQ706352	BQ706352 AGENCOURT
c	11	519.8	26.5	563	13	BM509302	BM509302 ih16b08.y
c	12	519.6	26.5	643	14	BQ573939	BQ573939 UI-H-EZ0-
c	13	519.2	26.5	618	10	AW575927	AW575927 UI-HF-BL0
c	14	518.8	26.5	731	14	BQ181514	BQ181514 UI-H-EU0-
c	15	518.4	26.4	539	10	AW575346	AW575346 UI-HF-BL0
c	16	518.4	26.4	549	14	BQ004403	BQ004403 UI-H-EI0-
c	17	518.4	26.4	555	13	BI711498	BI711498 id97e11.x
c	18	518.4	26.4	558	10	AW575963	AW575963 UI-HF-BL0
c	19	518.4	26.4	573	14	BQ008802	BQ008802 UI-H-EI0-
c	20	518.4	26.4	576	14	BM894026	BM894026 ij62c12.x
c	21	518.4	26.4	608	14	BM991141	BM991141 UI-H-DI0-
c	22	518.4	26.4	620	13	BM511892	BM511892 ij75d09.x
c	23	518.4	26.4	626	13	BM510477	BM510477 ij46b08.x
c	24	518.4	26.4	662	14	BQ008754	BQ008754 UI-H-EI0-
c	25	518.4	26.4	696	14	BQ573999	BQ573999 UI-H-EZ0-
c	26	518.4	26.4	703	14	BQ007693	BQ007693 UI-H-EI0-
c	27	518.4	26.4	705	14	BQ007821	BQ007821 UI-H-EI0-
c	28	518.4	26.4	737	14	BQ007971	BQ007971 UI-H-EI0-
c	29	518.4	26.4	750	14	BQ004577	BQ004577 UI-H-EI0-
c	30	518.4	26.4	776	14	BQ008671	BQ008671 UI-H-EI0-
c	31	518	26.4	682	14	BQ008906	BQ008906 UI-H-EI0-
c	32	518	26.4	798	14	BQ008761	BQ008761 UI-H-EI0-
c	33	517.4	26.4	548	14	BQ030072	BQ030072 UI-H-DT0-
c	34	516.8	26.4	542	10	AW575415	AW575415 UI-HF-BL0
c	35	516.8	26.4	592	14	BQ614189	BQ614189 il04h07.x
c	36	516.8	26.4	602	14	BM990936	BM990936 UI-H-DI0-
c	37	516.8	26.4	608	14	BM973577	BM973577 UI-CF-EC1
c	38	516.8	26.4	624	13	BM510468	BM510468 ij46a10.x
c	39	516.8	26.4	636	14	BM993250	BM993250 UI-H-DT0-
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c	41	516.8	26.4	680	14	BQ004218	BQ004218 UI-H-EI0-
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c	43	516	26.3	530	13	BI711279	BI711279 id96d10.x
c	44	516	26.3	530	13	BM512311	BM512311 ij70d09.x
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ALIGNMENTS

RESULT 1
BM788938
LOCUS BM788938 672 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0068215 S19N665307 Homo sapiens cDNA clone S19N665307-2-D11 5', mRNA sequence.
ACCESSION BM788938
VERSION BM788938.1 GI:19137170
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 672)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: D column: 11
High quality sequence stop: 672.
FEATURES Location/Qualifiers
source 1. .672

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S19N665307-2-D11"
/clone_lib="S19N665307"
/sex="M"
/lab_host="Top10F'"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 164 a 199 c 141 g 168 t
ORIGIN

Query Match 34.3%; Score 672; DB 14; Length 672;
Best Local Similarity 100.0%; Pred. No. 1.1e-127;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        610 GATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTT 669
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Db          1 GATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTT 60

Qy        670 CTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTT 729
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Db         61 CTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTT 120

Qy        730 TGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGT 789
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Qy        790 CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT 849
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Db        181 CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCT 240

Qy        850 GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCA 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCA 300

Qy        910 ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT 969
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Db        301 ATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT 360

Qy        970 CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGA 1029
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Db        361 CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGA 420

Qy       1030 AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTA 1089
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Db        421 AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTA 480

Qy       1090 GAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGC 1149
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Db        481 GAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGC 540

Qy       1150 CTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCAC 1209
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Qy       1270 AAAGTGAATCTT 1281
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Db         661 AAAGTGAATCTT 672
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RESULT 2
BM819800
LOCUS BM819800 656 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0087997 S16N667673 Homo sapiens cDNA clone S16N667673-2-G02 5', mRNA sequence.
ACCESSION BM819800
VERSION BM819800.1 GI:19176213
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 656)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: G column: 02
High quality sequence stop: 656.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="S16N667673"
/sex="M"
/lab_host="Top10F'"
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

BASE COUNT 182 a 166 c 148 g 160 t
ORIGIN

Query Match 28.3%; Score 553.8; DB 14; Length 656;
Best Local Similarity 99.6%; Pred. No. 1.9e-103;
Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db        100 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 159

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
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Db        220 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 279

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
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Db        280 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 339

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
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Db        340 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 399

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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LOCUS       BM510472                552 bp    mRNA    linear   EST 15-FEB-2002
DEFINITION  ij46b02.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:5633978
            3' similar to SW:KAC_HUMAN P01834 IG KAPPA CHAIN C REGION. ;, mRNA
            sequence.
ACCESSION   BM510472
VERSION     BM510472.1  GI:18681615
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40UP from Gibco
            High quality sequence stop: 448.
FEATURES             Location/Qualifiers
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                     /clone_lib="Human insulinoma"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
BASE COUNT      118 a    118 c    162 g    154 t
ORIGIN
```

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  Query Match             26.7%;  Score 523.4;  DB 13;  Length 552;
  Best Local Similarity   99.8%;  Pred. No. 3.3e-97;
  Matches  524;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        770 ACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA 829
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Qy        830 ACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG 889
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Qy        890 AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC 949
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Db        432 AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGC 373

Qy        950 AAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAA 313

Qy       1010 CACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC 1069
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Db        312 CACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC 253

Qy       1070 TTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTG 1129
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Qy       1130 ACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGG 1189
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Qy       1190 TCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATG 1249
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Qy       1250 TTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTT 1294
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Db          72 TTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTT 28
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RESULT 4
BM768769
LOCUS       BM768769                557 bp    mRNA    linear   EST 04-MAR-2002
DEFINITION  K-EST0051794 S14K402 Homo sapiens cDNA clone S14K402-11-A06 5',
            mRNA sequence.
ACCESSION   BM768769
VERSION     BM768769.1  GI:19098384
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 557)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
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  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 11  row: A  column: 06
            High quality sequence stop: 557.
FEATURES             Location/Qualifiers
     source          1. .557
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S14K402-11-A06"
                     /clone_lib="S14K402"
                     /cell_line="K402"
                     /lab_host="Top10F'"
                     /note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;
                     Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including EcoR
                     I site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized from oligo dT-selected mRNA by
                     priming with dT-tailed vector. The dT-tailed vector was
                     adjusted to have about 60nt. The cDNA vector was
                     circularized with E. coli DNA ligase after digestion of
                     EcoRI which site is also included in vector. An RNA strand
                     converted to a DNA strand by Okayama-Berg method. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method.
                     The cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT      140 a    171 c    126 g    120 t
ORIGIN

  Query Match             26.6%;  Score 521.8;  DB 14;  Length 557;
  Best Local Similarity   99.6%;  Pred. No. 7.1e-97;
  Matches  523;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db         33 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 92

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 152

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 212

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 272

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 332

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 392

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 452

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 512

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
              |||||||||||||||||||||||||||||||||||||||||||||
Db        513 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 557


RESULT 5
BQ049622
LOCUS       BQ049622                610 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_7077241 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5787516
            5', mRNA sequence.
ACCESSION   BQ049622
VERSION     BQ049622.1  GI:19808962
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12877  row: p  column: 13
            High quality sequence stop: 595.
FEATURES             Location/Qualifiers
     source          1. .610
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5787516"
                     /clone_lib="NIH_MGC_85"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.867 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      161 a    179 c    140 g    130 t
ORIGIN

  Query Match             26.6%;  Score 521.8;  DB 14;  Length 610;
  Best Local Similarity   99.6%;  Pred. No. 7e-97;
  Matches  523;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 125

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 185

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 245

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 305

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Db        306 GAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 365
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Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
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Db        366 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 425

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db        426 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 485

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db        486 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 545

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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Db        546 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 590


RESULT 6
BQ712156
LOCUS       BQ712156                643 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8349876 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6280272
            5', mRNA sequence.
ACCESSION   BQ712156
VERSION     BQ712156.1  GI:21851055
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2471  row: d  column: 01
            High quality sequence stop: 594.
FEATURES             Location/Qualifiers
     source.         1. .643
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6280272"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      179 a    189 c    133 g    132 t     10 others
ORIGIN

  Query Match           26.6%;  Score 521.8;  DB 14;  Length 643;
  Best Local Similarity   99.4%;  Pred. No. 7e-97;
  Matches  523;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        763 CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 822
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Db         69 CCCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 128

Qy        823 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 882
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Db        129 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 188

Qy        883 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA 942
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Db        189 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA 248

Qy        943 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 308

Qy       1003 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC 1062
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Db        309 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC 368

Qy       1063 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC 1122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC 428

Qy       1123 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT 1182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT 488

Qy       1183 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTAT 1242
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Db        489 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTAT 548

Qy       1243 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
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Db        549 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGNCCCT 594


RESULT 7
BM974791/c
LOCUS       BM974791                648 bp    mRNA    linear   EST 21-MAR-2002
DEFINITION  UI-CF-EC1-acd-g-18-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-acd-g-18-0-UI 3', mRNA sequence.
ACCESSION   BM974791
VERSION     BM974791.1  GI:19592382
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .648
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="UI-CF-EC1"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
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                modified polylinker; Site_1: EcoR I; Site_2: Not I;
                UI-CF-EC1 is a normalized cDNA library containing the
                following tissue(s): Normal lung from adult and from fetal
                day 64, day 87, week 19 and week 42. The library was
                constructed according to Bonaldo, Lennon and Soares,
                Genome.Research, 6:791-806, 1996. First strand cDNA
                synthesis was primed with an oligo-dT primer containing a
                Not I site.  Double stranded cDNA was ligated to an EcoR I
                adaptor, digested with Not I, and cloned directionally
                into pT7T3-Pac vector. The oligonucleotide used to prime
                the synthesis of first-strand cDNA contains a library tag
                sequence that is located between the Not I site and the
                (dT)18 tail. The sequence tag for this library is
                AAGTGCTTAC.
                TAG_LIB=UI-CF-EC1
                TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                and 380-383
                TAG_SEQ=AAGTGCTTAC"
BASE COUNT      141 a    144 c    189 g    174 t
ORIGIN

  Query Match             26.6%;  Score 521.4;  DB 14;  Length 648;
  Best Local Similarity   99.8%;  Pred. No. 8.5e-97;
  Matches  522;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 482

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 422

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 362

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 302

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Db        301 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 242

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
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Db        241 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 182

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db        181 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 122

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db         121 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 62

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
              |||||||||||||||||||||||||||||||||||||||||||
Db          61 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 19


RESULT 8
AW575364/c
LOCUS       AW575364                 544 bp    mRNA    linear   EST 15-MAR-2000
DEFINITION  UI-HF-BL0-acw-e-03-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3060557 3', mRNA sequence.
ACCESSION   AW575364
VERSION     AW575364.1  GI:7246903
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 544)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .544
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3060557"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      116 a    117 c    162 g    148 t      1 others
ORIGIN

  Query Match             26.6%;  Score 520.4;  DB 10;  Length 544;
  Best Local Similarity   99.6%;  Pred. No. 1.4e-96;
  Matches  521;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 481

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 421

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 361

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        360 CAGCAAGGACAGCACNTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 301

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 241

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 181

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 121

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 61
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Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 1288
              ||||||||||||||||||||||||||||||||||||||||||||
Db         60 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCT 18


RESULT 9
BQ062789
LOCUS       BQ062789                641 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6826785 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924314
            5', mRNA sequence.
ACCESSION   BQ062789
VERSION     BQ062789.1  GI:19889923
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 641)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2094  row: d  column: 11
            High quality sequence start: 77
            High quality sequence stop: 596.
FEATURES             Location/Qualifiers
     source          1. .641
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5924314"
                     /clone_lib="NIH_MGC_99"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
BASE COUNT      181 a    182 c    140 g    138 t
ORIGIN

  Query Match           26.5%;  Score 520.2;  DB 14;  Length 641;
  Best Local Similarity   99.4%;  Pred. No. 1.5e-96;
  Matches  522;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 155

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 215

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        216 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAAGA 275

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 335

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        336 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAAGGCCTGAGCTCGCCCGTCACAAA 395

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 455

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 515

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 575

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
              |||||||||||||||||||||||||||||||||||||||||||||
Db        576 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 620


RESULT 10
BQ706352/c
LOCUS       BQ706352                927 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353549 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279733
            5', mRNA sequence.
ACCESSION   BQ706352
VERSION     BQ706352.1  GI:21845251
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: m  column: 14
            High quality sequence stop: 658.
FEATURES             Location/Qualifiers
     source          1. .927
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279733"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      247 a    202 c    278 g    200 t
ORIGIN

  Query Match           26.5%;  Score 520.2;  DB 14;  Length 927;
  Best Local Similarity   98.5%;  Pred. No. 1.5e-96;
  Matches  525;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        753 TGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG 812
              ||||     | | ||||||||||||||||||||||||||||||||||||||||||||||
Db        550 TGCTCTGGATCCCTGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG 491
```

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Qy        813 AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG 872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAG 431

Qy        873 AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTG 932
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTG 371

Qy        933 TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCA 992
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCA 311

Qy        993 AAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCT 1052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 AAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCT 251

Qy       1053 CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGC 1112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGC 191

Qy       1113 TCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGG 1172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGG 131

Qy       1173 ACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGG 1232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGG 71

Qy       1233 CTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          70 CTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 18
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RESULT 11
BM509302/c
LOCUS BM509302 563 bp mRNA linear EST 15-FEB-2002
DEFINITION ih16b08.y1 Human insulinoma Homo sapiens cDNA 5' similar to SW:KAC_HUMAN P01834 IG KAPPA CHAIN C REGION. ;, mRNA sequence.
ACCESSION BM509302
VERSION BM509302.1 GI:18680445
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 563)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T. , Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other_ESTs: ih16b08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 428.
FEATURES Location/Qualifiers
source 1. .563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human insulinoma"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1: XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library. "
BASE COUNT 119 a 128 c 169 g 146 t 1 others
ORIGIN

Query Match 26.5%; Score 519.8; DB 13; Length 563;
Best Local Similarity 99.4%; Pred. No. 1.8e-96;
Matches 521; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy         766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
               | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 ACGANCTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 482

Qy         826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 422

Qy         886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 362

Qy         946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 302

Qy        1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 GAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 242

Qy        1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 182

Qy        1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 122

Qy        1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 62

Qy        1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTG 1289
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Db          61 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTG 18
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RESULT 12
BQ573939/c
LOCUS BQ573939 643 bp mRNA linear EST 19-JUN-2002
DEFINITION UI-H-EZ0-bax-d-24-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone UI-H-EZ0-bax-d-24-0-UI 3', mRNA sequence.
ACCESSION BQ573939
VERSION BQ573939.1 GI:21477256
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 643)

```
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ0-bax-d-24-0-UI"
                     /clone_lib="NCI_CGAP_Ch1"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ch1 is a cDNA library containing the following
                     tissue(s): Chondrosarcoma Grade II. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_LIB=UI-H-EZ0
                     TAG_TISSUE=grade-2-chondrosarcoma
                     TAG_SEQ=ATCTAATATG"
BASE COUNT      142 a    142 c    182 g    176 t      1 others
ORIGIN

  Query Match           26.5%;  Score 519.6;  DB 14;  Length 643;
  Best Local Similarity   99.2%;  Pred. No. 2e-96;
  Matches  522;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AAGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 485

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 425

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 365

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        364 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGTTGAGCAAAGCAGACTACGA 305

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GAAACACAAAGTTTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 245

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 185

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 125

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        124 GCGGTCCTCCAGCTCATTTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 65

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 1291
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Db         64 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 19


RESULT 13
AW575927/c
LOCUS       AW575927                 618 bp    mRNA    linear   EST 15-MAR-2000
DEFINITION  UI-HF-BL0-acl-e-02-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3059426 3', mRNA sequence.
ACCESSION   AW575927
VERSION     AW575927.1  GI:7247382
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 618)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .618
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                     /clone="IMAGE:3059426"
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                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      136 a    136 c    180 g    165 t      1 others
ORIGIN

  Query Match           26.5%;  Score 519.2;  DB 10;  Length 618;
  Best Local Similarity   98.5%;  Pred. No. 2.4e-96;
  Matches  524;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        754 GCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA 813
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Db        548 GCTGGAGTCCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA 489

Qy        814 GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGA 873
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Db        488 GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGA 429

Qy        874 GGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT 933
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Db        428 GGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT 369

Qy        934 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAA 993

Db        368 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAA 309

Qy        994 AGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC 1053

Db        308 AGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC 249

Qy       1054 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCT 1113

Db        248 GCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCT 189

Qy       1114 CCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGA 1173

Db        188 CCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGA 129

Qy       1174 CCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGC 1233

Db        128 CCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGC 69

Qy       1234 TTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285

Db          68 TTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 17
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RESULT 14
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LOCUS BQ181514 731 bp mRNA linear EST 30-APR-2002
DEFINITION UI-H-EU0-azu-i-21-0-UI.s1 NCI_CGAP_Car1 Homo sapiens cDNA clone IMAGE: 5853788 3', mRNA sequence.
ACCESSION BQ181514
VERSION BQ181514.1 GI:20357006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 731)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .731
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/note="Organ: Knee; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_Car1 is a cDNA library containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCACGCT.
/tag_lib=UI-H-EU0
/tag_tissue=osteoarthritic cartilage
/tag_seq=TGATCACGCT"

BASE COUNT 158 a 165 c 214 g 194 t
ORIGIN

Query Match 26.5%; Score 518.8; DB 14; Length 731;
Best Local Similarity 99.6%; Pred. No. 2.9e-96;
Matches 520; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825

Db        540 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 481

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885

Db        480 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 421

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945

Db        420 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 361

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005

Db        360 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 301

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065

Db        300 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 241

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125

Db        240 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 181

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185

Db        180 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 121

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245

Db        120 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 61

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACC 1287

Db         60 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCCCC 19
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RESULT 15
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LOCUS AW575346 539 bp mRNA linear EST 15-MAR-2000
DEFINITION UI-HF-BL0-acv-b-06-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3060418 3', mRNA sequence.
ACCESSION AW575346
VERSION AW575346.1 GI:7246885
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A

```
          tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: M.B. Soares Lab
           cDNA Library Arrayed by: M.B. Soares Lab
           DNA Sequencing by: M.B. Soares Lab
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          www-bio.llnl.gov/bbrp/image/image.html
          Seq primer: M13 Forward
          POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      114 a    117 c    161 g    147 t
ORIGIN

  Query Match             26.4%;  Score 518.4;  DB 10;  Length 539;
  Best Local Similarity   99.8%;  Pred. No. 3.5e-96;
  Matches  519;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 477

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db        476 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 417

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
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Db        416 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 357

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
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Db        356 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 297

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 237

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 177

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db         116 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 57

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db          56 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 17


Search completed: July 18, 2003, 09:25:54
Job time : 3400.49 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:14:58 ; Search time 508.109 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-09-627-896B-21
Perfect score: 1960
Sequence: 1 tctagaccaccatggattca.....cccacttctaggatcaattc 1960

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1682.8	85.9	1950	22	AAS11981	DNA encoding Human
	2	1635.4	83.4	8897	19	AAV18692	Plasmid pTWD-cJVK.
	3	1625.8	82.9	8897	19	AAV18693	Plasmid pD16hJ1.L1
	4	1611.8	82.2	8858	20	AAZ10202	Expression vector
	5	1611.8	82.2	8858	24	AAH43777	Chi220 light chain
	6	1429.4	72.9	1701	13	AAQ30919	pMDR1006 insert.
	7	1427.8	72.8	1701	13	AAQ30920	Vector pMDR1007.
	8	1184.2	60.4	13999	14	AAQ43845	Plasmid pAH4611.
	9	1181.4	60.3	1276	13	AAQ30918	pMDR986 insert. S
	10	1181.2	60.3	1241	13	AAQ30916	pSAB153 insert. S
	11	1044	53.3	3880	19	AAV39242	Plasmid pCK7-96 nu
	12	1044	53.3	3881	18	AAT78801	Kappa light chain
	13	1044	53.3	3881	20	AAZ21996	Nucleotide sequenc
	14	1044	53.3	3881	24	ABK85575	Human IgGkappa lig
c	15	1040.4	53.1	7059	15	AAQ55004	Humanised anti-CD1
c	16	1040.4	53.1	8400	15	AAQ62611	Humanised anti-CD1
	17	776.4	39.6	1721	22	AAS22530	Human cDNA encodin
	18	776.4	39.6	1736	22	AAS22532	Human cDNA encodin
	19	776.4	39.6	1741	22	AAS22531	Human cDNA encodin
	20	758.4	38.7	1178	22	AAF57572	Humanised anti-car
	21	736	37.6	1552	22	AAF57571	Light chain constr
	22	709.4	36.2	3819	18	AAT78825	Kappa light chain
	23	709.4	36.2	3819	19	AAV39266	Plasmid pLC6G5 nuc
	24	709.4	36.2	3819	20	AAZ22020	Nucleotide sequenc
	25	698	35.6	8068	20	AAZ32781	pKN100 F19 chimeri
	26	694.2	35.4	1710	22	AAS22533	Human cDNA encodin
	27	667.6	34.1	8068	20	AAZ32784	pKN100 human resha
	28	595.8	30.4	1244	24	ABK64543	Human benign prost
	29	595.8	30.4	1244	24	ABL65461	Lung cancer relate
	30	593.8	30.3	1242	12	AAQ11878	1B1 IgG aberrant l
c	31	590.6	30.1	1517	22	AAH98191	Human EST-derived
	32	523.4	26.7	948	24	AAS99475	Anti-human AILIM m
	33	523	26.7	941	22	AAF97954	Human secreted pro
	34	522.8	26.7	913	24	AAS62744	cDNA sequence #531
	35	522.4	26.7	1404	22	AAS22861	Human cDNA encodin
	36	520.2	26.5	944	22	AAF44892	Human breast cance
c	37	518.4	26.4	851	22	AAH98251	Human EST-derived
	38	518.4	26.4	931	22	AAC66524	Human immune syste
	39	518.4	26.4	936	21	AAA27390	Human IGFAM-10 imm
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	41	518.4	26.4	962	21	AAA09154	Human BMDSP-1 codi
	42	518.4	26.4	970	24	AAS99477	Anti-human AILIM m
	43	518.4	26.4	974	24	AAS99473	Anti-human AILIM m
	44	518.4	26.4	990	22	AAF97952	Human secreted pro
	45	518.4	26.4	1033	22	AAS00145	Human cDNA clone H

ALIGNMENTS

RESULT 1
AAS11981
ID AAS11981 standard; DNA; 1950 BP.
XX
AC AAS11981;
XX
DT 04-DEC-2001 (first entry)
XX
DE DNA encoding Humanised monoclonal antibody Hu266, light chain.
XX
KW Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW light chain; ds; gene therapy.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
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FT		/*tag= c
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FT                   /note= "The figure indicates that the intron
FT                   finishes at nucleotide 762 but this would alter the
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FT                   mistake by the authors"
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FT                   /number= 2
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PN   WO200162801-A2.
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PD   30-AUG-2001.
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PF   26-FEB-2001; 2001WO-US06191.
XX
PR   24-FEB-2000; 2000US-0184601.
PR   08-DEC-2000; 2000US-0254465.
PR   08-DEC-2000; 2000US-0254498.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM,  Demattos R,  Bales KR,  Paul SM,  Tsurushita N;
PI   Vasquez M;
XX
DR   WPI; 2001-550087/61.
DR   P-PSDB; AAU07744.
XX
PT   New humanised antibody for the treatment of Alzheimer's comprises the
PT   inhibition and reduction of the formation of amyloid plaques  -
XX
PS   Example 13; Fig 4; 63pp; English.
XX
CC   The invention relates a humanised antibody that specifically binds
CC   an epitope contained within positions 13-28 of amyloid beta peptide,
CC   Abeta. The antibody is useful to inhibit and reduce the formation of
CC   amyloid plaques or the effects of toxic soluble Abeta species in humans
CC   their fragments are used for the manufacture of a medicant. This includes
CC   the prolonged expression of recombinant sequences of them in human
CC   tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC   Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC   Specifically, the antibody is used to sequester Abeta into plasma, brain
CC   or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC   peptide within the brain thereby improving cognition. The present
CC   sequence encodes the light chain of a humanised monoclonal antibody,
CC   Hu266, based on the mouse antibody 266.
XX
SQ   Sequence 1950 BP; 547 A; 488 C; 383 G; 532 T; 0 other;

  Query Match             85.9%;  Score 1682.8;  DB 22;  Length 1950;
  Best Local Similarity   93.2%;  Pred. No. 0;
  Matches 1795;  Conservative    0;  Mismatches  122;  Indels    9;  Gaps    3;

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Db         30 CTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGGTGTGATGTTGTGATGACCCAGAGC 89

Qy         93 CCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACTATTAGCTGCAAATCCAGTCAG 152
              |||    ||||||  ||||  |  |  |  |||  |     |||  |  ||     ||||  |||  ||||||
Db         90 CCACTCTCCCTGCCTGTCACCCTTGGACAACCAGCCTCCATCTCTTGCAGATCTAGTCAG 149

Qy        153 AGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGG 212
              ||  ||   |  |   |||       ||  |    |||  ||    |||||  |   ||||||  |||||
Db        150 AGCCTTATATA---TAGTGATGGAAACGCCTATTTACATTGGTTCTTGCAGAAGCCAGGC 206

Qy        213 CAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGC 272
              |||  ||||  |   ||  |||||||||    |   ||||    |    ||||||||||  ||   |
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Qy        273 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAA 332
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Qy        333 GACGTGGCAGTTTATTACTGCAGCCAA---TCTTATAATCTTTACACGTTCGGACAGGGG 389
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Db        327 GATGTGGGAGTTTATTACTGTTCTCAAAGTACACATGTTCCGTGGACGTTCGGTCAAGGC 386

Qy        390 ACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGG 449
              ||||||||||||||  ||||||  ||||   ||      |  ||||||||||||||||||||||||
Db        387 ACCAAGGTGGAAATCAAACGTGAGTAGAATT---TAATCTAGAAATTCTAAACTCTGAGG 443

Qy        450 GGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAA 509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAA 503

Qy        510 GCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATT 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATT 563

Qy        570 AAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTG 629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 AAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTG 623

Qy        630 GTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCC 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 GTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCC 683

Qy        690 CTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCT 749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCT 743

Qy        750 GTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTG 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 GTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTG 803

Qy        810 ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCA 869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCA 863

Qy        870 GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGA 929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 GAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGA 923

Qy        930 GTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGA 989
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 GTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGA 983

Qy        990 GCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA 1049
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 GCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGA 1043

Qy       1050 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACC 1109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 GCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACC 1103

Qy       1110 TGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAG 1169
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 TGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAG 1163

Qy       1170 GGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCT 1229
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 GGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCT 1223

Qy       1230 TGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTG 1289
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 TGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTG 1283

Qy       1290 TGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTT 1349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 TGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTT 1343

Qy       1350 CTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCAT 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 CTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCAT 1403

Qy       1410 CCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGC 1469
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 CCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGC 1463

Qy       1470 CTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCT 1529
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 CTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCT 1523

Qy       1530 CCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTT 1589
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 CCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTT 1583

Qy       1590 GATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGCTATAAA 1649
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 GATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGCTATAAA 1643

Qy       1650 GAGAATCATTCATTGCAACATGATATAAAATAACAACACAATAAAAGCAATTAAATAAAC 1709
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 GAGAATCATTCATTGCAACATGATATAAAATAACAACACAATAAAAGCAATTAAATAAAC 1703

Qy       1710 AAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCT 1769
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1704 AAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCT 1763

Qy       1770 TATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTAC 1829
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1764 TATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTAC 1823

Qy       1830 TTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGT 1889
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1824 TTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGT 1883

Qy       1890 TGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCT 1949
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1884 TGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCT 1943

Qy       1950 AGGATC 1955
                ||||||
Db       1944 AGGATC 1949
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RESULT 2
AAV18692
ID AAV18692 standard; cDNA; 8897 BP.
XX
AC AAV18692;
XX
DT 03-AUG-1998 (first entry)
XX
DE Plasmid pTWD-cJVK.L1 expressing cBR96-light chain.
XX
KW plasmid; BR96; antibody; chimeric; humanised; immunotherapy;
KW immunoglobulin-induced toxicity; cancer; inhibition; BR-96-induced;
KW ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Simian virus 40.
XX
PN WO9805787-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13562.
XX
PR 02-AUG-1996; 96US-0023033.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Rosok MJ, Yelton DE;
XX
DR WPI; 1998-145622/13.
XX
PT Inhibiting immunoglobulin-induced toxicity resulting from
PT immuno:therapy - by administration of immunoglobulin fusion protein
PT modified prior to administration by inactivation of part of
PT the constant region
XX
PS Disclosure; Pages 58-60; 140pp; English.
XX
CC The sequence is that of a plasmid expressing a structurally
CC altered BR96 antibody, having the variable region of BR96 and
CC a modified variable region. It can be used in the production of the
CC structurally altered antibodies which are useful for the
CC treatment of cancer and carcinomas in vivo, especially when
CC conjugated to cytotoxic agents. Structurally altered BR96 Ab is
CC used, especially conjugated to doxorubicin, to treat proliferative
CC type diseases where a cell has a BR96 antigen on the cell surface.
CC The chimeric and humanised BR96 Ab are also used in the methods to
CC inhibit and prevent BR96-induced toxicity resulting from immunotherapy
CC for cancer.
XX
SQ Sequence 8897 BP; 2410 A; 2112 C; 1967 G; 2407 T; 1 other;

Query Match 83.4%; Score 1635.4; DB 19; Length 8897;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1780; Conservative 0; Mismatches 131; Indels 26; Gaps 4;

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Qy         33 CTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGGGACATTGTGCTGACACAGTCT 92
              ||  |  |||||  ||  |  |||  |  |||   ||  |  |  ||  ||  |||| ||  |
Db         60 CTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTTTGATGACCCAAATT 119

Qy         93 CCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACTATTAGCTGCAAATCCAGTCAG 152
              ||||  ||||| |||| ||  | |||||    ||  | ||    |||| ||| ||||||
Db        120 CCAGTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCGTCCATCTCTTGCAGATCTAGTCAG 179

Qy        153 AGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCTTGGTACCAGCAGAAACCAGGG 212
              |   |  |  |   ||  |   |  | | ||| || |  |||||| ||||||||||||
Db        180 ATCATTGTACA---TAATAATGGCAACACCTATTTAGAATGGTACCTGCAGAAACCAGGC 236

Qy        213 CAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGC 272
              ||| ||||  | || |||||||||  |  ||||  |    |||||||||| ||  |
Db        237 CAGTCTCCACAGCTCCTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGG 296

Qy        273 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGGCTGAA 332
              |||||  |||||||||| |||||||||||||| ||||  |||||||  || |||||||
Db        297 TTCAGCGGCAGTGGATCAGGGACAGATTTCACACTCAAGATCAGCAGAGTGGAGGCTGAG 356

Qy        333 GACGTGGCAGTTTATTACTGCAGCCAA---TCTTATAATCTTTACACGTTCGGACAGGGG 389
              ||  ||| ||||||||||||||  |||  ||  ||  ||  | |||||||||   ||||
Db        357 GATCTGGGAGTTTATTACTGCTTTCAAGGTTCACATGTTCCATTCACGTTCGGCTCGGGG 416

Qy        390 ACCAAGGTGGAAATAAAACGTAAG--------------TAGTCTTCTCAACTCTAGAAA 434
              || ||| ||||||||||||||||              ||  |     | |  | | ||
Db        417 ACAAAGTTGGAAATAAAACGTAAGTCTCGAGTCTCTAGATAACCGGTCAATCGATTGGAA 476

Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 536

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 596

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 656

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 716

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||     ||||||||||||||||||||||||||||||||||||||
Db        717 TGTCCCTAACATGCCC-----TTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 771

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
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Db        772 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 831

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854

Db        832 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 891

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914

Db        892 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 951

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974

Db        952 GTAACTCCCAGGAGAGTGTCACAGAGCAGGAGAGCAAGGACAGCACCTACAGCCTCAGCA 1011

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034

Db       1012 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1071

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094

Db       1072 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1131

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154

Db       1132 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1191

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214

Db       1192 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1251

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274

Db       1252 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1311

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTTTA 1334

Db       1312 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCATTTAATAATTATTATCTGTTGTTTTA 1371

Qy       1335 CCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAACC 1394

Db       1372 CCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCACGTAACC 1431

Qy       1395 ATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCC 1454

Db       1432 ATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTCC 1491

Qy       1455 CTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGCT 1514

Db       1492 CTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGCT 1551

Qy       1515 TCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTAC 1574

Db       1552 TCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTAC 1611

Qy       1575 AGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGAA 1634

Db       1612 AGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGAA 1671

Qy       1635 GAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATAAA 1694

Db       1672 GAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAATAACAACACAATAAA 1731

Qy       1695 AGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTTAA 1754

Db       1732 AGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATGGTACTTAGACTTAA 1791

Qy       1755 TGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCAAG 1814

Db       1792 TGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGACTCCTGTCTGCCAAG 1851

Qy       1815 GGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAA 1874

Db       1852 GGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATACTGTGAGATTAAAAA 1911

Qy       1875 CATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAACTC 1934

Db       1912 CATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAATATATTCTATAACTC 1971

Qy       1935 AGCAATCCCACTTCTAG 1951

Db       1972 AGCAATCCCACTTCTAG 1988
```

RESULT 3
AAV18693
ID AAV18693 standard; cDNA; 8897 BP.
XX
AC AAV18693;
XX
DT 03-AUG-1998 (first entry)
XX
DE Plasmid pD16hJ1.L1 expressing hBR96-light chain.
XX
KW plasmid; BR96; antibody; chimeric; humanised; immunotherapy;
KW immunoglobulin-induced toxicity; cancer; inhibition; BR-96-induced;
KW ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Simian virus 40.
XX
PN WO9805787-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US13562.
XX
PR 02-AUG-1996; 96US-0023033.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Rosok MJ, Yelton DE;
XX
DR WPI; 1998-145622/13.
XX
PT Inhibiting immunoglobulin-induced toxicity resulting from
PT immuno:therapy - by administration of immunoglobulin fusion protein
PT modified prior to administration by inactivation of part of
PT the constant region
XX
PS Disclosure; Pages 63-66; 140pp; English.
XX
CC The sequence is that of a plasmid expressing a structurally
CC altered BR96 antibody, having the variable region of BR96 and
CC a modified variable region. It can be used in the production of the
CC structurally altered antibodies which are useful for the
CC treatment of cancer and carcinomas in vivo, especially when
CC conjugated to cytotoxic agents. Structurally altered BR96 Ab is
CC used, especially conjugated to doxorubicin, to treat proliferative
CC type diseases where a cell has a BR96 antigen on the cell surface.
CC The chimeric and humanised BR96 Ab are also used in the methods to
CC inhibit and prevent BR96-induced toxicity resulting from immunotherapy
CC for cancer.
XX
SQ Sequence 8897 BP; 2407 A; 2119 C; 1972 G; 2398 T; 1 other;

Query Match 82.9%; Score 1625.8; DB 19; Length 8897;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1774; Conservative 0; Mismatches 137; Indels 26; Gaps 4;

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Qy         33 CTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGGGACATTGTGCTGACACAGTCT 92

Db       1058 CTGTTGGTGCTGATGTTCTGGATTCCTGCTTCCAGCAGTGATGTTGTCATGACCCAAACC 1117

Qy         93 CCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACTATTAGCTGCAAATCCAGTCAG 152
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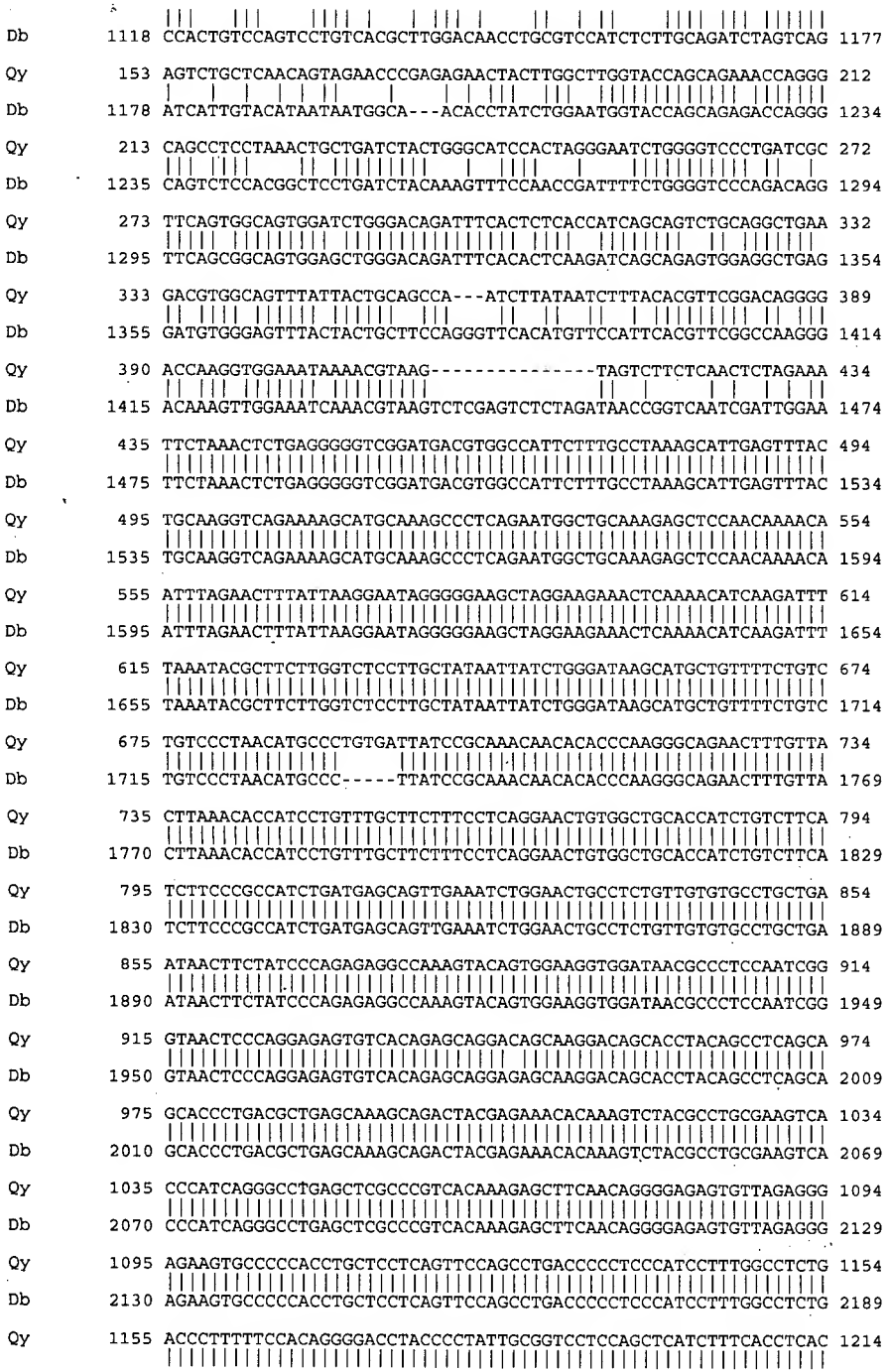

RESULT 4
AAZ10202
ID AAZ10202 standard; DNA; 8858 BP.
XX
AC AAZ10202;
XX
DT 01-NOV-1999 (first entry)
XX
DE Expression vector of light chain of chimeric anti-CD40 antibody chi22.
XX
KW Light chain variable region; chimeric antibody; anti-CD40 antibody;
KW chi220; humoral immune response; T cell dependent antigen;
KW collagen induced arthritis; transplant induced rejection;
KW T cell mediated disorder; autoimmune disease; inflammatory disease;
KW transplantation; ss.
XX
OS Synthetic.
XX

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FH   Key             Location/Qualifiers
FT   CDS             1065..1388
FT                   /*tag=  a
FT                   /note= "no termination sequence"
XX
PN   WO9942075-A2.
XX
PD   26-AUG-1999.
XX
PF   10-FEB-1999;   99WO-US02949.
XX
PR   19-FEB-1998;   98US-0026291.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Aruffo AA,  Bajorath J,  Berry KK,  Harris LJ,  Hollenbaugh D;
PI   Huse WD, Siadak AW,  Thorne BA,  Watkins JD,  Wu H;
XX
DR   WPI; 1999-527408/44.
XX
PT   Antibody that binds human CD40, for treating T cell mediated
PT   disorders
XX
PS   Claim 18; Fig 14A-C; 77pp; English.
XX
CC   The present sequence represents an expression vector for expressing
CC   the light chain of a chimeric anti-CD40 antibody designated chi220.
CC   The antibodies are effective in modulating humoral immune response
CC   against T cell dependent antigens, collagen induced arthritis and
CC   transplant induced rejection. They are also useful for their
CC   anti-inflammatory properties. The antibodies have wide therapeutic
CC   applications, including autoimmune and inflammatory diseases and
CC   transplantation. The antibody can be used in a pharmaceutical composition
CC   for treating a patient suffering from a T cell mediated disorder. They
CC   can also be used to treat autoimmune diseases, inflammatory diseases,
CC   and transplantation.
XX
SQ   Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;

  Query Match             82.2%;  Score 1611.8;  DB 20;  Length 8858;
  Best Local Similarity   90.6%;  Pred. No. 0;
  Matches 1783;  Conservative    0;  Mismatches  137;  Indels   49;  Gaps    4;

Qy          9 ACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGT 68
              ||||||||  | |  || ||| ||||  |  | ||||| || ||| |  | |  |||
Db       1002 ACCATGGAAGCCCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACC 1061

Qy         69 GGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCC 128
              || ||||||||  ||||| ||||||||||    ||||| |||| |     |||||| || | |
Db       1062 GGAGACATTGTTCTGACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGAGTC 1121

Qy        129 ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTG 188
               || ||  |||||   |||| ||||||  |   |                 |||||||
Db       1122 TCTCTTTCCTGCAGGGCCAGCCAGAGTATTAGC----------------GACTACTTA 1163

Qy        189 GCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACT 248
                |||||  || || ||| ||    || |||| |  || || ||| | |  || |||  |
Db       1164 CACTGGTATCAACAAAAATCACATGAGTCTCCAAGGCTTCTCATCAAATATGCTTCCCAT 1223

Qy        249 AGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTC 308
                  ||||||  ||||      | |||||||||||||||| ||| ||||||||||||||
Db       1224 TCCATCTCTGGGATCCCCTCCAGGTTCAGTGGCAGTGGATCAGGGTCAGATTTCACTCTC 1283

Qy        309 ACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA-- 366
              |  |||| |||| || |  |||||||  || | | ||||||||||     ||   | | |
Db       1284 AGTATCAACAGTGTGGAACCTGAAGATGTTGGAATTTATTACTGTCAACATGGTCACAGC 1343

Qy        367 -ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGT----------- 414
               ||  |  ||||||||    || |||||| |||||||  ||||||||||
Db       1344 TTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGTAAGTCTCGAGTCTCT 1403

Qy        415 ------------AGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGGGGGTCGGATGACG 462
                         | ||     | |  | | ||||||||||||||||||||||||||||||
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Db       1404 AGATAACCGGTCAATCGGTCAATCGATTGGAATTCTAAACTCTGAGGGGGTCGGATGACG 1463

Qy        463 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC 522
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC 1523

Qy        523 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGG 582
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGG 1583

Qy        583 AAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT 642
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 AAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT 1643

Qy        643 AATTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCG 702
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1644 AATTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCC-----TTATCCG 1698

Qy        703 CAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTC 762
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1699 CAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTC 1758

Qy        763 CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 822
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1759 CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 1818

Qy        823 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 882
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1819 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 1878

Qy        883 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA 942
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1879 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA 1938

Qy        943 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1002
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1939 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1998

Qy       1003 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC 1062
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1999 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC 2058

Qy       1063 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC 1122
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2059 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC 2118

Qy       1123 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT 1182
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2119 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT 2178

Qy       1183 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTAT 1242
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2179 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTAT 2238

Qy       1243 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTT 1302
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2239 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTT 2298

Qy       1303 TCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGA 1362
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2299 TCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGA 2358

Qy       1363 CTAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATT 1422
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db       2359 CTAAATATGTAGTCATCCTAAGGCACGTAACCATTTATAAAAATCATCCTTCATTCTATT 2418

Qy       1423 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCAC 1482
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2419 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCAC 2478

Qy       1483 AGTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCC 1542
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2479 AGTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCC 2538
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Qy       1543 TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT 1602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2539 TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT 2598

Qy       1603 GGGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCAT 1662
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2599 GAGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCAT 2658

Qy       1663 TGCAACATGATATAAAATAACAACACAATAAAAGCAATTAAATAAACAAACAATAGGGAA 1722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2659 TGCAACATGATATAAAATAACAACACAATAAAAGCAATTAAATAAACAAACAATAGGGAA 2718

Qy       1723 ATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTT 1782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2719 ATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTT 2778

Qy       1783 AAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 1842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2779 AAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 2838

Qy       1843 ATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGTTGCAAAGGTTCTA 1902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2839 ATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGTTGCAAAGGTTCTA 2898

Qy       1903 TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG 1951
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db       2899 TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG 2947
```

RESULT 5
AAH43777
ID AAH43777 standard; DNA; 8858 BP.
XX
AC AAH43777;
XX
DT 30-JAN-2002 (first entry)
XX
DE Chi220 light chain expression vector.
XX
KW complementarity determining region; humanised; chimerised; light;
KW heavy; chain; F4; chi220; L3.17; human; CD40; monoclonal antibody;
KW gp39; variable; region; murine; CDR; humoral immune response;
KW kidney; transplant rejection; anti-inflammatory; autoimmune disease;
KW type I diabetes; psoriasis; multiple sclerosis; rheumatoid arthritis;
KW systemic lupus erythematosus; myasthenia gravis; inflammatory disease;
KW T cell-dependent antigen; collagen induced arthritis; skin; ds.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1005..1007
FT /*tag= a
FT /function= "Start codon of inserted signal sequence"
FT CDS 1065..1388
FT /*tag= b
FT /product= "Variable light chain"
FT /note= "No stop codon"
XX
PN US6312693-B1.
XX
PD 06-NOV-2001.
XX
PF 10-FEB-1999; 99US-0247352.
XX
PR 19-FEB-1998; 98US-0026291.
XX
PA (ARUF/) ARUFFO A A.
PA (HOLL/) HOLLENBAUGH D.
PA (SIAD/) SIADAK A W.
PA (BERR/) BERRY K K.
PA (HARR/) HARRIS L.
PA (THOR/) THORNE B A.
PA (BAJO/) BAJORATH J.
PA (HUSE/) HUSE W D.
PA (WUHH/) WU H.
PA (WATK/) WATKINS J D.
XX
PI Aruffo AA, Hollenbaugh D, Siadak AW, Berry KK, Harris L;
PI Thorne BA, Bajorath J, Huse WD, Wu H, Watkins JD;
XX
DR WPI; 2002-024899/03.
XX
PT New humanized anti-human CD40 antibodies which block interaction
PT between gp39 and CD40 for modulating humoral immune responses against T
PT cell-dependent antigens, collagen induced arthritis, and transplant
PT rejection -
XX
PS Example 2; Fig 14; 54pp; English.
XX
CC This sequence shows the expression vector encoding the light chain of
CC the chimerised anti-human monoclonal antibody (mAb), Chi220. Chi220
CC binds to human CD40 (or its active portion). It comprises murine
CC variable and human kappa and gamma 1 constant regions. It binds to
CC CD40 and effectively blocks humoral immune responses to T cell-dependent
CC antigens in a dose dependant fashion. The antibodies of the invention
CC are useful for modulating humoral immune responses against T cell-
CC dependent antigens, collagen induced arthritis, and skin and kidney
CC transplant rejection and are also useful for their anti-inflammatory
CC properties. They are useful for treating autoimmune disease such as
CC type I diabetes, psoriasis, multiple sclerosis, rheumatoid arthritis,
CC systemic lupus erythematosus and myasthenia gravis, inflammatory
CC diseases and transplantation.
XX
SQ Sequence 8858 BP; 2396 A; 2124 C; 1950 G; 2387 T; 1 other;

Query Match 82.2%; Score 1611.8; DB 24; Length 8858;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 137; Indels 49; Gaps 4;

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Qy          9 ACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGT 68
              |||||||  | |  || ||| ||||  |  | ||||| || ||| |  | |  |||
Db       1002 ACCATGGAAGCCCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACC 1061

Qy         69 GGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCC 128
              || |||||||| ||||| |||||||||||    ||||| |||| |    |||||| || | |
Db       1062 GGAGACATTGTTCTGACTCAGTCTCCAGCCACCCTGTCTGTGACTCCAGGAGATAGAGTC 1121

Qy        129 ACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTG 188
               ||  ||  |||||   |||| |||||| |   |                  |||||||
Db       1122 TCTCTTTCCTGCAGGGCCAGCCAGAGTATTAGC-----------------GACTACTTA 1163

Qy        189 GCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACT 248
               ||||| || || ||| ||     || |||| |  || || ||| | |  || |||  |
Db       1164 CACTGGTATCAACAAAAATCACATGAGTCTCCAAGGCTTCTCATCAAATATGCTTCCCAT 1223

Qy        249 AGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTC 308
                  |||||| ||||     | |||||||||||||||||| ||| ||||||||||||||
Db       1224 TCCATCTCTGGGATCCCCTCCAGGTTCAGTGGCAGTGGATCAGGGTCAGATTTCACTCTC 1283

Qy        309 ACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA-- 366
              |  |||| |||| || |  |||||| || | | ||||||||||     ||   | | |
Db       1284 AGTATCAACAGTGTGGAACCTGAAGATGTTGGAATTTATTACTGTCAACATGGTCACAGC 1343

Qy        367 -ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGT---------- 414
               ||  |  |||||||    || |||||| ||||||| |||||||||
Db       1344 TTTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGTAAGTCTCGAGTCTCT 1403

Qy        415 ------------AGTCTTCTCAACTCTAGAAATTCTAAACTCTGAGGGGGTCGGATGACG 462
                         | ||      | |  | | ||||||||||||||||||||||||||||
Db       1404 AGATAACCGGTCAATCGGTCAATCGATTGGAATTCTAAACTCTGAGGGGGTCGGATGACG 1463

Qy        463 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC 522
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 TGGCCATTCTTTGCCTAAAGCATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCC 1523
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Qy       523 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGG 582
Db      1524 TCAGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGG 1583

Qy       583 AAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT 642
Db      1584 AAGCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTAT 1643

Qy       643 AATTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCG 702
Db      1644 AATTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCC-----TTATCCG 1698

Qy       703 CAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTC 762
Db      1699 CAAACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTC 1758

Qy       763 CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 822
Db      1759 CTCAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAA 1818

Qy       823 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 882
Db      1819 ATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGT 1878

Qy       883 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA 942
Db      1879 ACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCA 1938

Qy       943 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1002
Db      1939 GGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTA 1998

Qy      1003 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC 1062
Db      1999 CGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAC 2058

Qy      1063 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC 1122
Db      2059 AAAGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTC 2118

Qy      1123 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT 1182
Db      2119 CAGCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCT 2178

Qy      1183 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTAT 1242
Db      2179 ATTGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTAT 2238

Qy      1243 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTT 1302
Db      2239 GCTAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTT 2298

Qy      1303 TCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGA 1362
Db      2299 TCCTCATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGA 2358

Qy      1363 CTAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATT 1422
Db      2359 CTAAATATGTAGTCATCCTAAGGCACGTAACCATTTATAAAAATCATCCTTCATTCTATT 2418

Qy      1423 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCAC 1482
Db      2419 TTACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCAC 2478

Qy      1483 AGTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCC 1542
Db      2479 AGTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCC 2538

Qy      1543 TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT 1602
Db      2539 TCATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCT 2598

Qy      1603 GGGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCAT 1662
Db      2599 GAGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCAT 2658

Qy      1663 TGCAACATGATATAAAATAACAACACAATAAAAGCAATTAAATAAACAAACAATAGGGAA 1722
Db      2659 TGCAACATGATATAAAATAACAACACAATAAAAGCAATTAAATAAACAAACAATAGGGAA 2718

Qy      1723 ATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTT 1782
Db      2719 ATGTTTAAGTTCATCATGGTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTT 2778

Qy      1783 AAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 1842
Db      2779 AAACAGGTACTGAGGGACTCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTA 2838

Qy      1843 ATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGTTGCAAAGGTTCTA 1902
Db      2839 ATTTAATCCACACTATACTGTGAGATTAAAAACATTCATTAAAATGTTGCAAAGGTTCTA 2898

Qy      1903 TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG 1951
Db      2899 TAAAGCTGAGAGACAAATATATTCTATAACTCAGCAATCCCACTTCTAG 2947
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RESULT 6
AAQ30919
ID AAQ30919 standard; DNA; 1701 BP.
XX
AC AAQ30919;
XX
DT 02-APR-1993 (first entry)
XX
DE pMDR1006 insert.
XX
KW Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
KW pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;
KW NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
KW melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
KW humanised; 5A8; light chain; variable region; LV; genomic; constant
KW antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
KW lymphocyte; helper; inducer; HIV; syncytia; formation; ss.
XX
OS Synthetic.
XX
PN WO9209305-A.
XX
PD 11-JUN-1992.
XX
PF 27-NOV-1991; 91WO-US08843.
XX
PR 27-NOV-1990; 90US-0618542.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
XX
DR WPI; 1992-398399/48.
XX
PT New anti-CD4 antibody homolognes - which bind CD4, do not block
PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT formation between CD4+ cells
XX
PS Disclosure; Page 162-3; 205pp; English.
XX
CC The sequence given is the insert of the intermediate plasmid pMDR1006.
CC This plasmid and pSAB132 (see AAQ30906) were used in the construction of
CC the vector pMDR1007 (see AAQ30920). Three fragments were ligated
CC together to generate pMDR1006; a 572 bp fragment of pMDR985 (see
CC AAQ30913), a 3442bp AatII/EcoRV fragment of pMDR986 (see AAQ30918) and a
CC 326 bp EcoRV/BglII fragment of pMDR1003 (see AAQ30900). The ligation
CC mixture was used to transform E. coli JA221(Iq) to ampicillin
CC resistance. pMDR1006 was cleaved with NotI and the 1693 bp fragment

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CC   isolated was ligated into NotI linearised pSAB132 which had been
CC   dephosphorylated by calf alkaline phosphatase.  This generates the
CC   plasmid pMDR1007.  The dephosphorylated mixture was fractionated
CC   through low temperature melting agarose and used to transform E. coli
CC   JA221(Iq) to ampicillin resistance.  The pMDR1007 insert comprises
CC   DNA encoding, in a 5' to 3' order, the immunoglobulin kappa chain
CC   signal peptide, amino acid (AA) 1-AA112 of the humanised 5A8 light
CC   chain variable region (LV) followed by genomic DNA encoding AA108-
CC   AA214 of the human kappa light chain, ie. the light chain constant
CC   region (LC).   The polypeptide encoded by pMDR1007 is an antibody
CC   homolog which was shown to bind to CD4 but did not block the binding
CC   of gp120 to CD4.  CD4 is a cell surface glycoprotein of CD4+
CC   lymphocytes (helper/inducer cells).  The homolog blocked HIV-induced
CC   syncytia formation.  This homolog can be used in the detection,
CC   prophylaxis and treatment of diseases caused by infective agents whose
CC   primary targets are CD4+ cells.
XX
SQ   Sequence 1701 BP; 435 A; 468 C; 361 G; 437 T; 0 other;

  Query Match             72.9%;  Score 1429.4;  DB 13;  Length 1701;
  Best Local Similarity   93.1%;  Pred. No. 0;
  Matches 1534;  Conservative    0;  Mismatches   96;  Indels   17;  Gaps    3;

Qy         11 CATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGG 70
Db         40 CATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTGCCAGGTGCCAGAGG 99

Qy         71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC 130
Db        100 TGATATCGTAATGACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGGCTAC 159

Qy        131 TATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGC 190
Db        160 TATAAACTGCAAGTCCAGTGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGC 219

Qy        191 TTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAG 250
Db        220 CTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATTTACTGGGCATCCACTAG 279

Qy        251 GGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC 310
Db        280 GGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCAC 339

Qy        311 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCT 370
Db        340 CATCAGCAGTTTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGCTA 399

Qy        371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTA 430
Db        400 TCGGACGTTCGGTCGAGGGACCAAGCTGGAGATCAAACGTAAGTGCACT---------- 448

Qy        431 GAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 490
Db        449 ----TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 504

Qy        491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 550
Db        505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 564

Qy        551 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAG 610
Db        565 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAG 624

Qy        611 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 670
Db        625 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 684

Qy        671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 730
Db        685 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 744

Qy        731 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 790
Db        745 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 804

Qy        791 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 850
Db        805 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 864

Qy        851 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 910
Db        865 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 924

Qy        911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 970
Db        925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 984

Qy        971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1030
Db        985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1044

Qy       1031 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1090
Db       1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1104

Qy       1091 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1150
Db       1105 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1164

Qy       1151 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1210
Db       1165 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1224

Qy       1211 TCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1270
Db       1225 TCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1284

Qy       1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTG 1329
Db       1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG 1344

Qy       1330 TTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1389
Db       1345 -TTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1403

Qy       1390 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1449
Db       1404 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1463

Qy       1450 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGAC 1509
Db       1464 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGAC 1523

Qy       1510 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1569
Db       1524 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1583

Qy       1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
Db       1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA 1643

Qy       1630 AAGAAGAAACCTGCTATAAAGAGAATC 1656
Db       1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670


RESULT 7
AAQ30920
ID   AAQ30920 standard; DNA; 1701 BP.
XX
AC   AAQ30920;
XX
DT   02-APR-1993  (first entry)
XX
DE   Vector pMDR1007.
XX
```

```
KW   Plasmid; pMDR1006; pSAB132; vector; pMDR1007; pMDR985; AatII; EcoRV;
KW   pMDR986; BglII; pMDR1003; JA221(Iq); E. coli; ampicillin resistance;
KW   NotI; dephosphorylate; calf; alkaline phosphatase; low temperature;
KW   melting agarose; immunoglobulin; kappa chain; signal peptide; LC;
KW   humanised; 5A8; light chain; variable region; LV; genomic; constant
KW   antibody; homolog; CD4; gp120; cell surface; glycoprotein; CD4+;
KW   lymphocyte; helper; inducer; HIV; syncytia; formation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     35..100
FT                   /*tag=  a
FT                   /note= "Immunoglobulin kappa chain signal sequence"
FT   mat_peptide     101..1101
FT                   /*tag=  b
FT   exon            35..436
FT                   /*tag=  c
FT                   /number= 1
FT                   /note= "AA1-AA112 of humanised 5A8 LV"
FT   intron          438..781
FT                   /*tag=  d
FT                   /number= 1
FT   exon            782..1101
FT                   /*tag=  e
FT                   /number= 2
FT                   /note= "AA108-AA214 of human kappa LC"
FT   CDS             35..1104
FT                   /*tag=  f
XX
PN   WO9209305-A.
XX
PD   11-JUN-1992.
XX
PF   27-NOV-1991;   91WO-US08843.
XX
PR   27-NOV-1990;   90US-0618542.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Burkly LC,  Chisholm PL,  Rosa JJ,  Rosa MD,  Thomas DW;
XX
DR   WPI; 1992-398399/48.
DR   P-PSDB; AAR28809.
XX
PT   New anti-CD4 antibody homolognes - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Claim 27; Page 164-5; 205pp; English.
XX
CC   The sequence given is the insert of the vector pMDR1007.  pMDR1006
CC   (see AAQ30919) and pSAB132 (see AAQ30906) were used in the construction
CC   of this vector.  Three fragments were ligated together to generate
CC   pMDR1006; a 572 bp fragment of pMDR985 (see AAQ30913), a 3442bp AatII/
CC   EcoRV fragment of pMDR986 (see AAQ30918) and a 326 bp EcoRV/BglII
CC   fragment of pMDR1003 (see AAQ30900).  The ligation mixture was used to
CC   transform E. coli JA221(Iq) to ampicillin resistance.  pMDR1006 was
CC   cleaved with NotI and the 1693 bp fragment isolated was ligated into
CC   NotI linearised pSAB132 which had been dephosphorylated by calf
CC   alkaline phosphatase.  This generates the plasmid pMDR1007.  The
CC   dephosphorylated mixture was fractionated through low temperature
CC   melting agarose and used to transform E. coli JA221(Iq) to ampicillin
CC   resistance.  The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
CC   order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
CC   1-AA112 of the humanised 5A8 light chain variable region (LV) followed
CC   by genomic DNA encoding AA108-AA214 of the human kappa light chain,
CC   ie. the light chain constant region (LC).  The polypeptide encoded by
CC   pMDR1007 is an antibody homolog which was shown to bind to CD4 but did
CC   not block the binding of gp120 to CD4.  CD4 is a cell surface
CC   glycoprotein of CD4+ lymphocytes (helper/inducer cells).  The homolog
CC   blocked HIV-induced syncytia formation.  This homolog can be used in
CC   the detection, prophylaxis and treatment of diseases caused by
CC   infective agents whose primary targets are CD4+ cells.
XX
SQ   Sequence 1701 BP; 435 A; 469 C; 361 G; 436 T; 0 other;

  Query Match             72.8%;  Score 1427.8;  DB 13;  Length 1701;
  Best Local Similarity   93.1%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches   97;  Indels   17;  Gaps    3;

Qy         11 CATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGG 70
Db         40 CATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTGCCAGGTGCCAGAGG 99

Qy         71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC 130
Db        100 TGATATCGTAATGACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGGCTAC 159

Qy        131 TATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGC 190
Db        160 TATAAACTGCAAGTCCAGTGGGAGCCTTTTATATAGTACCAATCAAAAGAACTACTTGGC 219

Qy        191 TTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAG 250
Db        220 CTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATTTACTGGGCATCCACTAG 279

Qy        251 GGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAC 310
Db        280 GGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCAC 339

Qy        311 CATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCT 370
Db        340 CATCAGCAGTTTGCAGGCTGAAGACGTGGCAGTTTATTACTGTCAGCAATATTATAGCTA 399

Qy        371 TTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTA 430
Db        400 TCGGACGTTCGGTCGAGGGACCAAGCTGGAGATCAAACGTAAGTGCACT---------- 448

Qy        431 GAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 490
Db        449 ----TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 504

Qy        491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 550
Db        505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 564

Qy        551 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAG 610
Db        565 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAG 624

Qy        611 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 670
Db        625 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGCTTTC 684

Qy        671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 730
Db        685 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 744

Qy        731 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 790
Db        745 GTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTC 804

Qy        791 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 850
Db        805 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG 864

Qy        851 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 910
Db        865 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 924

Qy        911 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 970
Db        925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 984

Qy        971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1030
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1044

Qy       1031 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1090
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1104

Qy       1091 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1150
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1164

Qy       1151 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1210
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1224

Qy       1211 TCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1270
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225 TCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1284

Qy       1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTG 1329
                |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG 1344

Qy       1330 TTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1389
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 -TTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1403

Qy       1390 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1449
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1463

Qy       1450 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGAC 1509
                ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1464 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGAC 1523

Qy       1510 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1569
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1583

Qy       1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA 1643

Qy       1630 AAGAAGAAACCTGCTATAAAGAGAATC 1656
                |||||||||||||||     |  || ||
Db       1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670


RESULT 8
AAQ43845
ID   AAQ43845 standard; DNA; 13999 BP.
XX
AC   AAQ43845;
XX
DT   20-OCT-1993  (first entry)
XX
DE   Plasmid pAH4611.
XX
KW   Polymerase chain reaction; primer; PCR; amplify; murine;
KW   heavy;light; chain; variable; constant; region; anti-human;
KW   transferrin; receptor; antibody; brain; capillary;
KW   endothelial cell; conjugate; neuropharmaceutical;
KW   diagnostic; agent; tumour; AIDS; stroke; epilepsy;
KW   Parkinsons disease; Alzheimers disease; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   unsure          3396..5095
FT                   /*tag=  a
FT   CDS             5233..5616
FT                   /*tag=  b
FT                   /note= "128.1 VL region"
FT   unsure          6920..7218
FT                   /*tag=  c
FT   CDS             8424..8741
FT                   /*tag=  d
FT                   /note= "Undefined ORF"
FT   unsure          9300..12092
FT                   /*tag=  e
XX
PN   WO9310819-A.
XX
PD   10-JUN-1993.
XX
PF   24-NOV-1992;   92WO-US10206.
XX
PR   26-NOV-1991;   91US-0800458.
XX
PA   (ALKE-) ALKERMES INC.
XX
PI   Friden PM;
XX
DR   WPI; 1993-196742/24.
DR   P-PSDB; AAR41686-87.
XX
PT   Antibody conjugates specific for transferrin receptor - used
PT   for diagnosis and treatment of cancer, AIDS and neurological
PT   disorders
XX
PS   Disclosure; Fig 13A-F; 151pp; English.
XX
CC   This sequence represents the expression vector pAH4611.
CC   This vector was produced from the plasmid pAG4270.  pAG4270
CC   is the expression vector for the light chain variable region
CC   (VL) of the antibody 128.1 which was obtained by PCR with
CC   leader/J region priming (see also AAQ43842).  The vector also
CC   contains an ampicillin resistance gene, a gpt (mycophenolic
CC   acid resistance) selected marker, an immunoglobulin H
CC   enhancer and an intron for V-constant region splicing.
CC   Transcription of the CH gene is from the VH promoter of the
CC   murine 27.44 gene.  The cloning of the 128.1 VL region was
CC   accomplished in two stages with the production of plasmid
CC   pSV4271 as an intermediate vector which lacks the promoter
CC   region.  This plasmid was used in conjunction with pAH4602
CC   in the production of the chimeric antibody 128.1.  128.1 is
CC   an anti-human transferrin receptor antibody which binds to
CC   the transferrin receptor on brain capillary endothelial
CC   cells.  This antibody may be used in a conjugate in which it
CC   is linked to a neuropharmaceutical or diagnostic agent.  The
CC   conjugate may be used to treat or prevent neurological
CC   disorders eg. brain tumours, AIDS, stroke, epilepsy,
CC   Parkinsons and Alzheimers disease.  It may also be used for
CC   diagnostic methods.
XX
SQ   Sequence 13999 BP; 2534 A; 2085 C; 2104 G; 2472 T; 4804 other;

  Query Match             60.4%;  Score 1184.2;  DB 14;  Length 13999;
  Best Local Similarity   99.5%;  Pred. No. 4e-268;
  Matches 1208;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8087 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 8146

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8147 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 8206

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8207 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 8266

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8267 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 8326
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```
Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8327 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 8386

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8387 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 8446

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8447 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 8506

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8507 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 8566

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8567 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 8626

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8627 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 8686

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8687 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 8746

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8747 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 8806

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8807 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 8866

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8867 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 8926

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||| | |
Db       8927 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 8985

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8986 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 9045

Qy       1392 ACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9046 ACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 9105

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTT 1511
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       9106 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTT 9165

Qy       1512 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 1571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9166 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 9225

Qy       1572 TACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAA 1631
              ||| |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       9226 TACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAA 9285

Qy       1632 GAAGAAACCTGCTA 1645
              |||||||||||| |
Db       9286 GAAGAAACCTGCNA 9299
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RESULT 9
AAQ30918
ID AAQ30918 standard; DNA; 1276 BP.

XX
AC AAQ30918;
XX
DT 02-APR-1993 (first entry)
XX
DE pMDR986 insert.
XX
KW Primer; polymerase chain reaction; PCR; amplify; intermediate;
KW plasmid; pMDR986; genomic; DNA; human; kappa; light; chain; constant;
KW region; LC; placenta; EcoRI; pUC8; pAB8; EcoRV; pNN03; pSAB153;
KW dephosphorylated; calf; alkaline phosphatase; E. coli; JA221(Iq);
KW Eco0109 I; E. coli; GM2929; methylate; cloning artifact; NotI; PvuI;
KW CD4; CD4+; HIV; gp120; syncytia; formation; ss.
XX
OS Synthetic.
XX
PN WO9209305-A.
XX
PD 11-JUN-1992.
XX
PF 27-NOV-1991; 91WO-US08843.
XX
PR 27-NOV-1990; 90US-0618542.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
XX
DR WPI; 1992-398399/48.
XX
PT New anti-CD4 antibody homolognes - which bind CD4, do not block
PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT formation between CD4+ cells
XX
PS Disclosure; Page 161-2; 205pp; English.
XX
CC The sequence given is the insert of the intermediate plasmid pMDR986.
CC pMDR986 was constructed to carry genomic DNA encoding amino acid (AA)
CC 108-AA214 of a human kappa light chain ie. the light chain constant
CC region (LC). Human placental genomic DNA was prepared and cleaved
CC with EcoRI to give a 2.5 kb fragment. This fragment comprising the
CC kappa chain constant region was cloned into the EcoRI site of pUC8 to
CC give pAB8. The DNA encoding LC was amplified from pAB8 using the
CC primer sequences given in AAQ30914-15. The 1240 bp reaction product
CC was ligated into EcoRV linearised pNN03 (see AAQ30566) that had been
CC dephosphorylated. This generated plasmid pSAB153 (see AAQ30916). LC
CC was amplified from pSAB153 using the primers given in AAQ30915 and
CC AAQ30917 to generate an approx. 1276 bp fragment. This fragment was
CC ligated to EcoRV linearised pNN03 that had been dephosphorylated by
CC calf alkaline phosphatase. The ligation mixture was used to transform
CC E. coli JA221(Iq) to ampicillin resistance. Plasmid pMDR986 was
CC identified by the presence of a 1122 bp Eco0109 I restriction fragment.
CC pMDR986 was used to transform E. coli GM2929, which does not methylate
CC its own DNA. Sequence analysis of pMDR986 showed that a cloning
CC artifact caused a NotI site 3' of the constant region to be been
CC replaced with a PvuI site.
XX
SQ Sequence 1276 BP; 340 A; 352 C; 244 G; 340 T; 0 other;

Query Match 60.3%; Score 1181.4; DB 13; Length 1276;
Best Local Similarity 98.9%; Pred. No. 7.6e-268;
Matches 1210; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        144 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 203

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 563

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 683

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 743

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 803

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTGTTTT 923

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
              |||||||||||||||||||||||||||||||||||||||  ||||||||| |||||||||
Db        924 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTACTCCTAAGGCG-ATAAC 982

Qy       1394 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1102

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162

Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1163 CAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGA 1222

Qy       1634 AGAAACCTGCTATAAAGAGAATC 1656
              |||||||||     |  || ||
Db       1223 AGAAACCTGCGGCCGATCGATTC 1245
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RESULT 10
AAQ30916
ID AAQ30916 standard; DNA; 1241 BP.
XX
AC AAQ30916;
XX
DT 02-APR-1993 (first entry)
XX
DE pSAB153 insert.
XX
KW Primer; polymerase chain reaction; PCR; amplify; intermediate;
KW plasmid; pMDR986; genomic; DNA; human; kappa; light; chain; constant;
KW region; LC; placenta; EcoRI; pUC8; pAB8; EcoRV; pNN03; pSAB153;
KW dephosphorylated; calf; alkaline phosphatase; E. coli; JA221(Iq);
KW Eco0109 I; E. coli; GM2929; methylate; cloning artifact; NotI; PvuI;
KW CD4; CD4+; HIV; gp120; syncytia; formation; ss.
XX
OS Synthetic.
XX
PN WO9209305-A.
XX
PD 11-JUN-1992.
XX
PF 27-NOV-1991; 91WO-US08843.
XX
PR 27-NOV-1990; 90US-0618542.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
XX
DR WPI; 1992-398399/48.
XX
PT New anti-CD4 antibody homolognes - which bind CD4, do not block
PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT formation between CD4+ cells
XX
PS Disclosure; Page 159-60; 205pp; English.
XX
CC The sequence given is the insert from the intermediate plasmid pSAB153.
CC This plasmid was used in the construction of the intermediate plasmid
CC pMDR986 (see AAQ30918). pMDR986 was constructed to carry genomic DNA
CC encoding amino acid (AA) 108-AA214 of a human kappa light chain ie.
CC the light chain constant region (LC). Human placental genomic DNA was
CC prepared and cleaved with EcoRI to give a 2.5 kb fragment. This
CC fragment comprising the kappa chain constant region was cloned into
CC the EcoRI site of pUC8 to give pAB8. The DNA encoding LC was amplified
CC from pAB8 using the primer sequences given in AAQ30914-15. The 1240 bp
CC reaction product was ligated into EcoRV linearised pNN03 (see AAQ30566)
CC that had been dephosphorylated. This generated plasmid pSAB153. LC
CC was amplified from pSAB153 using the primers given in AAQ30915 and
CC AAQ30917 to generate an approx. 1276 bp fragment. This fragment was
CC ligated to EcoRV linearised pNN03 (see AAQ30566) that had been
CC dephosphorylated by calf alkaline phosphatase. The ligation mixture
CC was used to transform E. coli JA221(Iq) to ampicillin resistance.
CC Plasmid pMDR986 was identified by the presence of a 1122 bp Eco0109 I
CC restriction fragment. pMDR986 was used to transform E. coli GM2929,
CC which does not methylate its own DNA. Sequence analysis of pMDR986
CC showed that a cloning artifact caused a NotI site 3' of the constant
CC region to be been replaced with a PvuI site.
XX
SQ Sequence 1241 BP; 329 A; 340 C; 242 G; 330 T; 0 other;

Query Match 60.3%; Score 1181.2; DB 13; Length 1241;
Best Local Similarity 99.6%; Pred. No. 8.4e-268;
Matches 1205; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

```
Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83
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Qy       495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

Qy       555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       144 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 203

Qy       615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263

Qy       675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy       735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383

Qy       795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443

Qy       855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy       915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 563

Qy       975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy      1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 683

Qy      1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       684 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 743

Qy      1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 803

Qy      1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       804 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

Qy      1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
            |||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db       864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-TTT 922

Qy      1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       923 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 982

Qy      1394 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       983 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy      1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      1043 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTTGC 1102

Qy      1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1103 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162

Qy      1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1163 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1222

Qy      1634 AGAAACCTGC 1643
             ||||||||||
Db      1223 AGAAACCTGC 1232
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RESULT 11
AAV39242
ID AAV39242 standard; DNA; 3880 BP.
XX
AC AAV39242;
XX
DT 18-DEC-1998 (first entry)
XX
DE Plasmid pCK7-96 nucleotide sequence.
XX
KW Transgenic animal; human heterologous antibody; transgene;
KW isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW autoimmune reaction; inflammatory response; transplant rejection;
KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US21803.
XX
PR 02-DEC-1996; 96US-0758417.
XX
PA (GENP-) GENPHARM INT.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1998-333306/29.
XX
PT Hybridoma producing antibody specific for interleukin-8 - used to
PT prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX
PS Example 42; Pages 310-312; 452pp; English.
XX
CC The present sequence represents the kappa light chain plasmid, pCK7-96,
CC which includes the kappa constant region and polyadenylation site. The
CC plasmid is used in the construction of minigenes for expression of
CC IgGkappa anti-CD4 antibodies, in the transgenic mouse of the invention.
CC The specification describes transgenic non-human animals, especially a
CC mouse, which are capable of producing a human heterologous antibodies of
CC multiple isotypes by undergoing isotype switching. The transgenic animals
CC have human heavy and light chain transgenes. The transgenes are capable
CC of functionally rearranging a heterologous diversity (D) gene in a
CC variable-diversity-junction (V-D-J) recombination. The transgenes include
CC a heavy chain transgene comprising at least one V, D and J gene segment,
CC and one constant region gene segment. The immunoglobulin (Ig) light chain
CC transgene comprises at least one V and J gene segment and one constant
CC region gene segment. The gene segments are heterologous to the transgenic
CC animal. The antibody can be used to prevent efflux of neutrophils from
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC antibodies are used to reduce undesirable autoimmune reactions,
CC inflammatory responses and rejection of transplanted organs. The
CC anti-IL-8 antibodies can reduce tissue damage and prolong survival in
CC animal models of acute adult respiratory distress syndrome (ARDS) and
CC acid induced lung injury. The anti-IL-8 antibodies can also be used for
CC the treatment of vasculitis, septic shock, allergic reactions
CC (e.g. asthma) and cystic fibrosis.
XX
SQ Sequence 3880 BP; 981 A; 1013 C; 921 G; 965 T; 0 other;

```
  Query Match           53.3%;  Score 1044;  DB 19;  Length 3880;
  Best Local Similarity  99.8%;  Pred. No. 2.3e-235;
  Matches 1066;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2613

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2673

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2733

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2734 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2793

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2853

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2913

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2973

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2974 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3033

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3093

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3153

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3213

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3273

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3333

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3393

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db       3394 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3452

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3453 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3512

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3513 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3572

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3573 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3620
```

RESULT 12
AAT78801
ID AAT78801 standard; DNA; 3881 BP.
XX
AC AAT78801;
XX
DT 23-JAN-1998 (first entry)
XX
DE Kappa light chain plasmid pCK7-96.
XX
KW Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection; immunoglobulin; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9713852-A1.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US16433.
XX
PR 10-OCT-1995; 95US-0544404.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1997-235888/21.
XX
PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Example 42; Page 260-262; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The
CC present sequence represents the kappa light chain plasmid pCK7-96
CC which includes the kappa constant region and polyadenylation site. Anti-
CC CD4 antibodies may be used in therapeutic and diagnostic applications,
CC especially for the treatment of human diseases. These antibodies reduce
CC activity of CD4 cells and reduce undesirable autoimmune reactions,
CC inflammatory response and transplant rejection. Transgenic animals are
CC capable of producing heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. These animals produce a first Ig type
CC that is necessary for antigen-stimulated B-cell maturation and can
CC switch to encode and produce one or more subsequent heterologous
CC isotypes.
XX
SQ Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;

```
  Query Match           53.3%;  Score 1044;  DB 18;  Length 3881;
  Best Local Similarity  99.8%;  Pred. No. 2.3e-235;
  Matches 1066;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2734
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Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3215 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3334

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db       3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621
```

RESULT 13
AAZ21996
ID AAZ21996 standard; DNA; 3881 BP.
XX
AC AAZ21996;
XX
DT 24-NOV-1999 (first entry)
XX
DE Nucleotide sequence of plasmid pCK7-96.
XX
KW Transgenic animal; heterologous antibody; hybridoma; B cell;
KW transgenic mouse; human heavy chain transgene; digoxin;
KW human light chain transgene; immortalized cell; immunoglobulin;
KW Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS Synthetic.
XX
PN WO9945962-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05535.
XX
PR 13-MAR-1998; 98US-0042353.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Fishwild DM, Ball WJ;
XX
DR WPI; 1999-551219/46.
XX
PT Novel transgenic non-human animals used to produce heterologous
PT antibodies
XX
PS Example 42; Page 311-313; 484pp; English.
XX
CC The specification describes transgenic animals that are capable of
CC producing a heterologous antibody. The antibodies are isolated form a
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC having a genome comprising a human heavy chain transgene and a human
CC light chain transgene. The B cells are fused to immortalized cells
CC suitable for generating a hybridoma, which produces a detectable
CC amount of an immunoglobulin that specifically binds digoxin or
CC Shinga-like toxin. B cells from transgenic animals can be used to
CC generate hybridomas expressing monoclonal high affinity human sequence
CC antibodies. Antibodies produced from the transgenic animals of the
CC invention can be used to treat human diseases, e.g. autoimmune
CC diseases, cancer, infectious disease, transplant rejection, blood
CC disorders such as coagulation disorders and other diseases. The
CC present sequence is used in the course of the invention.
XX
SQ Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;

Query Match 53.3%; Score 1044; DB 20; Length 3881;
Best Local Similarity 99.8%; Pred. No. 2.3e-235;
Matches 1066; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2734

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3215 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3334

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db       3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy       1392 ACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 ACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
              |||||||||||||||||||||||||||||||||||||||||||||||
Db       3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621
```

RESULT 14
ABK85575
ID ABK85575 standard; DNA; 3881 BP.
XX
AC ABK85575;
XX
DT 03-SEP-2002 (first entry)
XX
DE Human IgGkappa light chain plasmid pCK7-96.
XX
KW Transgenic; rodent; immunoglobulin; Ig; transchromosome; B-cell;
KW human antibody display library; immune-related disorder; mutant;
KW immunomodulatory; IgGkappa light chain; pCK7-96; cyclic;
KW circular; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200243478-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US45293.
XX
PR 30-NOV-2000; 2000US-250340P.
XX
PA (MEDA-) MEDAREX INC.
PA (KIRI) KIRIN BEER KK.
XX
PI Tomizuka K, Ishida I, Lonberg N, Halk E;
XX
DR WPI; 2002-500300/53.
XX
PT New transgenic nonhuman mammal, useful for generating B-cells
PT expressing human antibody sequences and generating antigen-specific
PT hybridomas secreting human sequence antibody, comprises two human
PT immunoglobulin loci -
XX
PS Disclosure; Page 46-47; 110pp; English.
XX
CC The present invention relates to novel transgenic nonhuman mammals,
CC particularly rodents, comprising two human immunoglobulin (Ig) loci,
CC where one of two the human immunoglobulin loci is a human heavy chain
CC locus and the other locus is a human light chain locus, and where
CC only one of the loci is of a transchromosome. The transgenic animals
CC are useful for generating a number of B-cell expressing human
CC antibody sequences. They are also useful for producing rearranged
CC immunoglobulin sequences, producing human antibody display libraries,
CC and generating a human sequence antibody that binds to a predetermined
CC antigen. The produced antibodies are useful for treating immune-related
CC disorders. The present sequence represents a plasmid used in the
CC construction of expression vectors for human IgG.
XX
SQ Sequence 3881 BP; 981 A; 1014 C; 921 G; 965 T; 0 other;

Query Match 53.3%; Score 1044; DB 24; Length 3881;
Best Local Similarity 99.8%; Pred. No. 2.3e-235;
Matches 1066; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

```
Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2734

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154
```

```
Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3215 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3334

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Db       3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy       1392 ACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 ACCATTTATAAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621
```

RESULT 15
AAQ55004/c
ID AAQ55004 standard; DNA; 7059 BP.
XX
AC AAQ55004;
XX
DT 06-JUL-1994 (first entry)
XX
DE Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11).
XX
KW Monoclonal antibody; MAb; heavy chain; light chain;
KW constant region; variable region; amplification; primer;
KW polymerase chain reaction; PCR; chimera; Ig;
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
XX
OS Chimeric: Homo sapiens.
OS Chimeric: Mus sp.
XX
PN EP578515-A.
XX
PD 12-JAN-1994.
XX
PF 24-MAY-1993; 93EP-0401328.
XX
PR 26-MAY-1992; 92US-0888233.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
XX
DR WPI; 1994-010334/02.
XX
PT Humanised monoclonal antibodies prepn. - using comparative model
PT building, by computer database searching
XX
PS Disclosure; Page 27-31; 68pp; English.
XX
CC NB: Humanised anti-CD18 Ab 60.3 variable light chain (pGk.11)
CC sequences are given in Fig 10 and Sequence ID 10 of the
CC specification; corresp. to AAQ62611 and AAQ55004 respectively.
CC These two sequences are not identical; AAQ55004 comprising 7059 bases
CC and AAQ62611 comprising 8400 bases. Fig 10 should consist of
CC 4 pages (1/4, 2/4, 3/4 and 4/4), however, page 2/4 is duplicated
CC and page 4/4 is missing. The sequence found in AAQ62611 represents
CC pages 1/4 - 3/4.
CC A humanised monoclonal antibody corresponding to the murine anti-CD18
CC antibody 60.3 was prepared. The variable (V) region sequences from
CC both the heavy (H) and light (L) chains were determined from cDNA
CC (amplified by PCR), and spliced onto human constant (C) regions,
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC expressed in tissue culture (Ag8.653 mouse myeloma cells, detected
CC by ELISA), and examined in binding assays. The results from
CC competition and inhibition assays showed that the chimeric Ab was
CC as effective as the murine 60.3 MAb. The deduced murine VH and VL
CC protein sequences were compared to the protein sequence data base,
CC and two human Ig protein sequences were selected to be used as
CC templates. A murine 60.3 Fv was modeled according to the deduced
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC human template sequences selected from the protein data base, a
CC humanised Fv was modeled. Construction of the humanised 60.3 was
CC done by piecing 5 pairs of complementary oligonucleotides together
CC (spanning the entire V region) to form the VH and VL. These were
CC then attached onto vectors containing genes for appropriate C regions
CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC expressed in Ag8.653 cells and binding assays were done. FACS analyses
CC indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
CC and assayed for Ig.
XX
SQ Sequence 7059 BP; 1938 A; 1576 C; 1659 G; 1886 T; 0 other;

Query Match 53.1%; Score 1040.4; DB 15; Length 7059;
Best Local Similarity 98.1%; Pred. No. 2e-234;
Matches 1065; Conservative 0; Mismatches 16; Indels 5; Gaps 1;

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OM nucleic - nucleic search, using sw model

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Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1091.2	55.7	1708	15	US-10-027-075-31	Sequence 31, Appl
3	1044	53.3	3881	15	US-10-000-433-1	Sequence 1, Appli
4	595.8	30.4	1244	11	US-09-954-456-771	Sequence 771, App
5	523.4	26.7	948	11	US-09-859-053-33	Sequence 33, Appl
6	523.4	26.7	1045	15	US-10-198-846-13629	Sequence 13629, A
7	523	26.7	941	10	US-09-800-729-81	Sequence 81, Appl
8	523	26.7	968	12	US-09-992-600A-7	Sequence 7, Appli
9	523	26.7	968	12	US-09-924-340-7	Sequence 7, Appli
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12	522.8	26.7	913	11	US-09-822-830A-531	Sequence 531, App
13	518.4	26.4	970	11	US-09-859-053-37	Sequence 37, Appl
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17	518.4	26.4	1230	15	US-10-158-646-59	Sequence 59, Appl
18	517.4	26.4	1184	15	US-10-158-646-60	Sequence 60, Appl
19	514.4	26.2	1458	15	US-10-158-646-66	Sequence 66, Appl
20	509.4	26.0	1775	15	US-10-158-646-64	Sequence 64, Appl
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c 24	491.4	25.1	2272	15	US-10-158-646-63	Sequence 63, Appl
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c 37	416.8	21.3	520	11	US-09-292-758-57	Sequence 57, Appl
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ALIGNMENTS

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; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1960
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(408)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (768)..(1087)
US-09-249-011A-21

Query Match 100.0%; Score 1960; DB 11; Length 1960;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1960; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1501 AGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGG 1560

Qy       1561 GTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAA 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAA 1620

Qy       1621 ATTTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAAT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATTTTTCAAAAGAAGAAACCTGCTATAAAGAGAATCATTCATTGCAACATGATATAAAAT 1680

Qy       1681 AACAACACAATAAAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AACAACACAATAAAAGCAATTAAATAAACAAACAATAGGGAAATGTTTAAGTTCATCATG 1740

Qy       1741 GTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGAC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GTACTTAGACTTAATGGAATGTCATGCCTTATTTACATTTTTAAACAGGTACTGAGGGAC 1800

Qy       1801 TCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATAC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCCTGTCTGCCAAGGGCCGTATTGAGTACTTTCCACAACCTAATTTAATCCACACTATAC 1860

Qy       1861 TGTGAGATTAAAAACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAAT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TGTGAGATTAAAAACATTCATTAAAATGTTGCAAAGGTTCTATAAAGCTGAGAGACAAAT 1920

Qy       1921 ATATTCTATAACTCAGCAATCCCACTTCTAGGATCAATTC 1960
              |||||||||||||||||||||||||||||||||||||||
Db       1921 ATATTCTATAACTCAGCAATCCCACTTCTAGGATCAATTC 1960
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RESULT 2
US-10-027-075-31
; Sequence 31, Application US/10027075
; Publication No. US20020114814A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston

```
;           STATE: Massachusetts
;           COUNTRY: USA
;           ZIP: 02109-1875
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/027,075
;           FILING DATE: 20-Dec-2001
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/227,595
;           FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Amy E. Mandragouras
;           REGISTRATION NUMBER: 36,207
;           REFERENCE/DOCKET NUMBER: <Unknown>
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (617)227-7400
;           TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 31:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 1708 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-027-075-31

  Query Match           55.7%;  Score 1091.2;  DB 15;  Length 1708;
  Best Local Similarity  99.6%;  Pred. No. 2.1e-267;
  Matches 1115;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        525 AGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAA 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 AGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAA 649

Qy        585 GCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAA 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        650 GCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAA 709

Qy        645 TTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCA 769

Qy        705 AACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCT 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        770 AACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCT 829

Qy        765 CAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAT 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        830 CAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAT 889

Qy        825 CTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTAC 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        890 CTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTAC 949

Qy        885 AGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 AGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG 1009

Qy        945 ACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 ACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG 1069

Qy       1005 AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA 1129

Qy       1065 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCA 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCA 1189

Qy       1125 GCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTAT 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 GCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTAT 1249

Qy       1185 TGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGC 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 TGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGC 1309

Qy       1245 TAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1310 TAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1369

Qy       1305 CTC-ATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGAC 1363
              ||| |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1370 CTCAATTTAATAATTATTATCTGTTG-TTTACCAACTACTCAATTTCTCTTATAAGGGAC 1428

Qy       1364 TAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTT 1423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 TAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTT 1488

Qy       1424 TACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACA 1483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACA 1548

Qy       1484 GTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCT 1543
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 GTCCCCTGGGCCGTGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCT 1608

Qy       1544 CATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCTG 1603
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1609 CATAGTCCTTTTTAAGGGTGACAGGTCTTACGGTCATATATCCTTTGATTCAATTCCCTG 1668

Qy       1604 GGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGC 1643
              |||||||||||| ||||||||||||||||||||||||||||
Db       1669 GGAATCAACCAAGGCAAATTTTTCAAAAGAAGAAACCTGC 1708


RESULT 3
US-10-000-433-1
; Sequence 1, Application US/10000433
; Publication No. US20020199213A1
; GENERAL INFORMATION:
;  APPLICANT: Tomizuka, Kazuma
;  APPLICANT:  Ishida, Isao
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Halk, Ed
;  TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 014643-012110US
;  CURRENT APPLICATION NUMBER: US/10/000,433
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: US 60/250,340
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3881
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Kappa light
;   OTHER INFORMATION: chain plasmid
;   OTHER INFORMATION: pCK7-96
US-10-000-433-1

  Query Match           53.3%;  Score 1044;  DB 15;  Length 3881;
  Best Local Similarity  99.8%;  Pred. No. 3.7e-255;
  Matches 1066;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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Db       2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552

Db       2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612

Db       2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2734

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672

Db       2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732

Db       2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792

Db       2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852

Db       2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912

Db       2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972

Db       3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032

Db       3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092

Db       3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152

Db       3215 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212

Db       3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3334

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272

Db       3335 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331

Db       3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391

Db       3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451

Db       3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499

Db       3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621

RESULT 4
```

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US-09-954-456-771
; Sequence 771, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Ca
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 771
;   LENGTH: 1244
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-771

  Query Match             30.4%;  Score 595.8;  DB 11;  Length 1244;
  Best Local Similarity   69.3%;  Pred. No. 2.8e-141;
  Matches  882;  Conservative    0;  Mismatches  362;  Indels   29;  Gaps    4;

Qy          12 ATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGGG 71

Db           1 ATGGAAGCCCCAGCTCAGCTTCTCTTCCTCCTGCTACTCTGGCTCCCAGATACCACCGGA 60

Qy          72 GACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCACT 131

Db          61 GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACC 120

Qy         132 ATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGCT 191

Db         121 CTCTCCTGCAGGGCCAGTCAGAGTGT----------------TGGCAGCTACTTAGCC 162

Qy         192 TGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCACTAGG 251

Db         163 TGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCCCCTCATCTATGATGCATCCAACAGG 222

Qy         252 GAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACC 311

Db         223 GCCACTGGCATCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACC 282

Qy         312 ATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATAATCTT 371

Db         283 ATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAACACCGTGACAA--TT 340

Qy         372 TACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTCAACTCTAG 431

Db         341 GGCCTCCGGGGGCCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACATACCACCGGAG 400

Qy         432 AAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTT 491

Db         401 AAATTGTGT----TGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGGAAAGAGCC 456
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Qy        492 TACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAA 551
Db        457 ACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCTACTTAGCCTGGTACCAACAGAAA 516

Qy        552 ACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGA 611
Db        517 CCTGGCCAGGCTCCCAGGCCCCTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCA 576

Qy        612 TTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCT 671
Db        577 GCCAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGCCTA--- 633

Qy        672 GTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTG 731
Db        634 --GAGCCTGAAGATTTTGCAGTTTATTACTGTCAACACCGTGACAATTGGCCTCCGGGGG 691

Qy        732 TTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCT 791
Db        692 CCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTGTGGCTGCACCATCTGTCT 751

Qy        792 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGC 851
Db        752 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGC 811

Qy        852 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAT 911
Db        812 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAAT 871

Qy        912 CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA 971
Db        872 CGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA 931

Qy        972 GCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG 1031
Db        932 GCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAG 991

Qy       1032 TCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGA 1091
Db        992 TCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGA 1051

Qy       1092 GGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCT 1151
Db       1052 GGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCT 1111

Qy       1152 CTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCT 1211
Db       1112 CTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCT 1171

Qy       1212 CACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAA 1271
Db       1172 CACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAA 1231

Qy       1272 AGTGAATCTTTGC 1284
Db       1232 AGTGAATCTTTGC 1244
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RESULT 5
US-09-859-053-33
; Sequence 33, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(27)
; NAME/KEY: CDS
; LOCATION: (28)...(735)
; NAME/KEY: 3'UTR
; LOCATION: (739)...(948)
; NAME/KEY: sig_peptide
; LOCATION: (28)...(87)
; NAME/KEY: misc_feature
; LOCATION: (1)...(948)
; OTHER INFORMATION: n = A,T,C or G
US-09-859-053-33

Query Match 26.7%; Score 523.4; DB 11; Length 948;
Best Local Similarity 99.6%; Pred. No. 6.7e-123;
Matches 524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
Db        414 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 473

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
Db        474 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 533

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
Db        534 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 593

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
Db        594 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 653

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
Db        654 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 713

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
Db        714 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAANTGCCCCCACCTGCTCCTCAGTTCCAG 773

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
Db        774 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 833

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
Db        834 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 893

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 1291
Db        894 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 939
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RESULT 6
US-10-198-846-13629
; Sequence 13629, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen

```
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
;  TITLE OF INVENTION:  FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF BREAST CANCER
;  FILE REFERENCE: MRI-049
;  CURRENT APPLICATION NUMBER: US/10/198,846
;  CURRENT FILING DATE:  2002-07-18
;  PRIOR APPLICATION NUMBER: 60/306,220
;  PRIOR FILING DATE: 2001-07-18
;  NUMBER OF SEQ ID NOS: 14084
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13629
;   LENGTH: 1045
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-198-846-13629

  Query Match             26.7%;  Score 523.4;  DB 15;  Length 1045;
  Best Local Similarity   99.8%;  Pred. No. 7.1e-123;
  Matches  524;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db        493 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 552

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 612

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 672

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 732

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 792

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 852

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 912

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db        913 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 972

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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Db        973 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1017


RESULT 7
US-09-800-729-81
; Sequence 81, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
;  APPLICANT:  Ni et al.
;  TITLE OF INVENTION:  32 Human secreted proteins
;  FILE REFERENCE:  PZ044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  PCT/US00/26013
;  PRIOR FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER:  60/155,709
;  PRIOR FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  217
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 81
;   LENGTH: 941
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-800-729-81

  Query Match             26.7%;  Score 523;  DB 10;  Length 941;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-123;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 460

Qy        828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        461 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 520

Qy        888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 580

Qy        948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        581 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 640

Qy       1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 1067
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        641 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 700

Qy       1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        701 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 760

Qy       1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        761 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 820

Qy       1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 1247
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        821 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 880

Qy       1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
              |||||||||||||||||||||||||||||||||||||||||||||
Db        881 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 923


RESULT 8
US-09-992-600A-7
; Sequence 7, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US4.DIV
;  CURRENT APPLICATION NUMBER: US/09/992,600A
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 114
;  SOFTWARE: JPatent
; SEQ ID NO 7
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;   LENGTH: 968
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..31
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 32..748
;   FEATURE:
;   NAME/KEY: 3'UTR
;   LOCATION: 749..968
;   FEATURE:
;   NAME/KEY: polyA_signal
;   LOCATION: 928..933
;   FEATURE:
;   NAME/KEY: polyA_site
;   LOCATION: 953..968
US-09-992-600A-7

  Query Match           26.7%;  Score 523;  DB 12;  Length 968;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-123;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 488

Qy        828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 548

Qy        888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 608

Qy        948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 668

Qy       1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 728

Qy       1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         729 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 788

Qy       1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         789 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 848

Qy       1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 1247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 908

Qy       1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
              |||||||||||||||||||||||||||||||||||||||||||
Db         909 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 951


RESULT 9
US-09-924-340-7
; Sequence 7, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
;  APPLICANT: Bejanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/924,340
;  CURRENT FILING DATE:  2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: JPatent
; SEQ ID NO 7
;   LENGTH: 968
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..31
;   NAME/KEY: CDS
;   LOCATION: 32..748
;   NAME/KEY: 3'UTR
;   LOCATION: 749..968
;   NAME/KEY: polyA_signal
;   LOCATION: 928..933
;   NAME/KEY: polyA_site
;   LOCATION: 953..968
US-09-924-340-7

  Query Match           26.7%;  Score 523;  DB 12;  Length 968;
  Best Local Similarity  100.0%;  Pred. No. 8.5e-123;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 488

Qy        828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 548

Qy        888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 608

Qy        948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 668

Qy       1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 728

Qy       1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         729 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 788

Qy       1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         789 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 848

Qy       1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 1247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 908

Qy       1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
              |||||||||||||||||||||||||||||||||||||||||||
Db         909 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 951


RESULT 10
US-10-000-489-7
; Sequence 7, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
```

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;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US6.DIV
;  CURRENT APPLICATION NUMBER: US/10/000,489
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: JPatent
; SEQ ID NO 7
;   LENGTH: 968
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..31
;   NAME/KEY: CDS
;   LOCATION: 32..748
;   NAME/KEY: 3'UTR
;   LOCATION: 749..968
;   NAME/KEY: polyA_signal
;   LOCATION: 928..933
;   NAME/KEY: polyA_site
;   LOCATION: 953..968
US-10-000-489-7

  Query Match             26.7%;  Score 523;  DB 15;  Length 968;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-123;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 488

Qy        828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 548

Qy        888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 608

Qy        948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 668

Qy       1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 728

Qy       1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 788

Qy       1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
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Db        789 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 848

Qy       1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 1247
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Db        849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 908

Qy       1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
              |||||||||||||||||||||||||||||||||||||||||||
Db        909 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 951


RESULT 11
US-10-000-986-7
; Sequence 7, Application US/10000986
; Publication No. US20030096247A1
; GENERAL INFORMATION:
;  APPLICANT: Benjanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
;  FILE REFERENCE: 91.US9.DIV
;  CURRENT APPLICATION NUMBER: US/10/000,986
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: US 09/924,340
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: PCT/IB01/01715
;  PRIOR FILING DATE: 2001-08-06
;  PRIOR APPLICATION NUMBER: US 60/305,456
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/302,277
;  PRIOR FILING DATE: 2001-06-29
;  PRIOR APPLICATION NUMBER: US 60/298,698
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: US 60/293,574
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: JPatent
; SEQ ID NO 7
;   LENGTH: 968
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 1..31
;   NAME/KEY: CDS
;   LOCATION: 32..748
;   NAME/KEY: 3'UTR
;   LOCATION: 749..968
;   NAME/KEY: polyA_signal
;   LOCATION: 928..933
;   NAME/KEY: polyA_site
;   LOCATION: 953..968
US-10-000-986-7

  Query Match             26.7%;  Score 523;  DB 15;  Length 968;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-123;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        768 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 827
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG 488

Qy        828 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 887
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 GAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT 548

Qy        888 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACA 608

Qy        948 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 1007
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 GCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGA 668

Qy       1008 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 1067
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA 728

Qy       1068 GCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCC 1127
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Qy       1128 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 1187
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Db        789 TGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGC 848

Qy       1188 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 1247
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Db        849 GGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAA 908

Qy       1248 TGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGT 1290
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RESULT 12
US-09-822-830A-531
; Sequence 531, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 913
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-531

Query Match 26.7%; Score 522.8; DB 11; Length 913;
Best Local Similarity 99.6%; Pred. No. 9.3e-123;
Matches 524; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db        388 AAGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 447

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db        448 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 507

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 567

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 627

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Db        628 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 687

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
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Db        688 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 747

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Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db        808 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 867

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTG 1291
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RESULT 13
US-09-859-053-37
; Sequence 37, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(32)
; NAME/KEY: CDS
; LOCATION: (33)...(740)
; NAME/KEY: 3'UTR
; LOCATION: (744)...(970)
; NAME/KEY: sig_peptide
; LOCATION: (33)...(92)
US-09-859-053-37

Query Match 26.4%; Score 518.4; DB 11; Length 970;
Best Local Similarity 99.8%; Pred. No. 1.3e-121;
Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db        419 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 478

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db        479 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 538

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 598

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
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Db        599 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 658

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Db        659 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 718

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
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Db        779 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 838

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db        839 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 898

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db        899 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 938


RESULT 14
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
;  APPLICANT: Tsuji, Takashi
;  APPLICANT:  Tezuka, Katsunari
;  APPLICANT:  Hori, No. US20020102658A1uaki
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;  TITLE OF INVENTION:  COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;  TITLE OF INVENTION:  PHARMACEUTICAL USE THEREOF
;  FILE REFERENCE: 06501-079001
;  CURRENT APPLICATION NUMBER: US/09/859,053
;  CURRENT FILING DATE:  2001-05-16
;  PRIOR APPLICATION NUMBER: JP 2001-99508
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 974
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)...(38)
;   NAME/KEY: CDS
;   LOCATION: (39)...(746)
;   NAME/KEY: 3'UTR
;   LOCATION: (750)...(974)
;   NAME/KEY: sig_peptide
;   LOCATION: (39)...(104)
US-09-859-053-29

  Query Match             26.4%;  Score 518.4;  DB 11;  Length 974;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-121;
  Matches  519;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db        425 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 484

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db        485 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 544

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
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Db        545 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 604

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
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Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db        845 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 904

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Db        905 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 944


RESULT 15
US-09-800-729-79
; Sequence 79, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
;  APPLICANT:  Ni et al.
;  TITLE OF INVENTION:  32 Human secreted proteins
;  FILE REFERENCE:  PZ044P1
;  CURRENT APPLICATION NUMBER: US/09/800,729
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER:  PCT/US00/26013
;  PRIOR FILING DATE:  2000-09-22
;  PRIOR APPLICATION NUMBER:  60/155,709
;  PRIOR FILING DATE:  1999-09-24
;  NUMBER OF SEQ ID NOS:  217
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 79
;   LENGTH: 990
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (908)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-800-729-79

  Query Match             26.4%;  Score 518.4;  DB 10;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-121;
  Matches  519;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db        388 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 447

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db        448 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 507

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
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Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
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Db        688 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 747

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Db        748 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 807
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Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db        808 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 867

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCA 1285
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1429.4	72.9	1701	2	US-07-916-098A-54	Sequence 54, Appl
4	1429.4	72.9	1701	2	US-07-916-098A-55	Sequence 55, Appl
5	1184.2	60.4	13999	3	US-08-444-644-24	Sequence 24, Appl
6	1184.2	60.4	13999	4	US-08-232-246A-24	Sequence 24, Appl
7	1181.4	60.3	1276	2	US-07-916-098A-53	Sequence 53, Appl
8	1181.2	60.3	1241	2	US-07-916-098A-51	Sequence 51, Appl
9	1091.2	55.7	1708	4	US-09-227-595-31	Sequence 31, Appl
10	1044	53.3	3881	4	US-09-042-353-369	Sequence 369, App
11	1044	53.3	3881	4	US-08-758-417A-217	Sequence 217, App
12	709.4	36.2	3819	4	US-09-042-353-393	Sequence 393, App
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16	518.4	26.4	931	3	US-09-049-672A-19	Sequence 19, Appl
17	518.4	26.4	958	3	US-09-049-672A-15	Sequence 15, Appl
18	518.4	26.4	1066	1	US-08-157-101A-4	Sequence 4, Appli
19	450	23.0	1149	3	US-08-477-460B-5	Sequence 5, Appli
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30	323.4	16.5	711	4	US-08-487-283A-15	Sequence 15, Appl
31	323.4	16.5	726	4	US-08-487-283A-9	Sequence 9, Appli
32	323.4	16.5	726	4	US-08-487-283A-13	Sequence 13, Appl
33	323.4	16.5	726	4	US-08-487-283A-14	Sequence 14, Appl
34	322.4	16.4	2143	3	US-09-097-309-5	Sequence 5, Appli
35	322.4	16.4	2143	4	US-09-097-171A-9	Sequence 9, Appli
36	322.4	16.4	2143	4	US-09-460-587-5	Sequence 5, Appli
37	322.4	16.4	2178	1	US-08-463-587A-24	Sequence 24, Appl
38	322.4	16.4	2178	2	US-08-463-667A-2	Sequence 2, Appli
39	322.4	16.4	2178	3	US-08-923-854-24	Sequence 24, Appl
40	322.4	16.4	2178	5	PCT-US91-09133-25	Sequence 25, Appl
41	322.4	16.4	6550	4	US-09-422-712B-1	Sequence 1, Appli
42	322.4	16.4	6550	4	US-09-607-756-1	Sequence 1, Appli
43	322.4	16.4	7305	1	US-08-286-740-4	Sequence 4, Appli
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45	321.8	16.4	3169	3	US-08-630-820-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-247-352-6
; Sequence 6, Application US/09247352
; Patent No. 6312693
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffry D.
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2a SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/247,352
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: 09/026,291
; EARLIER FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-247-352-6

Query Match 82.2%; Score 1611.8; DB 4; Length 8858;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 137; Indels 49; Gaps 4;

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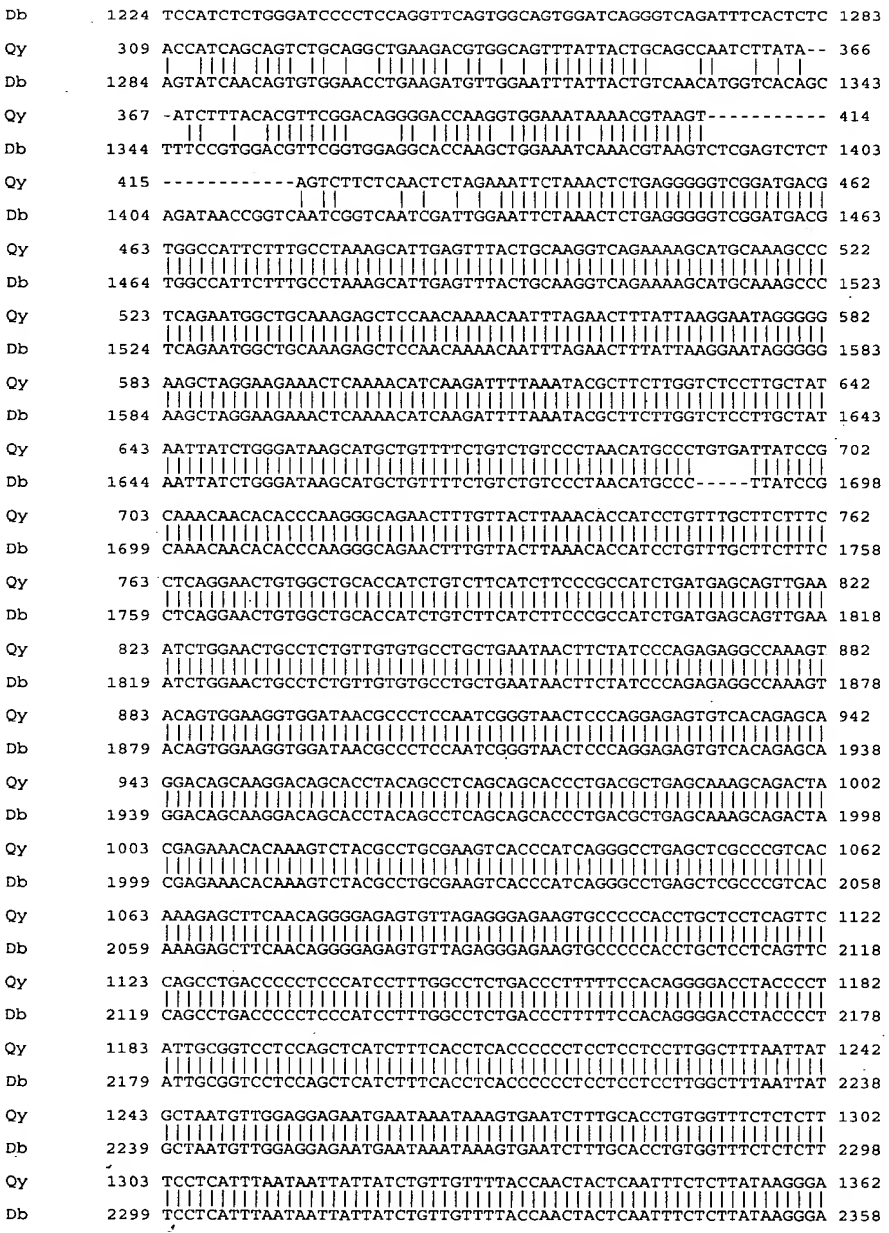
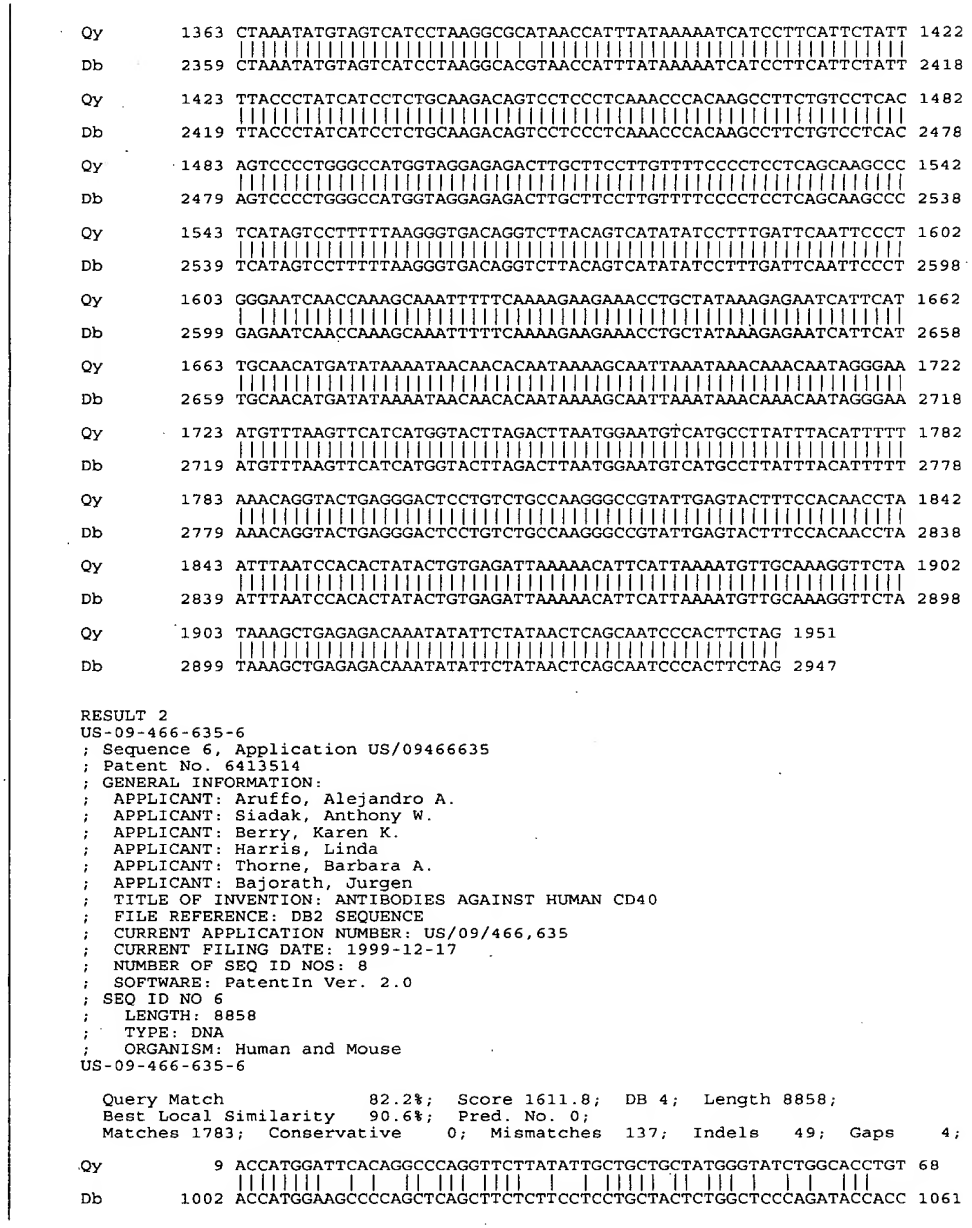
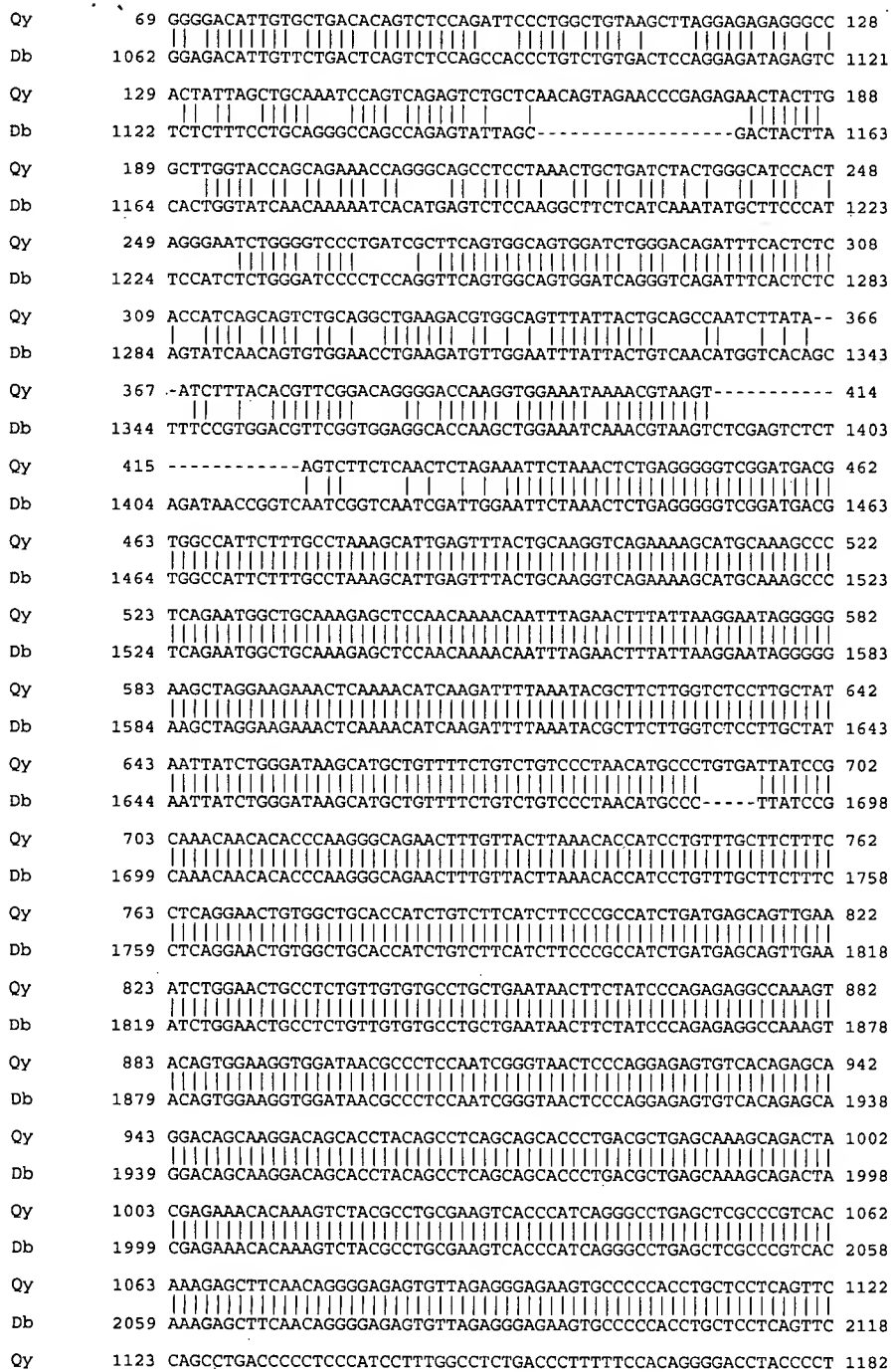
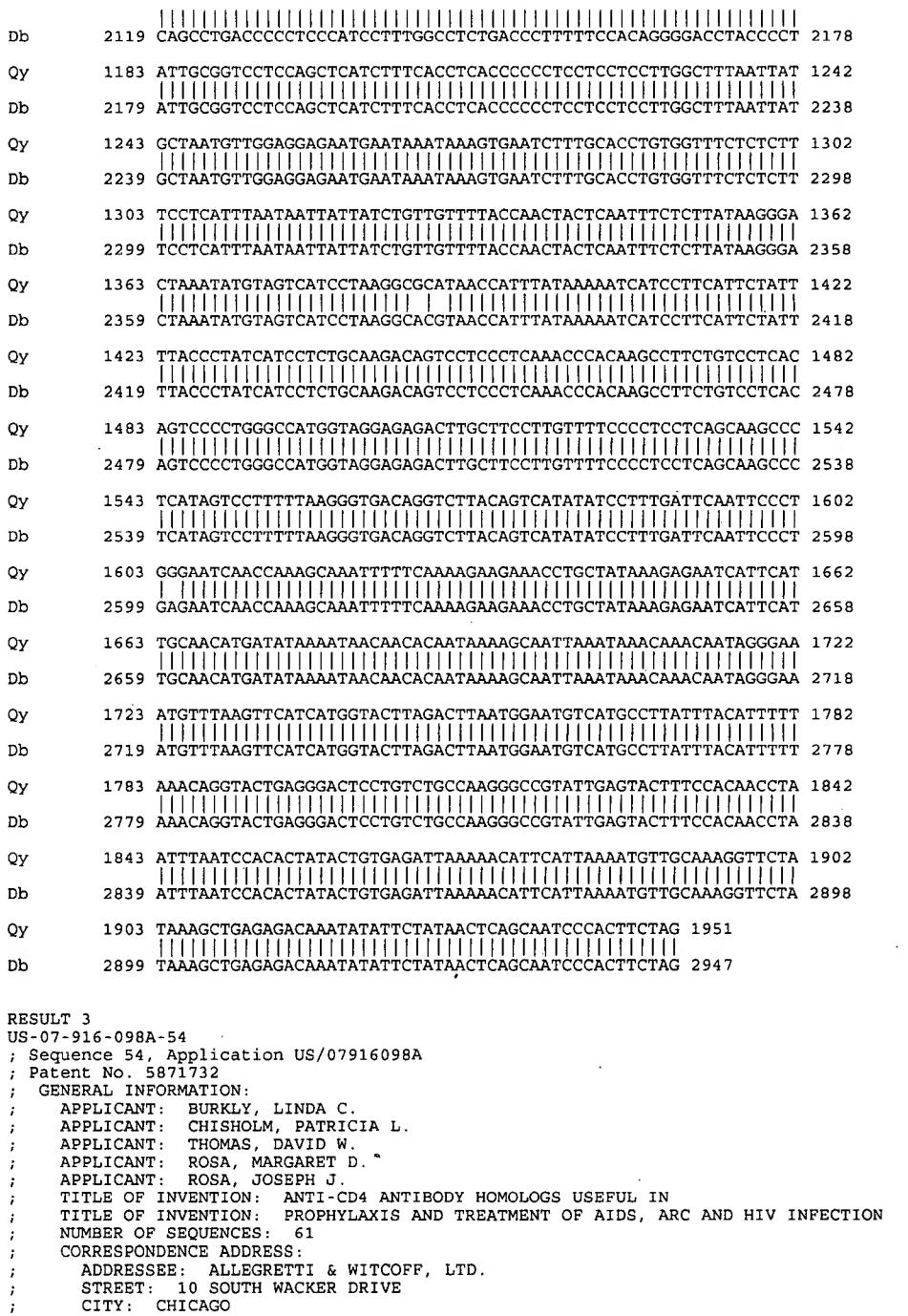




RESULT 2
US-09-466-635-6
; Sequence 6, Application US/09466635
; Patent No. 6413514
; GENERAL INFORMATION:
; APPLICANT: Aruffo, Alejandro A.
; APPLICANT: Siadak, Anthony W.
; APPLICANT: Berry, Karen K.
; APPLICANT: Harris, Linda
; APPLICANT: Thorne, Barbara A.
; APPLICANT: Bajorath, Jurgen
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD40
; FILE REFERENCE: DB2 SEQUENCE
; CURRENT APPLICATION NUMBER: US/09/466,635
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Human and Mouse
US-09-466-635-6

Query Match 82.2%; Score 1611.8; DB 4; Length 8858;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 137; Indels 49; Gaps 4;





RESULT 3
US-07-916-098A-54
; Sequence 54, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO

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;       STATE:  ILLINOIS
;       COUNTRY:  U.S.A.
;       ZIP:  60606
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/916,098A
;       FILING DATE:  July 24, 1992
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US91/08843
;       FILING DATE:  No. 5871732ember 27, 1991
;       CLASSIFICATION:  424
;       APPLICATION NUMBER:  07/618,542
;       FILING DATE:  No. 5871732ember 27, 1990
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  JOHN J. MC DONNELL
;       REGISTRATION NUMBER:  26,949
;       REFERENCE/DOCKET NUMBER:  92,310-G
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 715-1000
;       TELEFAX:  (312) 715-1234
;       TELEX:  910/221-5317
;   INFORMATION FOR SEQ ID NO:  54:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1701 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1
;       OTHER INFORMATION:  /note= "pMDR1006 insert"
US-07-916-098A-54

  Query Match             72.9%;  Score 1429.4;  DB 2;  Length 1701;
  Best Local Similarity   93.1%;  Pred. No. 0;
  Matches 1534;  Conservative    0;  Mismatches   96;  Indels   17;  Gaps    3;

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Qy         71 GGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGGCCAC 130
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Db        100 TGATATCGTAATGACCCAGTCTCCAGACTCCCTAGCTGTGTCACTTGGAGAGAGGGCTAC 159

Qy        131 TATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACTTGGC 190
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Db        280 GGAATCTGGGGTCCCTGATCGCTTCTCAGGCAGTGGATCTGGGACAGATTTCACTCTCAC 339

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Qy        491 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 550
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RESULT 4
US-07-916-098A-55
; Sequence 55, Application US/07916098A
; Patent No. 5871732
;  GENERAL INFORMATION:
;    APPLICANT:  BURKLY, LINDA C.
;    APPLICANT:  CHISHOLM, PATRICIA L.
;    APPLICANT:  THOMAS, DAVID W.
;    APPLICANT:  ROSA, MARGARET D.
;    APPLICANT:  ROSA, JOSEPH J.
;    TITLE OF INVENTION:  ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;    TITLE OF INVENTION:  PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
;      STREET:  10 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  U.S.A.
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,098A
;      FILING DATE:  July 24, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 5871732ember 27, 1991
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/618,542
;      FILING DATE:  No. 5871732ember 27, 1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JOHN J. MC DONNELL
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,310-G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;      TELEX:  910/221-5317
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1701 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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US-07-916-098A-55

  Query Match             72.9%;  Score 1429.4;  DB 2;  Length 1701;
  Best Local Similarity   93.1%;  Pred. No. 0;
  Matches 1534;  Conservative    0;  Mismatches   96;  Indels   17;  Gaps    3;

Qy         11 CATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCTGTGG 70
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Db        449 ----TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGT 504

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Db        505 TTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAA 564

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Db        565 AACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAG 624

Qy        611 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 670
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Db        625 ATTTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTC 684

Qy        671 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 730
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Db        685 TGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTT 744

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Db        925 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 984

Qy        971 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 1044

Qy       1031 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG 1104

Qy       1091 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 AGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCC 1164

Qy       1151 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 TCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACC 1224

Qy       1211 TCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225 TCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATA 1284

Qy       1271 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTG 1329
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1285 AAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG 1344

Qy       1330 TTTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1389
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Db       1345 -TTTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCA 1403

Qy       1390 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 TAACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGT 1463

Qy       1450 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGAC 1509
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1464 CCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGAC 1523

Qy       1510 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1524 TTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGT 1583

Qy       1570 CTTACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAA 1629
              ||||| |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1584 CTTACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAA 1643

Qy       1630 AAGAAGAAACCTGCTATAAAGAGAATC 1656
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Db       1644 AAGAAGAAACCTGCGGCCGATCGATTC 1670
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RESULT 5
US-08-444-644-24
; Sequence 24, Application US/08444644
; Patent No. 6015555
;  GENERAL INFORMATION:
;    APPLICANT:  Friden, Phillip M.
;    TITLE OF INVENTION:  TRANSFERRIN RECEPTOR SPECIFIC
;    TITLE OF INVENTION:  ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
;    TITLE OF INVENTION:  CONJUGATES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/444,644
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/232,246
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/800,458
;      FILING DATE:  26-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US90/05077
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/404,089
;      FILING DATE:  07-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wagner, Richard W.
;      REGISTRATION NUMBER:  34,480
;      REFERENCE/DOCKET NUMBER:  ALK88-15AAAZ
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13999 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  pAG4611
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..13999
;      OTHER INFORMATION:  /note= "Function = "Expression
;      OTHER INFORMATION:  Vector Coding Sequence""
US-08-444-644-24

  Query Match             60.4%;  Score 1184.2;  DB 3;  Length 13999;
  Best Local Similarity   99.5%;  Pred. No. 2.1e-298;
  Matches 1208;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

Qy         433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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Db        8087 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 8146

Qy         493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8147 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 8206

Qy         553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8207 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 8266

Qy         613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8267 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 8326

Qy         673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        8327 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 8386
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Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Db       8387 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 8446

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8447 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 8506

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8507 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 8566

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Db       8567 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 8626

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8627 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 8686

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8687 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 8746

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8747 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 8806

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8807 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 8866

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8867 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 8926

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db       8927 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 8985

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8986 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 9045

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
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Db       9046 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 9105

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTT 1511
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       9106 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTT 9165

Qy       1512 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 1571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9166 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 9225

Qy       1572 TACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAA 1631
              ||| |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       9226 TACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAA 9285

Qy       1632 GAAGAAACCTGCTA 1645
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Db       9286 GAAGAAACCTGCNA 9299


RESULT 6
US-08-232-246A-24
; Sequence 24, Application US/08232246A
; Patent No. 6329508
;  GENERAL INFORMATION:
;    APPLICANT:  Friden, Phillip M.
;    TITLE OF INVENTION:  TRANSFERRIN RECEPTOR SPECIFIC
;    TITLE OF INVENTION:  ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
;    TITLE OF INVENTION:  CONJUGATES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,246A
;      FILING DATE:  04-MAY-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/800,458
;      FILING DATE:  26-NOV-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US90/05077
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/404,089
;      FILING DATE:  07-SEP-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wagner, Richard W.
;      REGISTRATION NUMBER:  34,480
;      REFERENCE/DOCKET NUMBER:  ALK88-15AAA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13999 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  circular
;    MOLECULE TYPE:  DNA (genomic)
;    IMMEDIATE SOURCE:
;      CLONE:  pAG4611
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..13999
;      OTHER INFORMATION:  /note= "Function = "Expression
;      OTHER INFORMATION:  Vector Coding Sequence""
US-08-232-246A-24

  Query Match             60.4%;  Score 1184.2;  DB 4;  Length 13999;
  Best Local Similarity   99.5%;  Pred. No. 2.1e-298;
  Matches 1208;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8087 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 8146

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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Db       8147 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 8206

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
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Db       8207 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 8266

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
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Db       8267 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 8326

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
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Db       8387 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 8446

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8447 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 8506

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8507 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 8566

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
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Db       8567 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 8626

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8627 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 8686

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db       8687 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 8746

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db       8807 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 8866

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
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Db       8867 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 8926

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Db       8927 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 8985

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
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Db       8986 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 9045

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9046 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 9105

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTT 1511
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Db       9106 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTT 9165

Qy       1512 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 1571
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9166 GCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCT 9225

Qy       1572 TACAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAA 1631
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Db       9226 TACGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAA 9285

Qy       1632 GAAGAAACCTGCTA 1645
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Db       9286 GAAGAAACCTGCNA 9299


RESULT 7
US-07-916-098A-53
; Sequence 53, Application US/07916098A
; Patent No. 5871732
;  GENERAL INFORMATION:
;    APPLICANT:  BURKLY, LINDA C.
;    APPLICANT:  CHISHOLM, PATRICIA L.
;    APPLICANT:  THOMAS, DAVID W.
;    APPLICANT:  ROSA, MARGARET D.
;    APPLICANT:  ROSA, JOSEPH J.
;    TITLE OF INVENTION:  ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;    TITLE OF INVENTION:  PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
;      STREET:  10 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,098A
;      FILING DATE:  July 24, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 5871732ember 27, 1991
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/618,542
;      FILING DATE:  No. 5871732ember 27, 1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JOHN J. MC DONNELL
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,310-G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;      TELEX:  910/221-5317
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1276 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pMDR986 insert"
US-07-916-098A-53

  Query Match             60.3%;  Score 1181.4;  DB 2;  Length 1276;
  Best Local Similarity   98.9%;  Pred. No. 3.9e-298;
  Matches 1210;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    2;

Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 203

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263
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Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 563

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 683

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 743

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 803

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTGTTTT 923

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
              |||||||||||||||||||||||||||||||||||||  |||||||||| |||||
Db        924 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTACTCCTAAGGCG-ATAAC 982

Qy       1394 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1043 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1102

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1103 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162

Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1163 CAGTCATATATCCTTTGATTCAATTCCCTGAGAATCAACCAAAGCAAATTTTTCAAAAGA 1222

Qy       1634 AGAAACCTGCTATAAAGAGAATC 1656
              ||||||||||     |  || ||
Db       1223 AGAAACCTGCGGCCGATCGATTC 1245
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RESULT 8
US-07-916-098A-51
; Sequence 51, Application US/07916098A
; Patent No. 5871732

```
;  GENERAL INFORMATION:
;    APPLICANT:  BURKLY, LINDA C.
;    APPLICANT:  CHISHOLM, PATRICIA L.
;    APPLICANT:  THOMAS, DAVID W.
;    APPLICANT:  ROSA, MARGARET D.
;    APPLICANT:  ROSA, JOSEPH J.
;    TITLE OF INVENTION:  ANTI-CD4 ANTIBODY.HOMOLOGS USEFUL IN
;    TITLE OF INVENTION:  PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
;      STREET:  10 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
;      STATE:  ILLINOIS
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,098A
;      FILING DATE:  July 24, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 5871732ember 27, 1991
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/618,542
;      FILING DATE:  No. 5871732ember 27, 1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JOHN J. MC DONNELL
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,310-G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;      TELEX:  910/221-5317
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1241 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pSAB153 insert"
US-07-916-098A-51

  Query Match             60.3%;  Score 1181.2;  DB 2;  Length 1241;
  Best Local Similarity   99.6%;  Pred. No. 4.4e-298;
  Matches 1205;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        435 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 TTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTTAC 83

Qy        495 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAACA 143

Qy        555 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 ATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGATTT 203

Qy        615 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        204 TAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTGTC 263

Qy        675 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 TGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGTTA 323

Qy        735 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 CTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTTCA 383

Qy        795 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGA 443

Qy        855 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 ATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGG 503

Qy        915 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 GTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCA 563

Qy        975 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA 623

Qy       1035 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGGG 683

Qy       1095 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 AGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTCTG 743

Qy       1155 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 ACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTCAC 803

Qy       1215 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAAGT 863

Qy       1275 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTTTT 1333
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||
Db        864 GAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-TTT 922

Qy       1334 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 1393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 ACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATAAC 982

Qy       1394 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        983 CATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCCTC 1042

Qy       1454 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGGTAGGAGAGACTTGC 1513
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        1043 CCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCGTGGTAGGAGAGACTTGC 1102

Qy       1514 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1103 TTCCTTGTTTTCCCCTCCTCAGCAAGCCCTCATAGTCCTTTTTAAGGGTGACAGGTCTTA 1162

Qy       1574 CAGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAAGCAAATTTTTCAAAAGA 1633
              | ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        1163 CGGTCATATATCCTTTGATTCAATTCCCTGGGAATCAACCAAGGCAAATTTTTCAAAAGA 1222

Qy       1634 AGAAACCTGC 1643
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Db        1223 AGAAACCTGC 1232


RESULT 9
US-09-227-595-31
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; Sequence 31, Application US/09227595
; Patent No. 6444792
;  GENERAL INFORMATION:
;    APPLICANT:  Gray, Gary S. et al.
;    TITLE OF INVENTION:  CTLA4-Immunoglobulin Fusion Proteins
;    TITLE OF INVENTION:  Having Modified Effector Functions and Uses Therefor
;    NUMBER OF SEQUENCES:  32
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/227,595
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/595,590
;      FILING DATE:  February 2, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Amy E. Mandragouras
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1708 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-227-595-31

  Query Match             55.7%;  Score 1091.2;  DB 4;  Length 1708;
  Best Local Similarity   99.6%;  Pred. No. 1.4e-274;
  Matches 1115;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy        525 AGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAA 584
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Db        590 AGAATGGCTGCAAAGAGCTCCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAA 649

Qy        585 GCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAA 644
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Db        650 GCTAGGAAGAAACTCAAAACATCAAGATTTTAAATACGCTTCTTGGTCTCCTTGCTATAA 709

Qy        645 TTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        710 TTATCTGGGATAAGCATGCTGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCA 769

Qy        705 AACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCT 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        770 AACAACACACCCAAGGGCAGAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCT 829

Qy        765 CAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAT 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        830 CAGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAT 889

Qy        825 CTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTAC 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        890 CTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTAC 949

Qy        885 AGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        950 AGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGG 1009
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Qy        945 ACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 ACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACG 1069

Qy       1005 AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 AGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA 1129

Qy       1065 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCA 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 AGAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCA 1189

Qy       1125 GCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTAT 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 GCCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTAT 1249

Qy       1185 TGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGC 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 TGCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGC 1309

Qy       1245 TAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1310 TAATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTC 1369

Qy       1305 CTC-ATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGAC 1363
              ||| ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1370 CTCAATTTAATAATTATTATCTGTTG-TTTACCAACTACTCAATTTCTCTTATAAGGGAC 1428

Qy       1364 TAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTT 1423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1429 TAAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTT 1488

Qy       1424 TACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACA 1483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1489 TACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACA 1548

Qy       1484 GTCCCCTGGGCCATGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCT 1543
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1549 GTCCCCTGGGCCGTGGTAGGAGAGACTTGCTTCCTTGTTTTCCCCTCCTCAGCAAGCCCT 1608

Qy       1544 CATAGTCCTTTTTAAGGGTGACAGGTCTTACAGTCATATATCCTTTGATTCAATTCCCTG 1603
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1609 CATAGTCCTTTTTAAGGGTGACAGGTCTTACGGTCATATATCCTTTGATTCAATTCCCTG 1668

Qy       1604 GGAATCAACCAAAGCAAATTTTTCAAAAGAAGAAACCTGC 1643
              |||||||||||| ||||||||||||||||||||||||||||
Db       1669 GGAATCAACCAAGGCAAATTTTTCAAAAGAAGAAACCTGC 1708


RESULT 10
US-09-042-353-369
; Sequence 369, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  369:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3881 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-369

  Query Match             53.3%;  Score 1044;  DB 4;  Length 3881;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-262;
  Matches 1066;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
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Db       2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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Db       2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674

Qy        553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
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Db       2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2734

Qy        613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy        673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
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Db       2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy        733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Db       2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy        793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy        853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Db       2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy        913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy        973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Db       3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy       1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db       3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy       1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db       3215 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy       1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3334

Qy       1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy       1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db       3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy       1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
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Db       3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy       1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy       1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621


RESULT 11
US-08-758-417A-217
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; Sequence 217, Application US/08758417A
; Patent No. 6300129
;  GENERAL INFORMATION:
;       APPLICANT: Lonberg, Nils
;                  Kay, Robert M.
;       TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                           Producing Heterologous Antibodies
;       NUMBER OF SEQUENCES: 417
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/758,417A
;            FILING DATE: 02-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 217:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3881 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-08-758-417A-217

  Query Match           53.3%;  Score 1044;  DB 4;  Length 3881;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-262;
  Matches 1066;  Conservative    0;  Mismatches    0;  Indels    2;  Gaps    2;

Qy        433 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2555 AATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGCATTGAGTTT 2614

Qy        493 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 552
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Db       2615 ACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCTCCAACAAAA 2674
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Qy       553 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 612
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Db      2675 CAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAACATCAAGAT 2734

Qy       613 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 672
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Db      2735 TTTAAATACGCTTCTTGGTCTCCTTGCTATAATTATCTGGGATAAGCATGCTGTTTTCTG 2794

Qy       673 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 732
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2795 TCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCAGAACTTTGT 2854

Qy       733 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 792
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Db      2855 TACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACCATCTGTCTT 2914

Qy       793 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 852
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2915 CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCT 2974

Qy       853 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 912
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Db      2975 GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC 3034

Qy       913 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 972
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3035 GGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG 3094

Qy       973 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 1032
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Db      3095 CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGT 3154

Qy      1033 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 1092
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Db      3155 CACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAG 3214

Qy      1093 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 1152
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Db      3215 GGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCCTTTGGCCTC 3274

Qy      1153 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 1212
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Db      3275 TGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATCTTTCACCTC 3334

Qy      1213 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 1272
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3335 ACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGAATAAATAAA 3394

Qy      1273 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTC-ATTTAATAATTATTATCTGTTGTT 1331
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |
Db      3395 GTGAATCTTTGCACCTGTGGTTTCTCTCTTTCCTCAATTTAATAATTATTATCTGTTG-T 3453

Qy      1332 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 1391
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Db      3454 TTACCAACTACTCAATTTCTCTTATAAGGGACTAAATATGTAGTCATCCTAAGGCGCATA 3513

Qy      1392 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 1451
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Db      3514 ACCATTTATAAAAATCATCCTTCATTCTATTTTACCCTATCATCCTCTGCAAGACAGTCC 3573

Qy      1452 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 1499
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Db      3574 TCCCTCAAACCCACAAGCCTTCTGTCCTCACAGTCCCCTGGGCCATGG 3621
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RESULT 12
US-09-042-353-393
; Sequence 393, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
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;       TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  393:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  3819 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-393

  Query Match             36.2%;  Score 709.4;  DB 4;  Length 3819;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-175;
  Matches  732;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db       2826 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 2885

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2886 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 2945

Qy        886 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 945
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Db       2946 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 3005

Qy        946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
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Db       3006 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 3065

Qy       1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3066 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 3125

Qy       1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3126 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 3185

Qy       1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3186 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 3245

Qy       1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db       3246 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 3305

Qy       1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCC 1305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3306 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCC 3365

Qy       1306 TC-ATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGACT 1364
              || |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3366 TCAATTTAATAATTATTATCTGTTG-TTTACCAACTACTCAATTTCTCTTATAAGGGACT 3424

Qy       1365 AAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTTT 1424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3425 AAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTTT 3484

Qy       1425 ACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAG 1484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3485 ACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAG 3544

Qy       1485 TCCCCTGGGCCATGG 1499
              ||||||||||||||||
Db       3545 TCCCCTGGGCCATGG 3559


RESULT 13
US-08-758-417A-243
; Sequence 243, Application US/08758417A
; Patent No. 6300129
;   GENERAL INFORMATION:
;       APPLICANT: Lonberg, Nils
;                  Kay, Robert M.
;       TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                           Producing Heterologous Antibodies
;       NUMBER OF SEQUENCES: 417
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/758,417A
;            FILING DATE: 02-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;  INFORMATION FOR SEQ ID NO: 243:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 3819 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 243:
US-08-758-417A-243

  Query Match             36.2%;  Score 709.4;  DB 4;  Length 3819;
  Best Local Similarity   99.6%;  Pred. No. 4.9e-175;
  Matches  732;  Conservative    0;  Mismatches    1;  Indels    2;  Gaps    2;

Qy        766 AGGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 825
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Db       2826 ACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATC 2885

Qy        826 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 885
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Db       2886 TGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA 2945

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Db       2946 GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA 3005
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Qy       946 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 1005
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Db      3006 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGA 3065

Qy      1006 GAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAA 1065
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Qy      1066 GAGCTTCAACAGGGGAGAGTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAG 1125
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Qy      1126 CCTGACCCCCTCCCATCCTTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATT 1185
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Qy      1186 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 1245
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Db      3246 GCGGTCCTCCAGCTCATCTTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCT 3305

Qy      1246 AATGTTGGAGGAGAATGAATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCTCTTTCC 1305
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Qy      1306 TC-ATTTAATAATTATTATCTGTTGTTTTACCAACTACTCAATTTCTCTTATAAGGGACT 1364
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Qy      1365 AAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTTT 1424
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Db      3425 AAATATGTAGTCATCCTAAGGCGCATAACCATTTATAAAAATCATCCTTCATTCTATTTT 3484

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Db      3485 ACCCTATCATCCTCTGCAAGACAGTCCTCCCTCAAACCCACAAGCCTTCTGTCCTCACAG 3544

Qy      1485 TCCCCTGGGCCATGG 1499
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Db      3545 TCCCCTGGGCCATGG 3559
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RESULT 14
US-09-301-593-27
; Sequence 27, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890001
;  CURRENT APPLICATION NUMBER: US/09/301,593A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107925.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/086,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 8068
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-301-593-27

  Query Match             35.6%;  Score 698;  DB 4;  Length 8068;
  Best Local Similarity   76.5%;  Pred. No. 6.4e-172;
  Matches  992;  Conservative    0;  Mismatches   75;  Indels  229;  Gaps    2;
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Qy         7 CCACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCT 66
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Db      1594 CCACCATGGATTCACAGGCCCAGGTTCTTATGTTACTGCCGCTATGGGTATCTGGTACCT 1653

Qy        67 GTGGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGG 126
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Db      1654 GTGGGGACATTGTGATGTCACAGTCTCCATCCTCCCTAGCTGTGTCAGTTGGAGAGAAGG 1713

Qy       127 CCACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACT 186
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Db      1714 TTACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATTCTAGAAATCAAAAGAACTACT 1773

Qy       187 TGGCTTGGTACCAGCAGAAACCAGGGCAGCCTCCTAAACTGCTGATCTACTGGGCATCCA 246
             |||| |||| ||||||||| ||||||||| |||||||||||||||| | ||||||||||
Db      1774 TGGCCTGGTTCCAGCAGAAGCCAGGGCAGTCTCCTAAACTGCTGATTTTCTGGGCATCCA 1833

Qy       247 CTAGGGAATCTGGGGTCCCTGATCGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTC 306
             |||||||||||||||||||||||||||||  |||||||||| |||||| ||||||| ||
Db      1834 CTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATTTGGGACGGATTTCAATC 1893

Qy       307 TCACCATCAGCAGTCTGCAGGCTGAAGACGTGGCAGTTTATTACTGCAGCCAATCTTATA 366
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Db      1894 TCACCATCAGCAGTGTGCAGGCTGAGGACCTGGCAGTTTATGACTGTCAGCAATATTTTA 1953

Qy       367 ---ATCTTTACACGTTCGGACAGGGGACCAAGGTGGAAATAAAACGTAAGTAGTCTTCTC 423
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Db      1954 GCTATCCGCTCACGTTCGGTGCTGGGACCAAGCTGGAGCTGAAACGTGAGTGG------- 2006

Qy       424 AACTCTAGAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGC 483
Db      2007 ---------------------------------------------------------- 2006

Qy       484 ATTGAGTTTACTGCAAGGTCAGAAAAGCATGCAAAGCCCTCAGAATGGCTGCAAAGAGCT 543
Db      2007 ---------------------------------------------------------- 2006

Qy       544 CCAACAAAACAATTTAGAACTTTATTAAGGAATAGGGGGAAGCTAGGAAGAAACTCAAAA 603
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Db      2007 ----------------------------------------ATCCATCTGGGATAAGCATGC 2027

Qy       664 TGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCA 723
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Qy       784 ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT 843
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Qy       844 GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGC 903
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Qy       904 CCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA 963
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Db      2268 CCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA 2327

Qy       964 CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGC 1023
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Qy      1024 CTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGA 1083
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Qy      1084 GTGTTAGAGGGAGAAGTGCCCCCACCTGCTCCTCAGTTCCAGCCTGACCCCCTCCCATCC 1143
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Db       2508 TTTGGCCTCTGACCCTTTTTCCACAGGGGACCTACCCCTATTGCGGTCCTCCAGCTCATC 2567

Qy       1204 TTTCACCTCACCCCCCTCCTCCTCCTTGGCTTTAATTATGCTAATGTTGGAGGAGAATGA 1263
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Db       2628 ATAAATAAAGTGAATCTTTGCACCTGTGGTGGATCT 2663


RESULT 15
US-09-301-593-35
; Sequence 35, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
;  APPLICANT: Park, John E.
;  APPLICANT: Garin-Chesa, Pilar
;  APPLICANT: Bamberger, Uwe
;  APPLICANT: Leger, Olivier
;  APPLICANT: Saldanha, Jose W.
;  APPLICANT: Rettig, Wolfgang J.
;  TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
;  FILE REFERENCE: 0652.1890001
;  CURRENT APPLICATION NUMBER: US/09/301,593A
;  CURRENT FILING DATE: 1999-04-29
;  EARLIER APPLICATION NUMBER: EP 98107925.4
;  EARLIER FILING DATE: 1998-04-30
;  EARLIER APPLICATION NUMBER: US 60/086,049
;  EARLIER FILING DATE: 1998-05-18
;  NUMBER OF SEQ ID NOS: 108
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
;   LENGTH: 8068
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-301-593-35

  Query Match             34.1%;  Score 667.6;  DB 4;  Length 8068;
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  Matches  973;  Conservative    0;  Mismatches   94;  Indels  229;  Gaps    2;

Qy          7 CCACCATGGATTCACAGGCCCAGGTTCTTATATTGCTGCTGCTATGGGTATCTGGCACCT 66
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Db       1594 CCACCATGGAGACAGACACACTCCTGCTATGGGTGCTGCTGCTCTGGGTTCCAGGTTCCT 1653

Qy         67 GTGGGGACATTGTGCTGACACAGTCTCCAGATTCCCTGGCTGTAAGCTTAGGAGAGAGGG 126
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Db       1654 CCGGAGACATTGTGATGACCCAATCTCCAGACTCTTTGGCTGTGTCTCTAGGGGAGAGGG 1713

Qy        127 CCACTATTAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAGAGAACTACT 186
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Db       1714 CCACCATCAACTGCAAGTCCAGTCAGAGCCTTTTATATTCTAGAAATCAAAAGAACTACT 1773

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Db       1774 TGGCCTGGTATCAGCAGAAACCAGGACAGCCACCCAAACTCCTCATCTTTTGGGCTAGCA 1833

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Db       1954 GCTATCCGCTCACGTTCGGACAAGGGACCAAGGTGGAAATAAAACGTGAGTGG------- 2006

Qy        424 AACTCTAGAAATTCTAAACTCTGAGGGGGTCGGATGACGTGGCCATTCTTTGCCTAAAGC 483

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Qy        664 TGTTTTCTGTCTGTCCCTAACATGCCCTGTGATTATCCGCAAACAACACACCCAAGGGCA 723
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Qy        724 GAACTTTGTTACTTAAACACCATCCTGTTTGCTTCTTTCCTCAGGAACTGTGGCTGCACC 783
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Qy        844 GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGC 903
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Qy       1264 ATAAATAAAGTGAATCTTTGCACCTGTGGTTTCTCT 1299
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:46:48 ; Search time 6294.87 Seconds
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Title: US-09-627-896B-23
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Scoring table: IDENTITY_NUC
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Searched: 2054640 seqs, 14551402878 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1787.6	79.5	2009	9	HUMIGCD1	J00230 Human Ig ge
4	1765.2	78.5	56310	2	AC084717	AC084717 Homo sapi
5	1752.8	77.9	2193	9	AF237584	AF237584 Homo sapi
6	1651.6	73.4	2287	6	AR029004	AR029004 Sequence
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16	1610.8	71.6	2029	6	AR035227	AR035227 Sequence
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19	1584.6	70.5	2482	6	AR100741	AR100741 Sequence
20	1584.6	70.5	2482	6	AR125611	AR125611 Sequence
21	1584.6	70.5	2482	6	AR130196	AR130196 Sequence
22	1584.6	70.5	2482	6	AR184212	AR184212 Sequence
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24	1547.8	68.8	2252	9	HSIGHGP	X06766 Human immun
25	1547.2	68.8	2009	6	AX327474	AX327474 Sequence
26	1547.2	68.8	2009	6	E06998	E06998 DNA encodin
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28	1547.2	68.8	3133	6	I08115	I08115 Sequence 1
29	1545.6	68.7	2009	6	E10971	E10971 DNA sequenc
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33	1465.8	65.2	3108	6	E10974	E10974 Intron-incl
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35	1463.4	65.1	2071	6	E40080	E40080 Drug contai
36	1463.4	65.1	2071	6	E40888	E40888 Humanized a
37	1463.4	65.1	2071	6	E43434	E43434 Humanized a
38	1458.6	64.9	2077	6	E40055	E40055 Drug contai
39	1458.6	64.9	2077	6	E40863	E40863 Humanized a
40	1458.6	64.9	2077	6	E43409	E43409 Humanized a
41	1455.4	64.7	2073	6	E40910	E40910 Humanized a
42	1455.4	64.7	2073	6	E40911	E40911 Humanized a
43	1455.4	64.7	2077	6	E43441	E43441 Humanized a
44	1453.8	64.6	2073	6	E40912	E40912 Humanized a
45	1438.6	64.0	3282	6	AR038306	AR038306 Sequence

ALIGNMENTS

RESULT 1
AR035228
LOCUS AR035228 2560 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 44 from patent US 5871732.
ACCESSION AR035228
VERSION AR035228.1 GI:5951896
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2560)
AUTHORS Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.
TITLE Anti-CD4 antibody homologs useful in prophylaxis and treatment of AIDS, ARC and HIV infection
JOURNAL Patent: US 5871732-A 44 16-FEB-1999;

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FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      544 a    848 c    720 g    448 t
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  Query Match             80.2%;  Score 1804;  DB 6;  Length 2560;
  Best Local Similarity   89.2%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches  185;  Indels   64;  Gaps    7;

Qy          8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
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Db          8 CACCATGGACTGGACCTGGAGGGTCTTCTGCTTGCTGGCTGTAGCACCAGGTGCCCACTC 67

Qy         68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
              |||||||||  |||  | |||||||  |||||  |||||  |||||||||    ||||||||||
Db         68 CCAGGTCCAACTGCAGGAGTCTGGAGCTGAAGTGAAAAAGCCTGGGGCTTCAGTGAAGGT 127

Qy        128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
              ||||||||  |||||  ||  ||||||||||    ||||  ||||||  ||||||||  |||||
Db        128 GTCCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATACACTGGGTGAGGCAGGC 187

Qy        188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
               |||||  ||||||||  ||||||||||||   |||||||  ||||  |||||  |||  ||||
Db        188 GCCTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTGACTA 247

Qy        248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 307
              | |   |||||||  ||  ||||||||||||  |||||   ||  ||  |  |||||||||
Db        248 CGATGAGAAGTTCAAAGGCAAGGCCACAGTGACTTTAGACCCATCCACCAACACAGCCTA 307

Qy        308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAG---- 363
               |||||  ||  ||      ||||  ||||||||  ||  ||  ||  ||||||||||||||
Db        308 CATGGAGCTCAGCAGCCTGAGGTCTGAGGACACTGCGGTCTATTACTGTGCAAGAGAGAA 367

Qy        364 --------------CGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGT 409
                           |||     |   | |  ||||||||  |||||  |||||  ||||||||
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Qy        410 CTCCTCAGGTGAGTCCTTAAA----------------------------------ACCT 434
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Db        428 CTCCTCAGGTGAGTCCTAAGCTTGGTACCCGGGAATTCAGATCTGCAGCATGCTCGAGCT 487

Qy        435 CTAG-----AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
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Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
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Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              |||||||| ||||||  ||| ||||||||||||||||||||||||||||||||||||||||
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Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
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Db        667 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCC 726

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
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Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        787 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 846

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
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Db        847 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 906

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
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Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
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Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
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Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
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Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||| ||
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Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||||| |||||||||||||||||||| | || ||| ||||||||||  |||||||||
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Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
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Qy       1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
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Qy       1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
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Qy       1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
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Qy       1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
              |||||||||||||||||||||||||||||||||||||||||||||  || ||||||||||||||
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Qy       1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866
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Db       1865 TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACACGGACAGAGGCCAGCTC 1924

Qy       1867 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
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Db       1985 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC 2044
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Qy       1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
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Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
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Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
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Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
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Db       2225 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTG 2284

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RESULT 2
HSA250170

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LOCUS       HSA250170              2010 bp    DNA     linear   PRI 22-NOV-2001
DEFINITION  Homo sapiens partial IgG2 gene for immunoglobulin heavy chain
            constant region IgG2, exons 1-4.
ACCESSION   AJ250170
VERSION     AJ250170.1  GI:10799663
KEYWORDS    constant region; IgG2 gene; immunoglobulin; immunoglobulin heavy
            chain.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ellison,J. and Hood,L.
  TITLE     Linkage and sequence homology of two human immunoglobulin gamma
            heavy chain constant region genes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
  MEDLINE   82197621
   PUBMED   6804948
REFERENCE   2
  AUTHORS   Hougs,L., Svejgaard,A. and Barington,T.
  TITLE     The first constant-domain (CH1) exon of human IGHG2 is polymorphic
            and in strong linkage disequilibrium with the CH2 exon polymorphism
            encoding the G2m(n+) allotype in Caucasians
  JOURNAL   Immunogenetics 52 (3-4), 242-248 (2001)
  MEDLINE   21115140
   PUBMED   11220626
REFERENCE   3  (bases 1 to 2010)
  AUTHORS   Hougs,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1999) Hougs L., Dept. of Clinical Immunology,
            sect. 7631, National University Hospital, Rigshospitalet, Tagensvej
            20, DK-2200 Copenhagen N., DENMARK
COMMENT     Related sequences Z49801 and Z49802.
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     source          1. .2010
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BASE COUNT      413 a    702 c    566 g    329 t
ORIGIN
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Query Match 79.7%; Score 1793.2; DB 9; Length 2010;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1798; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy        439 AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGA 498
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Qy        499 GGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGC 558
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Db         61 GGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGC 120

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Db        121 CTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 180

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Qy        679 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGG 738
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Qy        739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 798
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Db        301 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 360

Qy        799 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 858
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Qy       859 TGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC 918
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Qy       919 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGT 978
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Qy       979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 1038
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Qy      1039 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 1098
Db       601 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 660

Qy      1099 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 1158
Db       661 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 720

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Db       841 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC 900

Qy      1339 AGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCC 1398
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Qy      1399 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1458
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Qy      1519 TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA 1578
Db      1081 TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA 1140

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RESULT 3
HUMIGCD1

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DEFINITION  Human Ig germline H-chain G-E-A region B: gamma-2 constant region,
            3' end.
ACCESSION   J00230 V00554
VERSION     J00230.1  GI:184750
KEYWORDS    .
SEGMENT     1 of 7
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 896 to 1256; 1749 to 1937)
  AUTHORS   Krawinkel,U. and Rabbitts,T.H.
  TITLE     Comparison of the hinge-coding segments in human immunoglobulin
            gamma heavy chain genes and the linkage of the gamma 2 and gamma 4
            subclass genes
  JOURNAL   EMBO J. 1 (4), 403-407 (1982)
  MEDLINE   84235992
   PUBMED   6329676
REFERENCE   2  (bases 1 to 2009)
  AUTHORS   Ellison,J. and Hood,L.
  TITLE     Linkage and sequence homology of two human immunoglobulin gamma
            heavy chain constant region genes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
  MEDLINE   82197621
   PUBMED   6804948
REFERENCE   3  (bases 475 to 1071; 1179 to 1330; 1461 to 1524)
  AUTHORS   Takahashi,N., Ueda,S., Obata,M., Nikaido,T., Nakai,S. and Honjo,T.
  TITLE     Structure of human immunoglobulin gamma genes: implications for
            evolution of a gene family
  JOURNAL   Cell 29 (2), 671-679 (1982)
  MEDLINE   83001943
   PUBMED   6811139
COMMENT     On Mar 2, 2000 this sequence version replaced gi:32759.
            [2] also reports sequences for gamma-3, gamma-4, and a gamma
            pseudogene. Most of this sequence is 95% homologous with gamma-4.
            The hinge exons are only 70% homologous. The authors estimate that
            gamma-2 and gamma-4 diverged 6.6 million years ago. The authors in
            [1] speculate that intron-mediated domain transfer played an
            important role in the evolution of human gamma genes. They also
            report the hinge regions of gamma-1, gamma-3, gamma-4, and a
            pseudo-gamma gene. [1] estimates the divergence of the human gamma
            genes to be between 7.7 and 4.4 million years ago. This entry is
            part of a multigene region containing the gamma-2, gamma-4,
            epsilon-1, and alpha-2 genes. The relative locations of the four
            genes were determined by Flanagan and Rabbitts (Nature 300, 709-713
```

(1982)"). They refer to this gene group as region B. The region A genes are gamma-3, gamma-1, pseudo-epsilon, alpha-1. Flanagan and Rabbits also determined the general locations of the two regions. They place region A between the JH/mu/delta region and region B.
Complete source information:
Human fetal liver DNA, library of T. Maniatis [3] and Lawn et al [2],[1]; clones p-gamma-2RPA3 [2], 5A [3], and Ig-gamma-2-15 [1].

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1801; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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RESULT 4
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DEFINITION  Homo sapiens clone RP11-815P21, WORKING DRAFT SEQUENCE, 3 unordered
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ACCESSION   AC084717
VERSION     AC084717.2  GI:12229387
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SOURCE      Homo sapiens.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 56310)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-815P21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 56310)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L.,
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  TITLE     Direct Submission
  JOURNAL   Submitted (08-NOV-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jan 15, 2001 this sequence version replaced gi:11120856.
            All repeats were identified using RepeatMasker:
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            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L11499
                Center clone name: 815_P_21
            -------------- Summary Statistics
                Sequencing vector: Plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
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                Consensus quality: 56050 bases at least Q20
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                Insert size: 56110; sum-of-contigs
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                Quality coverage: 8.6 in Q20 bases; sum-of-contigs
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 3 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
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Qy       1939 GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC 1998
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Qy       2179 ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAA 2238
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RESULT 5
AF237584
LOCUS AF237584 2193 bp DNA linear PRI 14-MAY-2001
DEFINITION Homo sapiens recombinant IgG2 heavy chain gene, partial cds.
ACCESSION AF237584
VERSION AF237584.1 GI:9857754
KEYWORDS .
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2193)
AUTHORS Vidarsson,G., van der Pol,W.L., van den Elsen,J.M.H., Vile,H., Jansen,M., Duijs,J., Morton,H.C., Boel,E., Daha,M.R., Corthesy,B. and van de Winkel,J.G.J.
TITLE Activity of human IgG and IgA subclasses in immune defense against Neisseria meningitidis serogroup B
JOURNAL J. Immunol. 166 (10), 6250-6256 (2001)
MEDLINE 21240692
PUBMED 11342648
REFERENCE 2 (bases 1 to 2193)
AUTHORS Vidarsson,G., Jansen,M., Boel,E. and van de Winkel,J.G.J.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Department of Immunology, University Medical Center Utrecht, Rm. KC.02-085.2, Lundlaan 6, Utrecht 3584 EA, The Netherlands
FEATURES Location/Qualifiers
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BASE COUNT 468 a 740 c 589 g 389 t 7 others
ORIGIN

Query Match 77.9%; Score 1752.8; DB 9; Length 2193;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 1954; Conservative 7; Mismatches 109; Indels 120; Gaps 2;

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Db          2 AGGTSMARCTGCAGSAGTCWGGGACTGTGCTGGCAAGGCCTGGGGCTTCCGTGAGGATGT 61

Qy        130 CCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGCTC 189
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Qy        190 CTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTACA 249
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Db        122 CTGGACAGGGTCTAGAATGGATTGGTGGTATTTATCCTGGAAATCGTGATACTAGGTACA 181

Qy        250 ACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTATA 309
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Db        182 CCCAGAGGTTTAAGGACAAGGCCAAACTGACTGCAGTCACATCCGCCAACACTGCCTACA 241

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Db        373 ----------------------------------------------------------GGCC 376

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Db        377 GCGAGCCCAGACACTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCT 436

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DEFINITION  Sequence 1 from patent US 5858983.
ACCESSION   AR029004
VERSION     AR029004.1  GI:5940977
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2287)
  AUTHORS   Seed,B. and Walz,G.
  TITLE     Inhibition of cell adhesion protein-carbohydrate interactions
  JOURNAL   Patent: US 5858983-A 1 12-JAN-1999;
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Best Local Similarity 87.2%; Pred. No. 3e-311;
Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14;

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Qy        63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
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Qy       123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
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Qy       243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302
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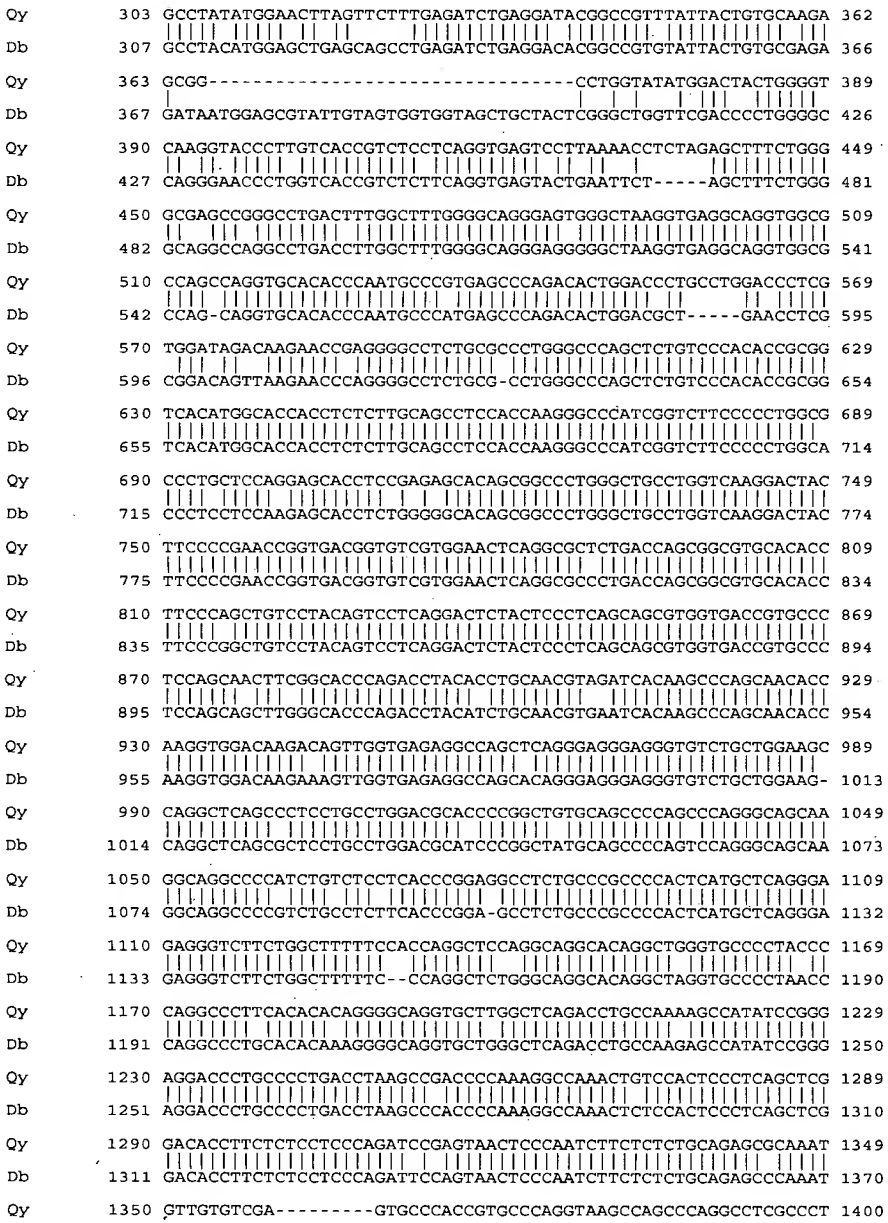

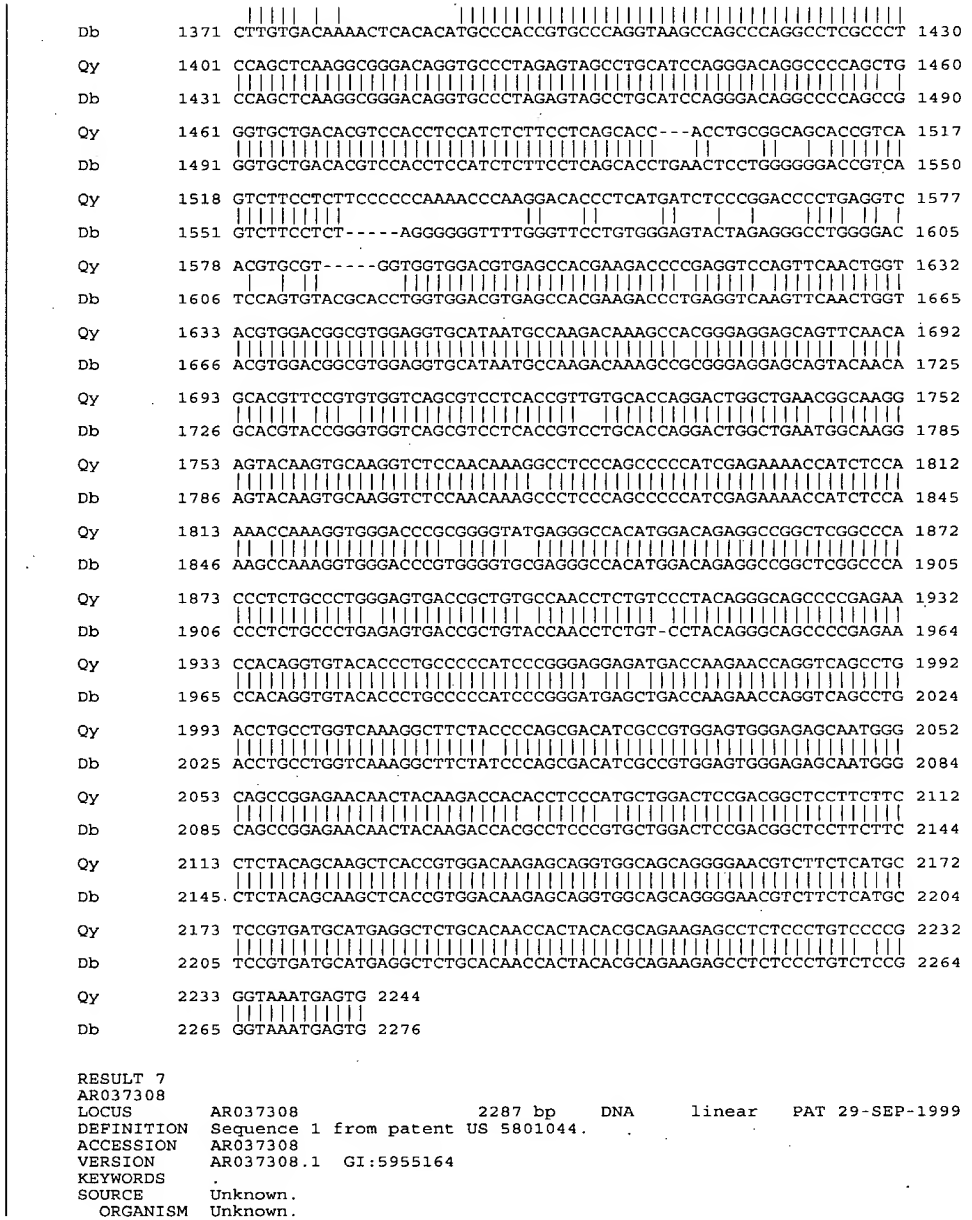

RESULT 7
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DEFINITION Sequence 1 from patent US 5801044.
ACCESSION AR037308
VERSION AR037308.1 GI:5955164
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

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          Unclassified.
REFERENCE   1  (bases 1 to 2287)
  AUTHORS   Seed,B. and Walz,G.
  TITLE     Nucleic acid encoding an antibody that inhibits cell adhesion
            protein-carbohydrate interactions
  JOURNAL   Patent: US 5801044-A 1 01-SEP-1998;
FEATURES             Location/Qualifiers
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              |||| |||||||||||||||||| |||||||||||||||||| ||      || |||||
Db        542 CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT-----GAACCTCG 595

Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
              ||| ||  ||||||| |||||||||||| ||||||||||||||||||||||||||||||
Db        596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCACACCGCGG 654

Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714

Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
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Db        715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy        750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Qy        810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
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Db        835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy        870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
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Db        895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy        930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC 989
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Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049
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Qy       1050 GGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109
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Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169
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Db       1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190

Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
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Db       1191 CAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG 1250

Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
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Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
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Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
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Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
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Db       1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy       1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGTCA 1517
              |||||||||||||||||||||||||||||||||||||||||||||||||||   ||  | |||||||
Db       1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA 1550

Qy       1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577
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Qy       1578 ACGTGCGT-----GGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT 1632
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Db       1606 TCCAGTGTACGCACCTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 1665

Qy       1633 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACA 1692
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Qy       1693 GCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG 1752
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Db       1726 GCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 1785

Qy       1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1812
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Db       1786 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1845

Qy       1813 AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1872
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Db       1846 AAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1905

Qy       1873 CCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA 1932
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Qy       1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG 1992
              ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
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Qy       1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2052
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Db       2025 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084

Qy       2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112
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Db       2085 CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC 2144

Qy       2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
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Qy       2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG 2232
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Db       2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG 2264

Qy       2233 GGTAAATGAGTG 2244
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Db       2265 GGTAAATGAGTG 2276


RESULT 8
BD000539
LOCUS       BD000539               2287 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Antibody capable of being used for inhibition of interaction
            between cell  adhesion protein and sugar ligand.
ACCESSION   BD000539
VERSION     BD000539.1  GI:18623652
KEYWORDS    JP 2000325092-A/1.
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2287)
  AUTHORS   Brian,S. and Gard,W.
  TITLE     Antibody capable of being used for inhibition of interaction
            between cell adhesion protein and sugar ligand
  JOURNAL   Patent: JP 2000325092-A 1 28-NOV-2000;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Unidentified
            PN   JP 2000325092-A/1
            PD   28-NOV-2000
            PF   04-APR-2000 JP 2000102880
            PR   23-NOV-1990 US    07/618314
            PI   SHEED BRIAN,WARTZ GARD
            PC   C12N15/09,A61K39/395,A61P9/10,A61P17/06,A61P29/00,A61P29/00,
            PC   A61P43/00,
            PC   C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/10,G01N33/53, PC
            C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .2287
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .2287
                     /organism="unidentified"
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BASE COUNT      478 a    739 c    667 g    403 t
ORIGIN

  Query Match           73.4%;  Score 1651.6;  DB 6;  Length 2287;
  Best Local Similarity   87.2%;  Pred. No. 3e-311;
  Matches 1998;  Conservative    0;  Mismatches  219;  Indels   75;  Gaps   14;

Qy          6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACAGCTACAGGTGTG 62
              |||||||||| |||| ||| |   || |||||||| |||| |  ||||||||||||||
Db          7 ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTGTGGTGGCAGCAGCTACAGGTGTC 66

Qy         63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
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Db         67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG 126

Qy        123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
              ||||| |||||||| ||||| ||   ||| ||||     ||||||||     |||||| ||
Db        127 AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy        183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
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Db        187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCA 246

Qy        243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302
              ||||||   |||||||| ||||||  | ||| || || |  ||| | || |||||||||
Db        247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA 306

Qy        303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA 362
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Db        307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 366

Qy        363 GCGG--------------------------------CCTGGTATATGGACTACTGGGGT 389
              |                                  | | |  | |||  ||||||
Db        367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGC 426

Qy        390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
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Db        427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT-----AGCTTTCTGGG 481

Qy        450 GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
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Db        482 GCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 541

Qy        510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGCCTGGACCCTCG 569
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Db        542 CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT----GAACCTCG 595

Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
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Db        596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCACACCGCGG 654

Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
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Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714

Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
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Db        715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy        750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy        810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
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Db        835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy        870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTGAGATCACAAGCCCAGCAACACC 929
              ||||||| ||| |||||||||||||||| |||||||||  ||||||||||||||||||||
Db        895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy        930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC 989
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Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049
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Db       1014 CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAA 1073

Qy       1050 GGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCCACTCATGCTCAGGGA 1109
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Db       1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA 1132
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Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169
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Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
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Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
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Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
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Db       1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370

Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
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Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
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Qy       1633 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACA 1692
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Db       1666 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 1725

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Qy       1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1812
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Db       1846 AAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1905

Qy       1873 CCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA 1932
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Db       1906 CCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAA 1964

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Db       2025 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084

Qy       2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112
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Qy       2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
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Db       2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2204

Qy       2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG 2232
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Db       2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG 2264

Qy       2233 GGTAAATGAGTG 2244
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Db       2265 GGTAAATGAGTG 2276
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RESULT 9
I90051
LOCUS I90051 2287 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 1 from patent US 5723583.
ACCESSION I90051
VERSION I90051.1 GI:3409991
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Seed,B. and Walz,G.
TITLE Antibody containing sialyl lewis X determinants
JOURNAL Patent: US 5723583-A 1 03-MAR-1998;
FEATURES Location/Qualifiers
source 1. .2287
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BASE COUNT 478 a 739 c 667 g 403 t
ORIGIN

Query Match 73.4%; Score 1651.6; DB 6; Length 2287;
Best Local Similarity 87.2%; Pred. No. 3e-311;
Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14;

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Qy         63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
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Qy        123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
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Qy        183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
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Qy        363 GCGG--------------------------------CCTGGTATATGGACTACTGGGGT 389
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Qy        390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
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Qy        450 GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
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Qy        510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGCCTGGACCCTCG 569
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Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
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Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714
Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
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Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049
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Qy       1578 ACGTGCGT-----GGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT 1632
Db       1606 TCCAGTGTACGCACCTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 1665
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Db       1846 AAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1905
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Qy       1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG 1992
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Qy       1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2052
Db       2025 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084
Qy       2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112
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DEFINITION  Sequence 41 from Patent WO0114424.
ACCESSION   AX088865
VERSION     AX088865.1  GI:13397636
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
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REFERENCE   1  (bases 1 to 4694)
  AUTHORS   Korman,A.J., Halk,E.L. and Lonberg,N.
  TITLE     Human ctla-4 antibodies and their uses
  JOURNAL   Patent: WO 0114424-A 41 01-MAR-2001;
            MEDAREX, INC. (US)
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Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
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Qy       550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
Db       127 GGACCCTGCATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 186

Qy       610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
Db       187 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCC 246

Qy       670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
Db       247 CATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGG 306

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Qy       790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
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Qy      1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
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Qy      1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
Db      1147 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCA 1206

Qy      1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
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Qy      1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866
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Qy      2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
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Qy      2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
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DEFINITION  Sequence 3 from Patent WO0243478.
ACCESSION   AX478055
VERSION     AX478055.1  GI:22217037
KEYWORDS    .
SOURCE      synthetic construct.
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            artificial sequences.
REFERENCE   1
  AUTHORS   Tomizuka,K., Ishida,I., Lonberg,N. and Halk,E.
  TITLE     Transgenic transchromosomal rodents for making human antibodies
  JOURNAL   Patent: WO 0243478-A 3 06-JUN-2002;
            Medarex, Inc. (US) ; KIRIN BEER KABUSHIKI KAISHA (JP)
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ORIGIN

  Query Match             72.8%;  Score 1638;  DB 6;  Length 4694;
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 Matches 1719;  Conservative    0;  Mismatches   95;  Indels    4;  Gaps    2;

Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
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Db        187 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCC 246

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
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Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
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Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
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Db       1507 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC 1566

Qy       1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
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Db       1567 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 1626

Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
              |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db       1627 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 1686

Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
              |||||||||||||||| ||| ||||||||||||||||||||||| ||||||| ||||||
Db       1687 TTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 1746

Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
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Qy       2227 TCCCCGGGTAAATGAGTG 2244
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Db       1807 TCTCTGGGTAAATGAGTG 1824
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RESULT 12
HUMIGCD2
LOCUS       HUMIGCD2                2028 bp    DNA     linear   PRI 11-APR-2001
DEFINITION  Human Ig germline H-chain G-E-A region B: gamma-4 constant region,
            3' end.
ACCESSION   K01316
VERSION     K01316.1  GI:184751
KEYWORDS    .
SEGMENT     2 of 7
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2028)
  AUTHORS   Ellison,J., Buxbaum,J. and Hood,L.
  TITLE     Nucleotide sequence of a human immunoglobulin C gamma 4 gene
  JOURNAL   DNA 1 (1), 11-18 (1981)
  MEDLINE   83157104
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   PUBMED   6299662
REFERENCE   2  (bases 894 to 1106)
  AUTHORS   Krawinkel,U. and Rabbitts,T.H.
  TITLE     Comparison of the hinge-coding segments in human immunoglobulin
            gamma heavy chain genes and the linkage of the gamma 2 and gamma 4
            subclass genes
  JOURNAL   EMBO J. 1 (4), 403-407 (1982)
  MEDLINE   84235992
   PUBMED   6329676
REFERENCE   3  (bases 1 to 2028)
  AUTHORS   Ellison,J. and Hood,L.
  TITLE     Linkage and sequence homology of two human immunoglobulin gamma
            heavy chain constant region genes
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 79 (6), 1984-1988 (1982)
  MEDLINE   82197621
   PUBMED   6804948
REFERENCE   4  (bases 475 to 1069; 1180 to 1331; 1432 to 1655)
  AUTHORS   Takahashi,N., Ueda,S., Obata,M., Nikaido,T., Nakai,S. and Honjo,T.
  TITLE     Structure of human immunoglobulin gamma genes: implications for
            evolution of a gene family
  JOURNAL   Cell 29 (2), 671-679 (1982)
  MEDLINE   83001943
   PUBMED   6811139
COMMENT     [1] reports that the human C-gamma-4 gene is equally homologous to
            the mouse gamma-1, gamma-2a, and gamma-2b genes (about 75%). [3]
            also reports partial sequences for human gamma-2, gamma-3, and a
            gamma pseudogene. [2] presents the gamma-1, gamma-2, gamma-3, and
            pseudo-gamma hinge regions.
            This entry is part of a multigene region (region B), which includes
            the gamma-2, gamma-4, epsilon-1, and alpha-2 genes. See segment 1
            for more comments.
            Complete source information:
            Human fetal liver DNA, library of T. Maniatis [3] and Lawn et al
            [1],[2]; clones 24B [1], lambda-HG4.1 [3], and Ig-gamma-4-2 [2].
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  Best Local Similarity  94.7%;  Pred. No. 9.9e-304;
  Matches 1713;  Conservative    0;  Mismatches   90;  Indels    6;  Gaps    4;

Qy        439 AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGA 498
              ||||||||||||  |||||||||||||||||| | |||||||||| ||||||||||||
Db          1 AGCTTTCTGGGGCAGGCCGGGCCTGACTTTGGC-TGGGGGCAGGGAGGGGGCTAAGGTGA 59

Qy        499 GGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGC 558
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Db         60 CGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACCCTGC 119

Qy        559 CTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 618
              |||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 ATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 179

Qy        619 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 678
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Db        180 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCCCATCCGTCT 239

Qy        679 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGG 738
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        240 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGG 299

Qy        739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 798
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Db        300 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG 359

Qy        799 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 858
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Db        360 GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 419

Qy        859 TGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC 918
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Db        420 TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGC 479

Qy        919 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGT 978
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Db        480 CCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGT 539

Qy        979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 1038
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Qy       1039 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 1098
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Qy       1099 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 1158
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Db        660 ATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCCGGCA-CCACAGGCTGGA 718

Qy       1159 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAG 1218
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Db        719 TGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAGAG 777

Qy       1219 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACT 1278
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Db        778 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACT 837

Qy       1279 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC 1338
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Db        838 CCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTGC 897

Qy       1339 AGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCC 1398
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Db        898 AGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCAGGCCTCGCC 957

Qy       1399 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1458
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Db        958 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1017

Qy       1459 TGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGT 1515

Db       1018 CGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGGGGGGACCAT 1077

Qy       1516 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 1575

Db       1078 CAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGG 1137

Qy       1576 TCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACG 1635

Db       1138 TCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACG 1197

Qy       1636 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCA 1695

Db       1198 TGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCA 1257

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Db       1318 ACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAG 1377

Qy       1816 CCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCC 1875

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Db       1438 TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAGCCA 1497

Qy       1936 CAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACC 1995

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Qy       2056 CCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTC 2115

Db       1618 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1677

Qy       2116 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 2175

Db       1678 TACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCC 1737

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Qy       2236 AAATGAGTG 2244

Db       1798 AAATGAGTG 1806
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RESULT 13
AR161379
LOCUS AR161379 4723 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 370 from patent US 6255458.
ACCESSION AR161379
VERSION AR161379.1 GI:16227241
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 4723)
AUTHORS Lonberg,N. and Kay,R.M.
TITLE High affinity human antibodies and human antibodies against digoxin
JOURNAL Patent: US 6255458-A 370 03-JUL-2001;

FEATURES Location/Qualifiers
source 1. .4723
/organism="unknown"
BASE COUNT 1072 a 1411 c 1253 g 987 t
ORIGIN

Query Match 71.7%; Score 1611.8; DB 6; Length 4723;
Best Local Similarity 94.3%; Pred. No. 1.5e-303;
Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4;

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Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609

Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669

Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729

Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789

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Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909

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Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
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Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
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Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
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Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
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Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
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Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828


RESULT 14
AX088864
LOCUS       AX088864               4723 bp    DNA     linear   PAT 17-MAR-2001
DEFINITION  Sequence 40 from Patent WO0114424.
ACCESSION   AX088864
VERSION     AX088864.1  GI:13397635
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4723)
  AUTHORS   Korman,A.J., Halk,E.L. and Lonberg,N.
  TITLE     Human ctla-4 antibodies and their uses
  JOURNAL   Patent: WO 0114424-A 40 01-MAR-2001;
            MEDAREX, INC. (US)
FEATURES             Location/Qualifiers
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BASE COUNT     1072 a   1411 c   1253 g    987 t
ORIGIN

  Query Match             71.7%;  Score 1611.8;  DB 6;  Length 4723;
  Best Local Similarity   94.3%;  Pred. No. 1.5e-303;
  Matches 1722;  Conservative    0;  Mismatches   87;  Indels   18;  Gaps    4;

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Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
AX478054
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DEFINITION  Sequence 2 from Patent WO0243478.
ACCESSION   AX478054
VERSION     AX478054.1  GI:22217036
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tomizuka,K., Ishida,I., Lonberg,N. and Halk,E.
  TITLE     Transgenic transchromosomal rodents for making human antibodies
  JOURNAL   Patent: WO 0243478-A 2 06-JUN-2002;
            Medarex, Inc. (US) ; KIRIN BEER KABUSHIKI KAISHA (JP)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Gamma1 heavy chain plasmid-pCG7-96"
BASE COUNT     1072 a   1411 c   1253 g    987 t
ORIGIN

  Query Match             71.7%;  Score 1611.8;  DB 6;  Length 4723;
  Best Local Similarity   94.3%;  Pred. No. 1.5e-303;
  Matches 1722;  Conservative    0;  Mismatches   87;  Indels   18;  Gaps    4;

Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              | |  ||  |||||||||||||  ||| |||||||| ||||||||||||||||||| |||
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
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Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
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Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||||||||||||||||| |||| ||||| ||||||||| | | ||||||||||||||||
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
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Job time : 6302.87 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:16:54 ; Search time 3897.3 Seconds
(without alignments)
9345.860 Million cell updates/sec

Title: US-09-627-896B-23
Perfect score: 2249
Sequence: 1 tctagaccaccatgggttgg.....ccgggtaaatgagtgaattc 2249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	504.2	22.4	871	12	BG753979	BG753979 602709506
6	504.2	22.4	965	12	BG754808	BG754808 602714385
7	504.2	22.4	983	14	BQ708975	BQ708975 AGENCOURT
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c 34	482.8	21.5	1074	12	BG745803	BG745803 602723944
35	480.8	21.4	958	14	BQ706140	BQ706140 AGENCOURT
36	480.6	21.4	1014	14	BM914505	BM914505 AGENCOURT
c 37	480.2	21.4	815	12	BG745709	BG745709 602723815
c 38	478.8	21.3	781	14	BM674851	BM674851 UI-E-EJ0-
39	478	21.3	925	14	BQ709853	BQ709853 AGENCOURT
c 40	474	21.1	1034	12	BG745946	BG745946 602724146
41	473.4	21.0	817	12	BG678806	BG678806 602624701
c 42	473	21.0	894	12	BG745916	BG745916 602724102
c 43	470.8	20.9	764	14	BQ009025	BQ009025 UI-H-EI0-
44	468.2	20.8	987	14	BQ881933	BQ881933 AGENCOURT
45	468.2	20.8	1020	14	BQ062878	BQ062878 AGENCOURT

ALIGNMENTS

RESULT 1
BI768933
LOCUS BI768933 856 bp mRNA linear EST 25-SEP-2001
DEFINITION 603058055F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5207605 5', mRNA sequence.
ACCESSION BI768933
VERSION BI768933.1 GI:15760511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11520 row: m column: 14
High quality sequence stop: 797.
FEATURES Location/Qualifiers
source 1. .856

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                 /organism="Homo sapiens"
                 /db_xref="taxon:9606"
                 /clone="IMAGE:5207605"
                 /clone_lib="NIH_MGC_122"
                 /lab_host="DH10B"
                 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
                 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
                 anonymous pool of 24 week female lung, 16 week female
                 spleen, and 20-22 week male spleens.  Library is oligo-dT
                 primed and directionally cloned (EcoRV site is destroyed
                 upon  cloning).  Average insert size 1.4 kb, insert size
                 range 1-3 kb. Library is normalized and enriched for
                 full-length clones and was  constructed by C. Gruber
                 (Invitrogen).  Research Genetics tracking  code 026. Note:
                 this is a NIH_MGC Library."
BASE COUNT      209 a    281 c    228 g    138 t
ORIGIN

  Query Match           23.7%;  Score 533;  DB 13;  Length 856;
  Best Local Similarity   85.8%;  Pred. No. 2e-118;
  Matches  646;  Conservative    0;  Mismatches   10;  Indels   97;  Gaps    1;

Qy       1486 CTTCCTCAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 1545
             | | | |||||||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db         92 CGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG 151

Qy       1546 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACG 1605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACG 211

Qy       1606 AAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 1665
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 AAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA 271

Qy       1666 CAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTG 1725
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 CAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTG 331

Qy       1726 TGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCC 1785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCC 391

Qy       1786 CAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGC 1845
             ||||||||||||||||||||||||||||||||
Db        392 CAGCCCCCATCGAGAAAACCATCTCCAAAACCAA---------------------------- 425

Qy       1846 CACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACC 1905

Db        426 ------------------------------------------------------------ 425

Qy       1906 TCTGTCCCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAG 1965
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 -----------AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAG 474

Qy       1966 GAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC 2025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 GAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGAC 534

Qy       2026 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCC 2085
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Db        535 ATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCC 594

Qy       2086 ATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 2145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 ATGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 654

Qy       2146 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC 2205
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Db        655 TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAAAACCACTAC 714

Qy       2206 ACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAA 2238
             |||||||||||||||||||||||| || ||  ||
Db        715 ACGCAGAAGAGCCTCTCCCTGTCTCCCGGGTAA 747
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RESULT 2
BG398446
LOCUS       BG398446                974 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602439729F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565862 5',
            mRNA sequence.
ACCESSION   BG398446
VERSION     BG398446.1  GI:13291894
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1283  row: j  column: 07
            High quality sequence stop: 801.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4565862"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      231 a    315 c    272 g    155 t      1 others
ORIGIN

  Query Match           23.6%;  Score 530.4;  DB 12;  Length 974;
  Best Local Similarity   83.0%;  Pred. No. 9.2e-118;
  Matches  722;  Conservative    0;  Mismatches   41;  Indels  107;  Gaps    6;

Qy       1371 GCCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAG 1430
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GCCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAG 61

Qy       1431 TAGCCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCC 1490
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         62 TAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCC 121

Qy       1491 TCAGCACC---ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 1547
             ||||||||   ||    ||  | ||||||||||||||||||||||||||||||||||||
Db        122 TCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC 181

Qy       1548 ACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAA 1607
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        182 ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA 241

Qy       1608 GACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 1667
             ||||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA 301
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Qy       1668 AAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTG 1727
             ||||| |||||||||||||| |||||||||| |||||||||||||||||||||||||  ||
Db        302 AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG 361

Qy       1728 CACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCA 1787
             |||||||||||||||| ||||||||||||||||||||||||||||||| |||||||
Db        362 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 421

Qy       1788 GCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCA 1847
             |||||||||||||||||||||||||| ||||
Db        422 GCCCCCATCGAGAAAACCATCTCCAAAGCCAA-------------------------- 453

Qy       1848 CATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTC 1907
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ------------------------------------------------------------ 453

Qy       1908 TGTCCCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGA 1967
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 ---------AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGA 504

Qy       1968 GATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACAT 2027
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 GCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACAT 564

Qy       2028 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCAT 2087
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT 624

Qy       2088 GCTGGACTCCGACGGCTCCTTCTT--CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGG 2145
             |||||||||||||||||||||||   |   ||||||||||||||||||||||||||||||
Db        625 GCTGGACTCCGACGGCTCCTTCTTTCCTCTTACAGCAAGCTCACCGTGGACAAGAGCAGG 684

Qy       2146 TGG--CAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT 2203
             |||        ||||||||||||||||||||||||||||||||||||||||||||||   |
Db        685 TGGGCAGCAGGGGGAACGTCTTCTCATGCTCCGTGATGCATGA-GCTCTGCACAAC--AT 741

Qy       2204 ACACGCAGAAGAGCCTCTCCCTGTCCCCGG 2233
             |||||||||||||    ||   || ||||
Db        742 ACACGCAGAAGAGCTCTCCCTGTTCTCCGG 771


RESULT 3
BG674795
LOCUS       BG674795                757 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602620925F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4746150 5',
            mRNA sequence.
ACCESSION   BG674795
VERSION     BG674795.1  GI:13906191
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10594  row: b  column: 07
            High quality sequence stop: 755.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4746150"
                     /clone_lib="NCI_CGAP_Skn3"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.5kb.  Library constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      187 a    248 c    203 g    118 t      1 others
ORIGIN

  Query Match             22.5%;  Score 506.4;  DB 12;  Length 757;
  Best Local Similarity   83.5%;  Pred. No. 5.5e-112;
  Matches  629;  Conservative    0;  Mismatches   27;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
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Db         68 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 127

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
             |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        128 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 187

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
             | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 247

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
             | |||||||||||||| |||||||||| |||||||||||||||||||||||  ||||||
Db        248 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 307

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
             |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||
Db        308 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 367

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
             |||||||||||||||||||||||| ||||
Db        368 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------- 395

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 ------------------------------------------------------------ 395

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 450

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        451 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 510

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||
Db        511 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 570

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db        571 GACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 630

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
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Db        631 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAANCACTACACGCAG 690

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
             |||||||||||||||||||||||||||||||||
Db        691 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 723


RESULT 4
BG756349
LOCUS       BG756349                990 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602713669F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853873 5',
            mRNA sequence.
ACCESSION   BG756349
VERSION     BG756349.1  GI:14067002
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KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1700  row: j  column: 18
            High quality sequence stop: 782.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      243 a    368 c    246 g    133 t
ORIGIN

  Query Match             22.5%;  Score 505.8;  DB 12;  Length 990;
  Best Local Similarity   83.5%;  Pred. No. 8.6e-112;
  Matches  629;  Conservative    0;  Mismatches   27;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
              || |   ||     || || ||||||||||||||||||||||||||||||||||| ||||
Db         35 CACCTGAACTCCTGGGAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGATACCC 94

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
              | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 TTATGATTTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 154

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        155 CCGAGGTCCAGTTCAAGTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 214

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
              | ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        215 CGCGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 274

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        275 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 334

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
              |||||||||||||||||||||||||
Db        335 CCATCGAGAAAACCATCTCCAAAACCAA---------------------------------- 362

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911
              |
Db        363 ------------------------------------------------------------ 362

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 -----AGGACAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 417

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
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Db        418 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 477

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
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Db        478 GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACAACTACAACACCACGCCTCCCATGCTG 537

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db        538 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 597

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
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Db        598 CAGGGGAACATCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCGCTTCACGCAG 657

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db        658 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 690


RESULT 5
BG753979
LOCUS       BG753979                871 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5',
            mRNA sequence.
ACCESSION   BG753979
VERSION     BG753979.1  GI:14064632
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 871)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1686  row: k  column: 02
            High quality sequence stop: 848.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4846201"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      220 a    284 c    231 g    136 t
ORIGIN

  Query Match             22.4%;  Score 504.2;  DB 12;  Length 871;
  Best Local Similarity   83.4%;  Pred. No. 2e-111;
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  Matches  628;  Conservative    0;  Mismatches   28;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
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Db         68 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 127

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
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Db        128 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 187

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
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Db        188 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 247

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
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Db        248 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 307

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
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Db        368 CCATCGAGAAAACCATCTCCAAAGCCAA---------------------------------- 395

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

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Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
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Db        396 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 450

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
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Db        451 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 510

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
             |||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Db        511 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 570

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db        571 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 630

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
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Db        631 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 690

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db        691 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 723


RESULT 6
BG754808
LOCUS       BG754808                965 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602714385F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854621 5',
            mRNA sequence.
ACCESSION   BG754808
VERSION     BG754808.1  GI:14065461
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 965)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1702  row: i  column: 22
            High quality sequence stop: 779.
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      229 a    361 c    247 g    127 t      1 others
ORIGIN

  Query Match           22.4%;  Score 504.2;  DB 12;  Length 965;
  Best Local Similarity   83.4%;  Pred. No. 2.1e-111;
  Matches  628;  Conservative    0;  Mismatches   28;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
             || |   ||    ||  | ||||||||||||||||||||||||||||||||||||||||||
Db          8 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 67

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
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Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
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Db        128 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 187

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
             | |||||||||||| |||||||||| |||||||||||||||||||||||||  ||||||
Db        188 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 247

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
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Db        308 CCATCGAGAAAACCATCTCCAAAGCCAA---------------------------------- 335

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

Db        336 ------------------------------------------------------------ 335

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
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Db        336 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 390

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
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Db        391 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 450

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Db        451 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 510
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Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db        511 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 570

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
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Db        571 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 630

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db        631 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 663


RESULT 7
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      251 a    306 c    265 g    161 t
ORIGIN

  Query Match             22.4%;  Score 504.2;  DB 14;  Length 983;
  Best Local Similarity   83.4%;  Pred. No. 2.1e-111;
  Matches  628;  Conservative    0;  Mismatches   28;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
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Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
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Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
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Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
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Db        355 CCATCGAGAAAACCATCTCCAAAGCCAA---------------------------------- 382

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911
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Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
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Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 8
BQ712021
LOCUS       BQ712021                941 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
            5', mRNA sequence.
ACCESSION   BQ712021
VERSION     BQ712021.1  GI:21850920
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474  row: c  column: 04
            High quality sequence stop: 638.
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                /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
BASE COUNT      239 a    301 c    236 g    145 t     20 others
ORIGIN

  Query Match            22.4%;  Score 503.2;  DB 14;  Length 941;
  Best Local Similarity  83.3%;  Pred. No. 3.6e-111;
  Matches  627;  Conservative    0;  Mismatches   29;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
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Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
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Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
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Db        409 ------------------------------------------------------------ 408

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
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Db        409 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 463

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
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Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
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Db        524 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 583

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 643

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
                |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        644 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACCACTACACGCAG 703

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
                |||||||||||||||| ||||||||||||||
Db        704 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 736


RESULT 9
BQ708562
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LOCUS       BQ708562                873 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7977052 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215953
            5', mRNA sequence.
ACCESSION   BQ708562
VERSION     BQ708562.1  GI:21847461
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 873)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2385  row: l  column: 02
            High quality sequence stop: 682.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      205 a    277 c    222 g    133 t     36 others
ORIGIN

  Query Match            22.3%;  Score 502.6;  DB 14;  Length 873;
  Best Local Similarity  83.3%;  Pred. No. 4.9e-111;
  Matches  627;  Conservative    0;  Mismatches   29;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
                || |   ||    ||  | ||||||||||||||||||||||||||||||||||||||||||
Db         22 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 81

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
                |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         82 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 141

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
                | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 201

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
                | |||||||||||| |||||||||| |||||||||||||||||||||||  ||||||
Db        202 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 261

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
                |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db        262 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 321

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
                |||||||||||||||||||||| ||||
Db        322 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------ 349

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911
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Db        350 ------------------------------------------------------------ 349

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||
Db        350 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 404

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        405 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 464

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Db        465 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 524

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 584

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        585 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAG 644

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db        645 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 677
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RESULT 10
BQ709152
LOCUS BQ709152 925 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245 5', mRNA sequence.
ACCESSION BQ709152
VERSION BQ709152.1 GI:21848051
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.
FEATURES Location/Qualifiers
source 1. .925
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/db_xref="taxon:9606"
/clone="IMAGE:6301245"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 230 a 292 c 225 g 144 t 34 others
ORIGIN

Query Match 22.3%; Score 502.6; DB 14; Length 925;
Best Local Similarity 83.3%; Pred. No. 5e-111;
Matches 627; Conservative 0; Mismatches 29; Indels 97; Gaps 1;

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Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
              || |   ||    ||  | ||||||||||||||||||||||||||||||||||||||||
Db          79 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 138

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         139 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 198

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
              | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         199 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 258

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
              | |||||||||||||| |||||||||| |||||||||||||||||||||||| ||||||
Db         259 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 318

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
              |||||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||
Db         319 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 378

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
              |||||||||||||||||||| ||||
Db         379 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------ 406

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

Db         407 ------------------------------------------------------------ 406

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||
Db         407 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 461

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         462 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 521

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Db         522 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 581

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         582 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 641

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         642 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAG 701

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
              ||||||||||||||| ||||||||||||||
Db         702 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 734
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RESULT 11
BQ709771
LOCUS BQ709771 947 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583 5', mRNA sequence.
ACCESSION BQ709771
VERSION BQ709771.1 GI:21848670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 947)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

```
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2466  row: m  column: 16
           High quality sequence start: 3
           High quality sequence stop: 675.
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      225 a    320 c    252 g    150 t
ORIGIN

  Query Match             22.3%;  Score 502.6;  DB 14;  Length 947;
  Best Local Similarity   83.3%;  Pred. No. 5.1e-111;
  Matches  627;  Conservative    0;  Mismatches   29;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
              || |   ||    ||  | ||||||||||||||||||||||||||||||||||||||||||
Db        228 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 287

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        288 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 347

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
              | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 407

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
              | |||||||||||| |||||||||| |||||||||||||||||||||||||  ||||||
Db        408 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 467

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
              |||||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||
Db        468 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 527

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
              |||||||||||||||||||| ||||
Db        528 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------ 555

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

Db        556 ------------------------------------------------------------ 555

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
                   ||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||
Db        556 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 610

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        611 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 670

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
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Db        671 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 730

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db        731 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 790

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        791 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACCACCACTACACGCAG 850

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
              |||||||||||||||||| ||||||||||||||
Db        851 AAGAGCCTCTCCCTGTCCTCGGGTAAATGAGTG 883


RESULT 12
BQ706204
LOCUS       BQ706204                973 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352308 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277592
            5', mRNA sequence.
ACCESSION   BQ706204
VERSION     BQ706204.1  GI:21845103
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 973)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464  row: d  column: 09
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      255 a    310 c    256 g    146 t      6 others
ORIGIN

  Query Match             22.3%;  Score 501.6;  DB 14;  Length 973;
  Best Local Similarity   83.1%;  Pred. No. 9e-111;
  Matches  626;  Conservative    0;  Mismatches   30;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
              || |   ||    ||  | ||||||||||||||||||||||||||||||||||||||||||
Db        139 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 198

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        199 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 258

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
              | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 318
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Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
             | ||||||||||||| |||||||||| |||||||||||||||||||||  ||||||
Db        319 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 378

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
             ||||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Db        379 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 438

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
             ||||||||||||||||||||| ||||
Db        439 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------ 466

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

Db        467 ------------------------------------------------------------ 466

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
                 |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||
Db        467 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 521

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        522 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 581

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
              |||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||
Db        582 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 641

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 701

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
              |||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        702 CAGGNGAACGTCTTCTCATGCTCCGTGATGCATGAAGCTCTGCACAACCACTACACGCAG 761

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
              |||||||||||||||| ||||||||||||||
Db        762 AAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 794
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RESULT 13
BQ709339

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LOCUS       BQ709339                 919 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976429 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214450
            5', mRNA sequence.
ACCESSION   BQ709339
VERSION     BQ709339.1  GI:21848238
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 919)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2381  row: m  column: 11
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      234 a    297 c    229 g    150 t      9 others
ORIGIN
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  Query Match             22.3%;  Score 501;  DB 14;  Length 919;
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  Matches  626;  Conservative    0;  Mismatches   30;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
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Db         88 CACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 147

Qy       1552 TCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACC 1611
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        148 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 207

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671
              | |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        208 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 267

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731
              | |||||||||||||| |||||||||| |||||||||||||||||||||  ||||||
Db        268 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 327

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
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Db        328 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 387

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851
              ||||||||||||||||||||| ||||
Db        388 CCATCGAGAAAACCATCTCCAAAGCCAA------------------------------ 415

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

Db        416 ------------------------------------------------------------ 415

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
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Db        416 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 470

Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
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Db        471 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 530

Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
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Db        531 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 590

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Db        591 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAAGTGGCAG 650

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
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Db        651 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAG 710

Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 14
BG741164

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LOCUS       BG741164                797 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602631842F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4776923 5',
            mRNA sequence.
ACCESSION   BG741164
VERSION     BG741164.1  GI:14051817
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
            Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10630  row: d  column: 12
            High quality sequence stop: 782.
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                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
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                     Technologies. Note: this is a NCI_CGAP Library."
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ORIGIN

  Query Match             22.2%;  Score 500.2;  DB 12;  Length 797;
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  Matches  618;  Conservative    0;  Mismatches   18;  Indels   97;  Gaps    1;

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Db         12 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 71

Qy       1565 GACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTT 1624
              |||||||||||||| |||||||||||||||||||||||||||||||| |||||| ||||
Db         72 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 131

Qy       1625 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCA 1684
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        132 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 191

Qy       1685 GTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAA 1744
              || |||||||||| |||||||||||||||||||||||  ||||||||||||||||||||
Db        192 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 251

Qy       1745 CGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAAC 1804
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Qy       1865 TCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGC 1924
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Qy       1925 CCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGG 1984
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Qy       1985 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGA 2044
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Qy       2165 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC 2224
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Db        575 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC 634

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Db        635 TGTCCCCGGGTAA 647


RESULT 15
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LOCUS       BM007897                843 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
            mRNA sequence.
ACCESSION   BM007897
VERSION     BM007897.1  GI:16522238
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939  row: d  column: 22
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                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      207 a    277 c    227 g    132 t
ORIGIN

  Query Match             22.2%;  Score 499.6;  DB 13;  Length 843;
  Best Local Similarity   83.2%;  Pred. No. 2.6e-110;
  Matches  624;  Conservative    0;  Mismatches   29;  Indels   97;  Gaps    1;

Qy       1492 CAGCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC 1551
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Db        199 TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACC 258

Qy       1612 CCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 1671

Db        259 CTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGC 318

Qy       1672 CACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACC 1731

Db        319 CGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACC 378

Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791

Db        379 AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCC 438

Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATG 1851

Db        439 CCATCGAGAAAACCATCTCCAAAGCCAA---------------------------------- 466

Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911

Db        467 ------------------------------------------------------------ 466

Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971

Db        467 -----AGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 521

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Db        582 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 641

Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151

Db        642 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 701

Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211

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Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGA 2241

Db        762 AAGAGCCTCTCCCTGTCTCCGGGTAAATGA 791
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Job time : 3905.3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:14:58 ; Search time 583.029 Seconds
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Searched: 2185239 seqs, 1125999159 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	80.2	2560	13	AAQ30910	pMDR1002 insert; p
2	1761.2	78.3	3223	22	AAS11982	DNA encoding Human
3	1739.4	77.3	2287	13	AAQ25443	Sequence encoding
4	1736.2	77.2	2287	18	AAT60739	IgG1 gene. Homo s
5	1638	72.8	4694	22	AAF55225	Nucleotide sequenc
6	1638	72.8	4694	24	ABK85577	Human IgGgamma4 he
7	1611.8	71.7	4723	18	AAT78802	Gamma heavy chain
8	1611.8	71.7	4723	20	AAZ21997	Nucleotide sequenc
9	1611.8	71.7	4723	22	AAF55224	Nucleotide sequenc
10	1611.8	71.7	4723	24	ABK85576	Human IgGgamma1 he
11	1610.2	71.6	4723	19	AAV39243	Plasmid pCG7-96 nu
12	1609.2	71.6	2029	13	AAQ30909	pBAG101 insert. S
13	1604.4	71.3	9201	15	AAQ55003	Humanised anti-CD1
14	1584.6	70.5	2482	13	AAQ28089	Encodes CD4-IgG2 c
15	1584.6	70.5	2482	21	AAZ98856	CD4-IgG2 chimeric
16	1584.6	70.5	2482	22	AAF77830	Coding sequence fo
17	1584.6	70.5	2482	22	AAF56396	CD4-IgG2 chimeric
18	1580.4	70.3	1999	21	AAA46891	DNA encoding the h
19	1578.2	70.2	2482	15	AAQ57751	CD4-IgG2 chimeric
20	1547.2	68.8	2009	24	AAD35054	Human death domain
21	1547.2	68.8	3133	10	AAN90356	Sequence of a gene
22	1547.2	68.8	3133	21	AAA50660	DNA encoding CD4-I
23	1547.2	68.8	3133	21	AAZ44061	Human fusion prote
24	1547.2	68.8	3133	21	AAZ48201	DNA sequence encod
25	1545.6	68.7	2009	17	AAT27385	Human immunoglobul
26	1543.8	68.6	3400	18	AAT62932	2A2 human G2/G4 ch
27	1541.8	68.6	3400	18	AAT62937	3F4 human G2/G4 ch
28	1494.8	66.5	1979	13	AAQ20293	SEQ ID No. 4 that
29	1493.8	66.4	2008	13	AAQ20294	SEQ ID No. 5 that
30	1487.4	66.1	10704	14	AAQ43846	Plasmid pAH4625.
31	1465.8	65.2	3108	17	AAT27388	Human IgG CH1-hing
32	1465.8	65.2	3147	17	AAT27389	Human IgG CH1-hing
33	1463.4	65.1	2071	19	AAV70080	Anti-Fas humanised
34	1463.4	65.1	2071	21	AAA72184	DNA encoding human
35	1463.4	65.1	2071	21	AAA11622	Humanised HFE7A de
36	1463.4	65.1	2071	24	ABL46001	Humanised anti-Fas
37	1463.4	65.1	2071	24	ABL48744	Humanised anti-Fas
38	1459.8	64.9	1719	24	ABK40183	Human/rabbit Cgamm
39	1458.6	64.9	2077	19	AAV70079	Anti-Fas humanised
40	1458.6	64.9	2077	21	AAA72159	DNA encoding human
41	1458.6	64.9	2077	21	AAA11597	Humanised HFE7A de
42	1458.6	64.9	2077	24	ABL45976	Humanised anti-Fas
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44	1455.4	64.7	2073	21	AAA11644	Humanised anti-Fas
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ALIGNMENTS

RESULT 1
AAQ30910
ID AAQ30910 standard; DNA; 2560 BP.
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AC AAQ30910;
XX
DT 02-APR-1993 (first entry)
XX
DE pMDR1002 insert; pre-5A8 humanised heavy chain.
XX
KW Vector; pMDR1002; NotI; HindIII; pMDR1001; pSAB132; pBAG101; E. coli;
KW JA221(Iq); ampicillin; resistance; immunoglobulin; signal sequence;
KW humanised; 5A8; heavy chain; variable; region; HV; IgG4; constant;
KW HC; antibody; homolog; CD4; gp120; cell surface glycoprotein; CD4+;
KW lymphocytes; helper; inducer; HIV; syncytia; formation; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
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PN   WO9209305-A.
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PD   11-JUN-1992.
XX
PF   27-NOV-1991;   91WO-US08843.
XX
PR   27-NOV-1990;   90US-0618542.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Burkly LC,  Chisholm PL,  Rosa JJ,  Rosa MD,  Thomas DW;
XX
DR   WPI; 1992-398399/48.
DR   P-PSDB; AAR28808.
XX
PT   New anti-CD4 antibody homolognes - which bind CD4, do not block
PT   binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT   formation between CD4+ cells
XX
PS   Claim 27; Page 152-55; 205pp; English.
XX
CC   This sequence represents the insert of the vector pMDR1002.  Three
CC   fragments were used in the construction of pMDR1002; a 443 bp NotI/
CC   HindIII fragment of pMDR1001 (see AAQ30905), the 7913 bp NotI linearised
CC   pSAB132 (see AAQ30906) and a 2109 bp NotI/HindIII fragment of pBAG101
CC   (see AAQ30909).  These fragments were ligated together and the ligation
CC   mixture was used to transform E. coli JA221(Iq) to ampicillin
CC   resistance.  The insert encodes the immunoglobulin signal sequence,
CC   amino acids (AA) 1-122 of the humanised 5A8 heavy chain variable
CC   region (HV) and AA114-AA478 of the human IgG4 heavy chain, ie. the
CC   constant region (HC).  The polypeptide encoded by this sequence is
CC   an antibody homolog which was shown to bind to CD4 but did not block
CC   the binding of gp120 to CD4.  CD4 is a cell surface glycoprotein of
CC   CD4+ lymphocytes (helper/inducer cells).  The homolog blocked HIV-
CC   induced syncytia formation.  This homolog can be used in the
CC   detection, prophylaxis and treatment of diseases caused by infective
CC   agents whose primary targets are CD4+ cells.
XX
SQ   Sequence 2560 BP; 544 A; 848 C; 720 G; 448 T; 0 other;

  Query Match             80.2%;  Score 1804;  DB 13;  Length 2560;
  Best Local Similarity   89.2%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches  185;  Indels   64;  Gaps    7;
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Db      128 GTCCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATACACTGGGTGAGGCAGGC 187

Qy      188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
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Qy      308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAG---- 363
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Qy      364 --------------CGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGT 409
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Qy      410 CTCCTCAGGTGAGTCCTTAAA----------------------------------ACCT 434
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Qy      435 CTAG-----AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
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Qy      970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
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Db       1745 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1804

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Db       1805 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCA 1864

Qy       1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866

Db       1865 TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACACGGACAGAGGCCAGCTC 1924

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Db       1925 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1984

Qy       1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986

Db       1985 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC 2044

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Db       2045 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2104

Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106

Db       2105 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 2164

Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166

Db       2165 TTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 2224

Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226

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RESULT 2
AAS11982
ID AAS11982 standard; DNA; 3223 BP.
XX
AC AAS11982;
XX
DT 04-DEC-2001 (first entry)
XX
DE DNA encoding Humanised monoclonal antibody Hu266, heavy chain.
XX
KW Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;
KW Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;
KW heavy chain; ds; gene therapy.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX

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PN WO200162801-A2.
XX
PD 30-AUG-2001.
XX
PF 26-FEB-2001; 2001WO-US06191.
XX
PR 24-FEB-2000; 2000US-0184601.

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PR   08-DEC-2000; 2000US-0254465.
PR   08-DEC-2000; 2000US-0254498.
XX
PA   (UNIW ) UNIV WASHINGTON.
PA   (ELIL ) LILLY & CO ELI.
XX
PI   Holtzman DM,  Demattos R,  Bales KR,  Paul SM,  Tsurushita N;
PI   Vasquez M;
XX
DR   WPI; 2001-550087/61.
DR   P-PSDB; AAU07745.
XX
PT   New humanised antibody for the treatment of Alzheimer's comprises the
PT   inhibition and reduction of the formation of amyloid plaques
XX
PS   Example 13; Fig 5; 63pp; English.
XX
CC   The invention relates a humanised antibody that specifically binds
CC   an epitope contained within positions 13-28 of amyloid beta peptide,
CC   Abeta. The antibody is useful to inhibit and reduce the formation of
CC   amyloid plaques or the effects of toxic soluble Abeta species in humans
CC   their fragments are used for the manufacture of a medicant. This includes
CC   the prolonged expression of recombinant sequences of them in human
CC   tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC   Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC   Specifically, the antibody is used to sequester Abeta into plasma, brain
CC   or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC   peptide within the brain thereby improving cognition. The present
CC   sequence encodes the heavy chain of a humanised monoclonal antibody,
CC   Hu266, based on the mouse antibody 266.
XX
SQ   Sequence 3223 BP; 659 A; 1135 C; 885 G; 544 T; 0 other;

Query Match             78.3%;  Score 1761.2;  DB 22;  Length 3223;
Best Local Similarity   88.1%;  Pred. No. 0;
Matches 1984;  Conservative    0;  Mismatches  238;  Indels   30;  Gaps    5;

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Qy         65 CTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAA 124
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Qy        425 CTTAAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGA 484
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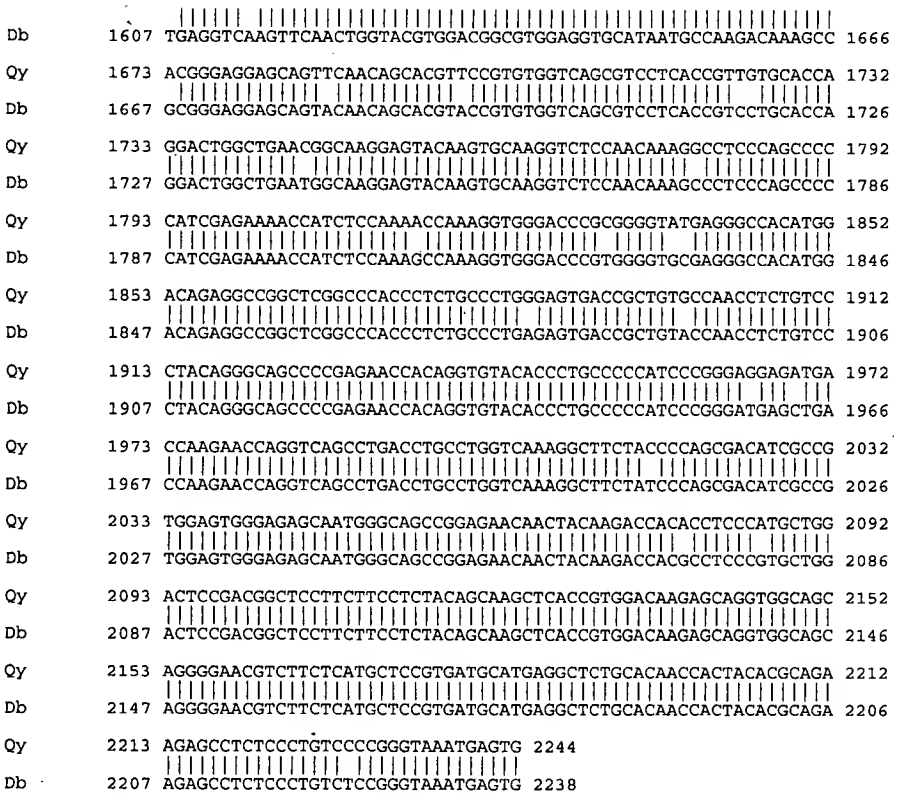

RESULT 3
AAQ25443
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AC AAQ25443;
XX
DT 02-JAN-1992 (first entry)
XX
DE Sequence encoding antibody molecule IgG1.
XX
KW Antibody; immunoglobulin G1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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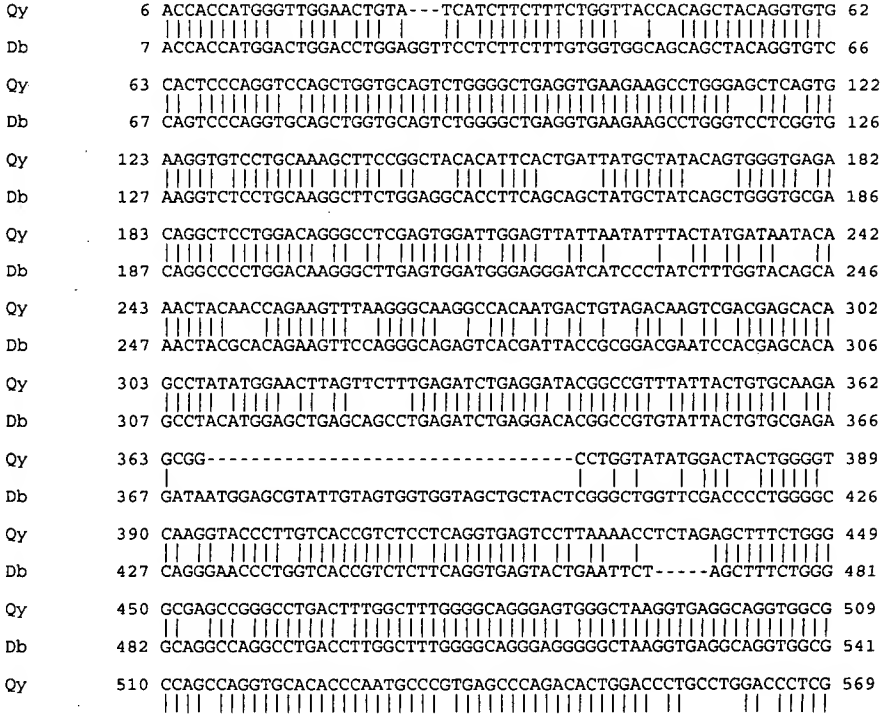
XX
PD 11-JUN-1992.
XX
PF 18-NOV-1991; 91WO-US08605.
XX
PR 23-NOV-1990; 90US-0618314.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B, Walz G;
XX
DR WPI; 1992-216789/26.
DR P-PSDB; AAR24442.
XX
PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PT - used in treating chronic inflammation, rheumatoid arthritis,
PT psoriasis, etc.
XX
PS Disclosure; Fig 1; 46pp; English.
XX
CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC inventors designed a molecule including several such sites for
CC attachment of sialyl-Lex side chains (see AAR24442, FT). The
CC additional N-linked glycosylation sites are introduced at locations
CC which impair complement fixing and Fc receptor binding ability. They
CC are preferably located in the CH2 region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for
CC disrupting undesirable interactions between cells or proteins.
CC Disrupting this interaction has therapeutic applications, for
CC example, in minimising inflammation following tissue injury.
XX
SQ Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;

Query Match 77.3%; Score 1739.4; DB 13; Length 2287;
Best Local Similarity 89.0%; Pred. No. 0;
Matches 2036; Conservative 0; Mismatches 186; Indels 65; Gaps 12;



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Db       1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGTA 1132
Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169
Db       1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190
Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
Db       1191 CAGGCCCTGCACACAAACGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG 1250
Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310
Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
Db       1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370
Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
Db       1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430
Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
Db       1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1490
Qy       1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGTCA 1517
Db       1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA 1550
Qy       1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577
Db       1551 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1610
Qy       1578 ACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTG 1637
Db       1611 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 1670

Qy       1638 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACG 1697
Db       1671 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 1730
Qy       1698 TTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTAC 1757
Db       1731 TACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 1790
Qy       1758 AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACC 1817
Db       1791 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 1850
Qy       1818 AAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTC 1877
Db       1851 AAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTC 1910
Qy       1878 TGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACA 1937
Db       1911 TGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAACCACA 1969
Qy       1938 GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG 1997
Db       1970 GGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG 2029
Qy       1998 CCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC 2057
Db       2030 CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC 2089
Qy       2058 GGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTA 2117
Db       2090 GGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTA 2149
Qy       2118 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT 2177
Db       2150 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT 2209
Qy       2178 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA 2237
Db       2210 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA 2269
Qy       2238 ATGAGTG 2244
Db       2270 ATGAGTG 2276
```

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RESULT 4
AAT60739
ID   AAT60739 standard; DNA; 2287 BP.
XX
AC   AAT60739;
XX
DT   22-APR-1997  (first entry)
XX
DE   IgG1 gene.
XX
KW   IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin;
KW   sialyl-Lewis X; antiinflammatory; inflammation;
KW   extravasation-dependent adverse reaction; organ damage; clotting;
KW   adult respiratory distress syndrome; glomerular nephritis;
KW   ischaemic myocardial injury; immune reaction; septic shock;
KW   septicaemia; therapy; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO9700079-A1.
XX
PD   03-JAN-1997.
XX
PF   11-JUN-1996;   96WO-US10043.
XX
PR   14-JUN-1995;   95US-0000213.
XX
```

PA (GEHO) GEN HOSPITAL CORP.
XX
PI Pouyani T, Seed B;
XX
DR WPI; 1997-077356/07.
DR P-PSDB; AAW10550.
XX
PT P-selectin and opt. E-selectin binding organic mol. - having
PT sialyl-Le(x) and sulphated determinant, useful for protecting
PT against inflammatory or immune reactions
XX
PS Disclosure; Page 40-41; 81pp; English.
XX
CC The gene (AAT60739) encoding IgG1 (AAW10550) can be subjected to site-
CC directed mutagenesis in order to introduce one or more N-linked
CC glycan addition sites into the IgG1 molecule (see also AAW10551).
CC Eukaryotic host cells co-transfected with a vector carrying the
CC the mutated IgG1 gene and with a vector that expresses an alpha-
CC (1,3)fucosyltransferase capable of attaching sialyl-Le(x) groups at
CC the glycosylation sites of the antibody molecule can be used in the
CC prodn. of sialyl-Le(x)-modified antibody. Such an antibody has
CC therapeutic applns., e.g. in minimising inflammation and
CC decreasing extravasation-dependent organ damage and/or clotting.
XX
SQ Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;

Query Match 77.2%; Score 1736.2; DB 18; Length 2287;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 2034; Conservative 0; Mismatches 188; Indels 65; Gaps 12;

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Qy          6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACAGCTACAGGTGTG 62
              |||||||||| |||| ||| |  || |||||||| |||| | ||||||||||||
Db          7 ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTGTGGTGGCAGCAGCTACAGGTGTC 66

Qy         63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
              || |||||||| |||||||||||||||||||||||||||||||||||  ||| |||
Db         67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG 126

Qy        123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
              ||||| |||||||| ||||| ||   ||| ||||     ||||||||    |||||| ||
Db        127 AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy        183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
              ||||| |||||||| || || |||||||| ||||  || |    |  || ||  ||   ||
Db        187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCA 246

Qy        243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302
              ||||||   ||||||||  ||||||  | ||| || || |  ||| | || |||||||||
Db        247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA 306

Qy        303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA 362
              ||||| ||||| || ||     |||||||||||||| |||||||| |||||||||| |||
Db        307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 366

Qy        363 GCGG----------------------------------CCTGGTATATGGACTACTGGGGT 389
              |                                    |  | |   | |||  ||||||
Db        367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGC 426

Qy        390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
              || || ||||| |||||||||| |||||||||| || ||  |      ||||||||||
Db        427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT-----AGCTTTCTGGG 481

Qy        450 GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
              ||  ||| |||||||| |||||||||||||||||| ||||||||||||||||||||||
Db        482 GCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 541

Qy        510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGCCTGGACCCTCG 569
              |||| |||||||||||||||||| ||||||||||||||||| ||     || |||||
Db        542 CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT-----GAACCTCG 595

Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
              ||| ||  ||||||| |||||||||||||| ||||||||||||||||||||||||||||
Db        596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCACACCGCGG 654
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Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714

Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
              |||| ||||| |||||||||| | | ||||||||||||||||||||||||||||||||||
Db        715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy        750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy        810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy        870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
              ||||||| ||| |||||||||||||| |||||||| ||||||||||||||||||||||
Db        895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy        930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC 989
              |||||||||||| |||||||||||||||||| ||||||||||||||||||||||||| |
Db        955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAA-C 1013

Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049
              |||||||||| |||||||||||||||| ||||||| |||||||||| ||||||||||||
Db       1014 CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAA 1073

Qy       1050 GGCAGGCCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109
              |||||||||| |||| ||| |||||||||||||||||||||||||||||||||||||||
Db       1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA 1132

Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169
              |||||||||||||||||| |||||||| |||||||||||||| |||||||||| ||
Db       1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190

Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
              |||||||| |||||| |||||||||| || |||||||||||||||| ||||||||||||
Db       1191 CAGGCCCTGCACACAAAGGGGCAGGTCCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG 1250

Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
              |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||||
Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
              |||||||||||||||||||||| | |||||||||||||||||||||||||||| |||||
Db       1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370

Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
              |||||  | |          |||||||||| ||||||||||||||||||||||||||||
Db       1371 CTTGTGACAAAACTCACACATGCCCACCGTCCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||| |
Db       1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTCCATCCAGGGACAGGCCCCAGCCG 1490

Qy       1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGTCA 1517
              |||||||||||||||||||||||||||||||||||||    ||    || | |||||||
Db       1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA 1550

Qy       1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1610

Qy       1578 ACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTG 1637
              || |||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||
Db       1611 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 1670

Qy       1638 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACG 1697
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1671 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 1730
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Qy       1698 TTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTAC 1757
Db            ||| |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy       1758 AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACC 1817
Db            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Qy       1818 AAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTC 1877
Db            ||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||||
Qy       1878 TGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACA 1937
Db            |||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Qy       1938 GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG 1997
Db            |||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Qy       1998 CCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC 2057
Db            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Qy       2058 GGAGAACAACTACAAGACCACGCCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTA 2117
Db            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Qy       2118 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT 2177
Db            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       2178 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAA 2237
Db            ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Qy       2238 ATGAGTG 2244
Db            |||||||
Db       2270 ATGAGTG 2276
```

RESULT 5
AAF55225
ID AAF55225 standard; DNA; 4694 BP.
XX
AC AAF55225;
XX
DT 29-MAY-2001 (first entry)
XX
DE Nucleotide sequence of pG4HE.
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease; ss.
XX
OS Unidentified.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
XX
PT Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient
XX
PS Example 10; Page 94-95; 127pp; English.
XX
CC The present sequence is used in the course of the specification. The
CC specification describes a human antibodies which specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging
CC an immune response to an antigen in a patient, where the antibodies
CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing a immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 4694 BP; 1068 A; 1396 C; 1248 G; 982 T; 0 other;

Query Match 72.8%; Score 1638; DB 22; Length 4694;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 1719; Conservative 0; Mismatches 95; Indels 4; Gaps 2;

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Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCGGGCCTGACTTTGGC-TGGGGGCAGGGAGGGGG 66
Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
Db         67 CTAAGGTGACGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 126
Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
Db        127 GGACCCTGCATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 186
Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
Db        187 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCC 246
Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
Db        247 CATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGG 306
Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
Db        307 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 366
Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
Db        367 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 426
Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
Db        427 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAG 486
Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
Db        487 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAG 546
Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
Db        547 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 606
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Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
             ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||| ||
Db        607 GCCCCAGCCCAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACC 666

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
             |||||||||||||||||||||||||||||||| |||||||||||||||| ||||| ||
Db        667 ACCCCACTCATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCGGGCAGCCA 726

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
             |||||||| |||||||||||||||||| | || ||||||||||||||  |||||||||
Db        727 CAGGCTGGATGCCCCTACCCCAGGCCCTGCGCATACAGGGGCAGGTGCTGCGCTCAGACC 786

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
             |||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        787 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 846

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
             || |||||||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db        847 CTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCT 906

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCA 1389
             |||||||||||||  ||||| | ||  |   |||||| | ||||||||||||||| ||||
Db        907 TCTCTCTGCAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCA 966

Qy       1390 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1026

Qy       1450 GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGG 1506
             |||||||| |||||||||| | |||||||||||||||||||||||||          ||
Db        1027 GGCCCCAGCCGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGG 1086

Qy       1507 CAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
               | ||| |||||||||||| |||||||||||||||||||||||||| ||||||||||||||
Db        1087 GGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGA 1146

Qy       1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        1147 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCA 1206

Qy       1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
             |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||
Db        1207 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1266

Qy       1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
             |||||||||||| |||||||||||||||||||||||| |||||||||||||||||||||
Db        1267 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1326

Qy       1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
             |||||||||||||||||||||||||||||||||||||||||||  || ||||||||||||||
Db        1327 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCA 1386

Qy       1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866
             |||||||| |||||||||||||| ||||||  |||||||||||||||||||| | ||||
Db        1387 TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACATGGACAGAGGTCAGCTC 1446

Qy       1867 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1447 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1506

Qy       1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
             ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1507 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC 1566

Qy       1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1567 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 1626

Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
             |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db        1627 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 1686

Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
             |||||||||||||||| ||| |||||||||||||||||||||||| ||||||| ||||||
Db        1687 TTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 1746

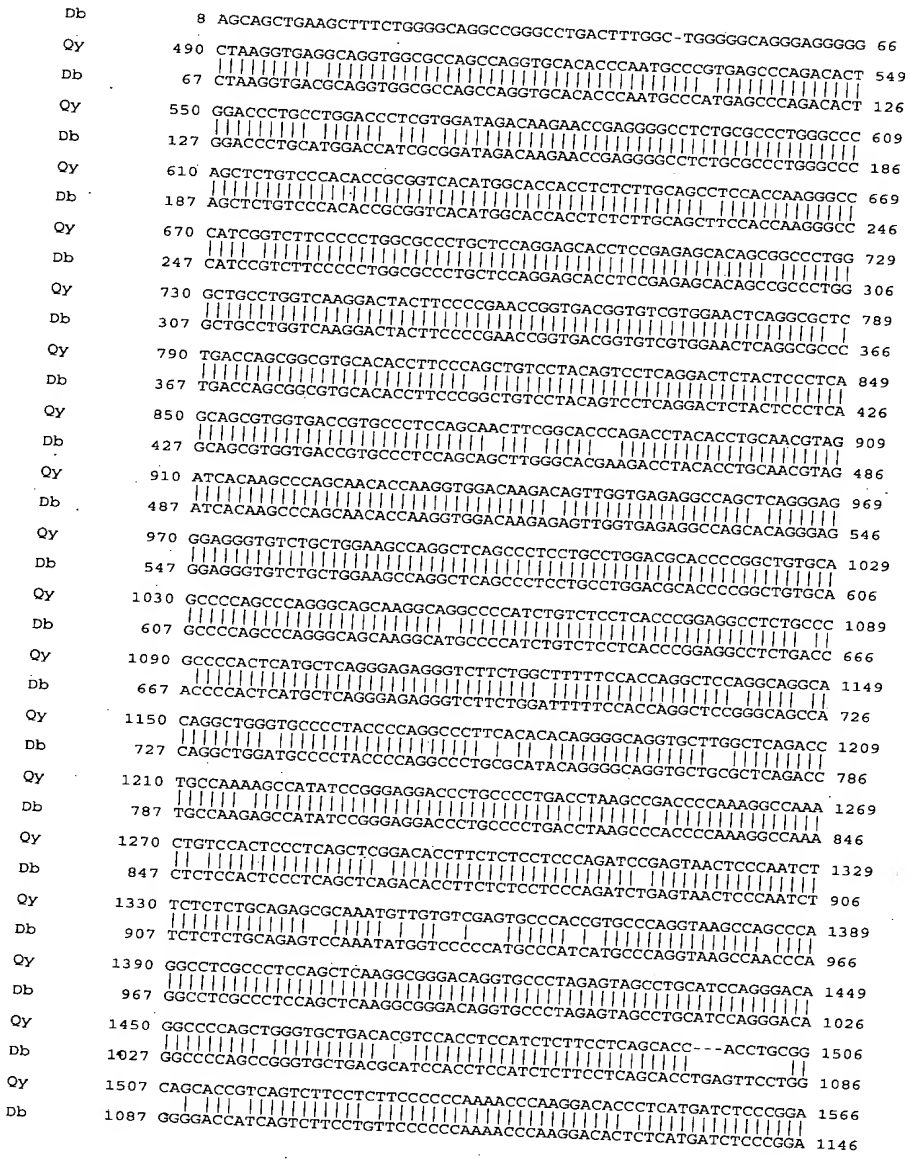
Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        1747 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTG 1806

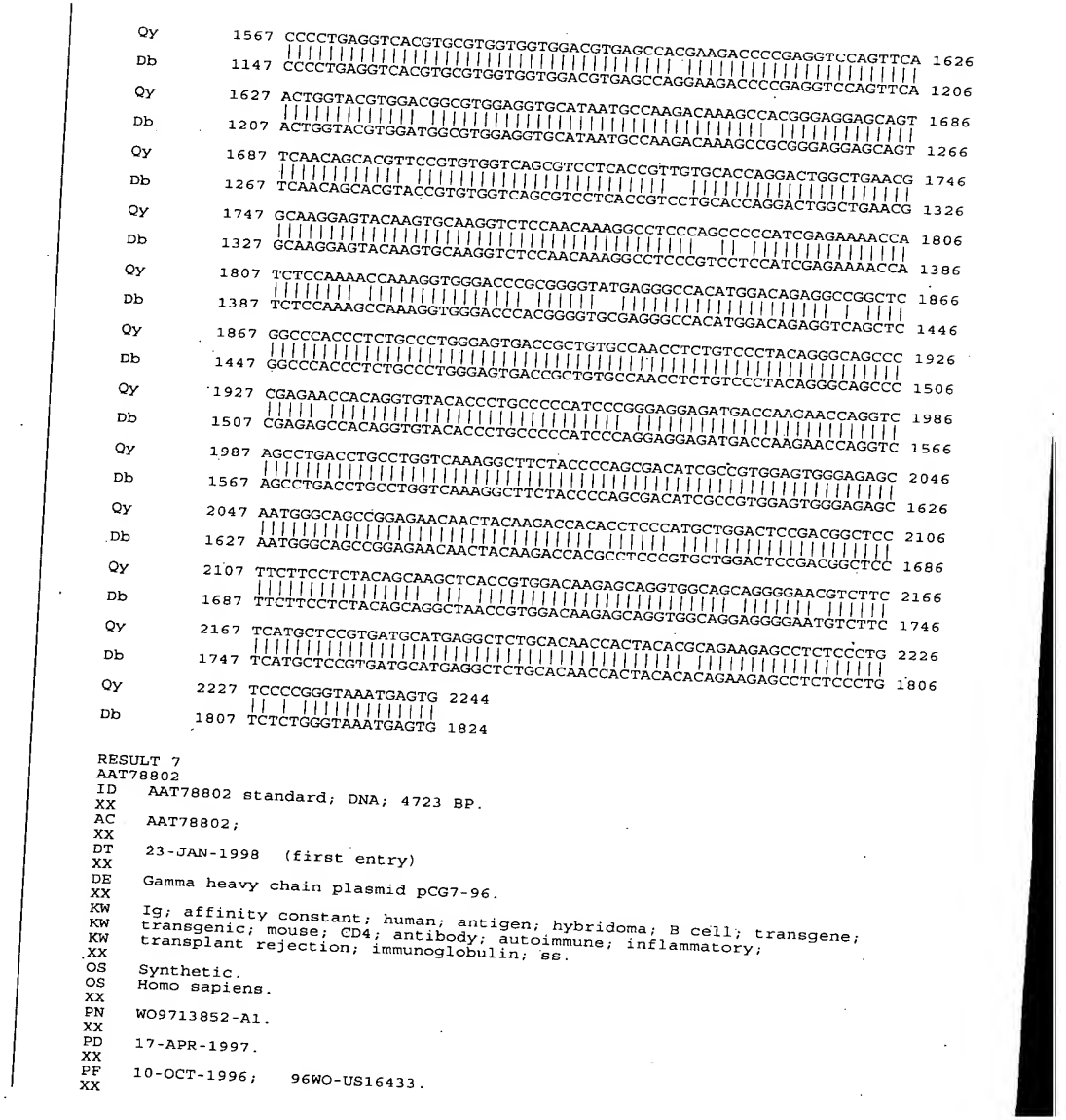
Qy       2227 TCCCCGGGTAAATGAGTG 2244
             || | ||||||||||||||
Db        1807 TCTCTGGGTAAATGAGTG 1824
```

RESULT 6
ABK85577
ID   ABK85577 standard; DNA; 4694 BP.
XX
AC   ABK85577;
XX
DT   03-SEP-2002 (first entry)
XX
DE   Human IgGgamma4 heavy chain plasmid pG4HE.
XX
KW   Transgenic; rodent; immunoglobulin; Ig; transchromosome; B-cell;
KW   human antibody display library; immune-related disorder; mutant;
KW   immunomodulatory; IgGgamma4 heavy chain; pG4HE; cyclic;
KW   circular; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200243478-A2.
XX
PD   06-JUN-2002.
XX
PF   30-NOV-2001; 2001WO-US45293.
XX
PR   30-NOV-2000; 2000US-250340P.
XX
PA   (MEDA-) MEDAREX INC.
PA   (KIRI) KIRIN BEER KK.
XX
PI   Tomizuka K, Ishida I, Lonberg N, Halk E;
XX
DR   WPI; 2002-500300/53.
XX
PT   New transgenic nonhuman mammal, useful for generating B-cells
PT   expressing human antibody sequences and generating antigen-specific
PT   hybridomas secreting human sequence antibody, comprises two human
PT   immunoglobulin loci -
XX
PS   Disclosure; Page 48-50; 110pp; English.
XX
CC   The present invention relates to novel transgenic nonhuman mammals,
CC   particularly rodents, comprising two human immunoglobulin (Ig) loci,
CC   where one of two the human immunoglobulin loci is a human heavy chain
CC   locus and the other locus is a human light chain locus, and where
CC   only one of the loci is of a transchromosome. The transgenic animals
CC   are useful for generating a number of B-cell expressing human
CC   antibody sequences. They are also useful for producing rearranged
CC   immunoglobulin sequences, producing human antibody display libraries,
CC   and generating a human sequence antibody that binds to a predetermined
CC   antigen. The produced antibodies are useful for treating immune-related
CC   disorders. The present sequence represents a plasmid used in the
CC   construction of expression vectors for human IgG.
XX
SQ   Sequence 4694 BP; 1068 A; 1396 C; 1248 G; 982 T; 0 other;

  Query Match   72.8%; Score 1638; DB 24; Length 4694;
  Best Local Similarity   94.6%; Pred. No. 0;
  Matches 1719; Conservative   0; Mismatches   95; Indels   4; Gaps   2;

```
Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              | |  ||  |||||||||||||  |||||||||||||||||| | ||||||||||| |||
```





RESULT 7
AAT78802
ID AAT78802 standard; DNA; 4723 BP.
XX
AC AAT78802;
XX
DT 23-JAN-1998 (first entry)
XX
DE Gamma heavy chain plasmid pCG7-96.
XX
KW Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection; immunoglobulin; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9713852-A1.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US16433.
XX

PR 10-OCT-1995; 95US-0544404.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1997-235888/21.
XX
PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Example 42; Page 262-264; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The present
CC sequence represents the kappa light chain plasmid pCK7-96 which includes
CC the human gammal constant region and polyadenylation site. Anti-CD4
CC antibodies may be used in therapeutic and diagnostic applications,
CC especially for the treatment of human diseases. These antibodies reduce
CC activity of CD4 cells and reduce undesirable autoimmune reactions,
CC inflammatory response and transplant rejection. Transgenic animals are
CC capable of producing heterologous antibodies of multiple isotypes by
CC undergoing isotype switching. These animals produce a first Ig type
CC that is necessary for antigen-stimulated B-cell maturation and can
CC switch to encode and produce one or more subsequent heterologous
CC isotypes.
XX
SQ Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

Query Match 71.7%; Score 1611.8; DB 18; Length 4723;
Best Local Similarity 94.3%; Pred. No. 1.7e-313;
Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4;

```
Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              |  |  ||  |||||||||||||  ||| ||||||||| |||||||||||||||||| |||
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              |||| ||     || ||||| ||| ||  ||||||| |||||||||||||||||||||||
Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||||||||||||||||| |||| ||||| ||||||||| | | ||||||||||||||||
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              |||||||||||||||||||||||||||||| ||| |||||||||||||||||| |||||||
Db        423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA 482

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              ||||||| |||||||||||||||||||||||||| |||| ||| |||||||||||||||||||
Db        603 GCCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||  ||||||||
Db        663 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGGCA 721

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||| |||||||||| |||||||||| |||||| |||||||||||| ||||||||||
Db        722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACC 781

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
              |||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 841

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              || |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAA 1380
              |||||||||||||||| ||||| ||||| | |         ||||||||||||||||||||||
Db        902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1022 CCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTG 1081

Qy       1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557
               ||  ||  | ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1141

Qy       1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| ||||
Db       1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy       1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy       1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
              ||||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857
              |||||||||||||||||||||||||||||||| |||||  ||||||||||||||||||||||
Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
              |||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681
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Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
             ||||||||||| ||||||||||||||||
Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
```

RESULT 8
AAZ21997
ID AAZ21997 standard; DNA; 4723 BP.
XX
AC AAZ21997;
XX
DT 24-NOV-1999 (first entry)
XX
DE Nucleotide sequence of plasmid pCG7-96.
XX
KW Transgenic animal; heterologous antibody; hybridoma; B cell;
KW transgenic mouse; human heavy chain transgene; digoxin;
KW human light chain transgene; immortalized cell; immunoglobulin;
KW Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS Synthetic.
XX
PN WO9945962-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05535.
XX
PR 13-MAR-1998; 98US-0042353.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Lonberg N, Fishwild DM, Ball WJ;
XX
DR WPI; 1999-551219/46.
XX
PT Novel transgenic non-human animals used to produce heterologous
PT antibodies
XX
PS Example 42; Page 313-316; 484pp; English.
XX
CC The specification describes transgenic animals that are capable of
CC producing a heterologous antibody. The antibodies are isolated form a
CC hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC having a genome comprising a human heavy chain transgene and a human
CC light chain transgene. The B cells are fused to immortalized cells
CC suitable for generating a hybridoma, which produces a detectable
CC amount of an immunoglobulin that specifically binds digoxin or
CC Shinga-like toxin. B cells from transgenic animals of the
CC generate hybridomas expressing monoclonal high affinity human sequence
CC antibodies. Antibodies produced from the transgenic animals of the
CC invention can be used to treat human diseases, e.g. autoimmune
CC diseases, cancer, infectious disease, transplant rejection, blood
CC disorders such as coagulation disorders and other diseases. The
CC present sequence is used in the course of the invention.
XX
SQ Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

Query Match   71.7%; Score 1611.8; DB 20; Length 4723;
Best Local Similarity 94.3%; Pred. No. 1.7e-313;
Matches 1722; Conservative   0; Mismatches   87; Indels   18; Gaps   4;

```
Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              |-| || ||||||||||||| ||| |||||||| ||||||||||||||||||||| |||
```

```
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              |||| ||  || |||||| ||| ||  |||||| |||||||||||||||||||||||||||
Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||||||||||||||||| |||| ||||| |||||||| | | ||||||||||||||||||
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACACCTGCAACGTGA 482

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 GCCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGGCA 721

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACC 781

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 841

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAA 1380
              |||||||||||||| ||||| | | |||||         |||||||||||||||||||||
Db        902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||--
Db       1022 CCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTG 1081

Qy       1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1141
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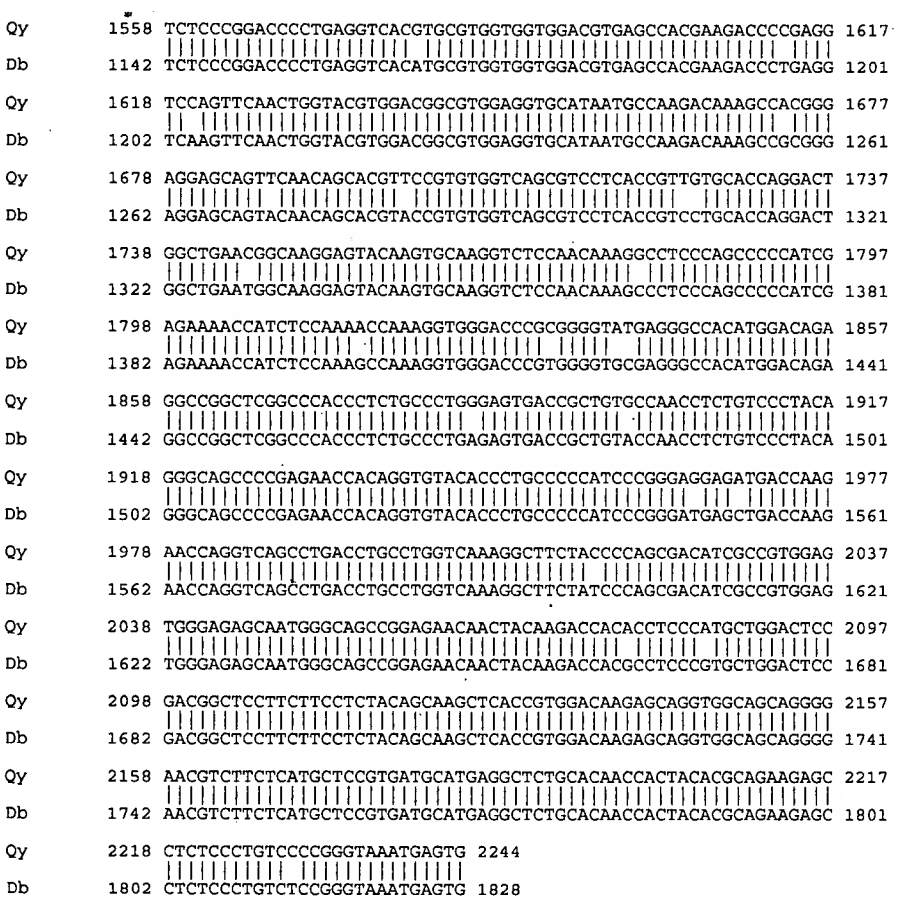

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Qy       1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
Db       1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy       1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
Db       1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy       1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
Db       1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
Db       1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857
Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917
Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

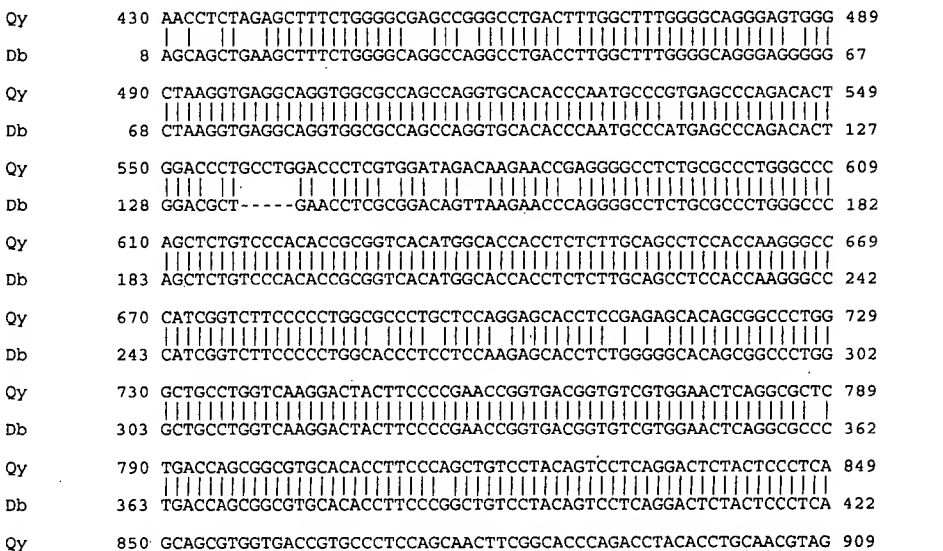
Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
```

RESULT 9
AAF55224
ID AAF55224 standard; DNA; 4723 BP.
XX
AC AAF55224;
XX
DT 29-MAY-2001 (first entry)
XX
DE Nucleotide sequence of pCG7-96.
XX
KW Complementarity determining region; CDR; immune response; antibody;
KW cytotoxic T lymphocyte associated antigen-4; CTLA-4; B7 ligand; cancer;
KW autoimmune disease; infectious disease; inflammation; allergy;
KW rheumatoid arthritis; myasthenia gravis; lupus erythematosus;
KW multiple sclerosis; insulin-dependent diabetes mellitus; inflammation;
KW transplant rejection; graft versus host disease; ss.
XX
OS Unidentified.
XX
PN WO200114424-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23356.
XX
PR 24-AUG-1999; 99US-0150452.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Korman AJ, Halk EL, Lonberg N;
XX
DR WPI; 2001-202933/20.
DR P-PSDB;
XX
PT Novel human sequence antibody that binds to human cytotoxic T
PT lymphocyte associated antigen-4, useful for inducing, augmenting or
PT prolonging immune response to antigen or for suppressing immune
PT response in patient -
XX
PS Example 10; Page 93-94; 127pp; English.
XX
CC The present sequence is used in the course of the specification. The
CC specification describes a human antibodies which specifically bind to
CC human cytotoxic T lymphocyte associated antigen-4 (CTLA-4). Such
CC antibodies are used in methods for inducing, augmenting or prolonging
CC an immune response to an antigen in a patient, where the antibodies
CC block binding of human CTLA-4 to human B7 ligands. The antibodies are
CC also useful for treating autoimmune disease in a subject caused or
CC exacerbated by increased activity of T cells and for treating prostate
CC cancer, melanoma or epithelial cancer. A polyvalent or polyclonal
CC antibody preparation comprising two antibodies of the invention are
CC useful for suppressing a immune response in a patient. They are used for
CC treating cancer, infectious diseases and promoting beneficial autoimmune
CC reactions for the treatment of diseases with inflammatory or allergic
CC components. The polyvalent or polyclonal preparations are useful for
CC treating autoimmune diseases such as rheumatoid arthritis, myasthenia
CC gravis and lupus erythematosus, multiple sclerosis, insulin-dependent
CC diabetes mellitus, transplant rejection, and inflammation, graft versus
CC host disease.
XX
SQ Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

Query Match 71.7%; Score 1611.8; DB 22; Length 4723;
Best Local Similarity 94.3%; Pred. No. 1.7e-313;
Matches 1722; Conservative 0; Mismatches 87; Indels 18; Gaps 4;



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Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
Db        363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
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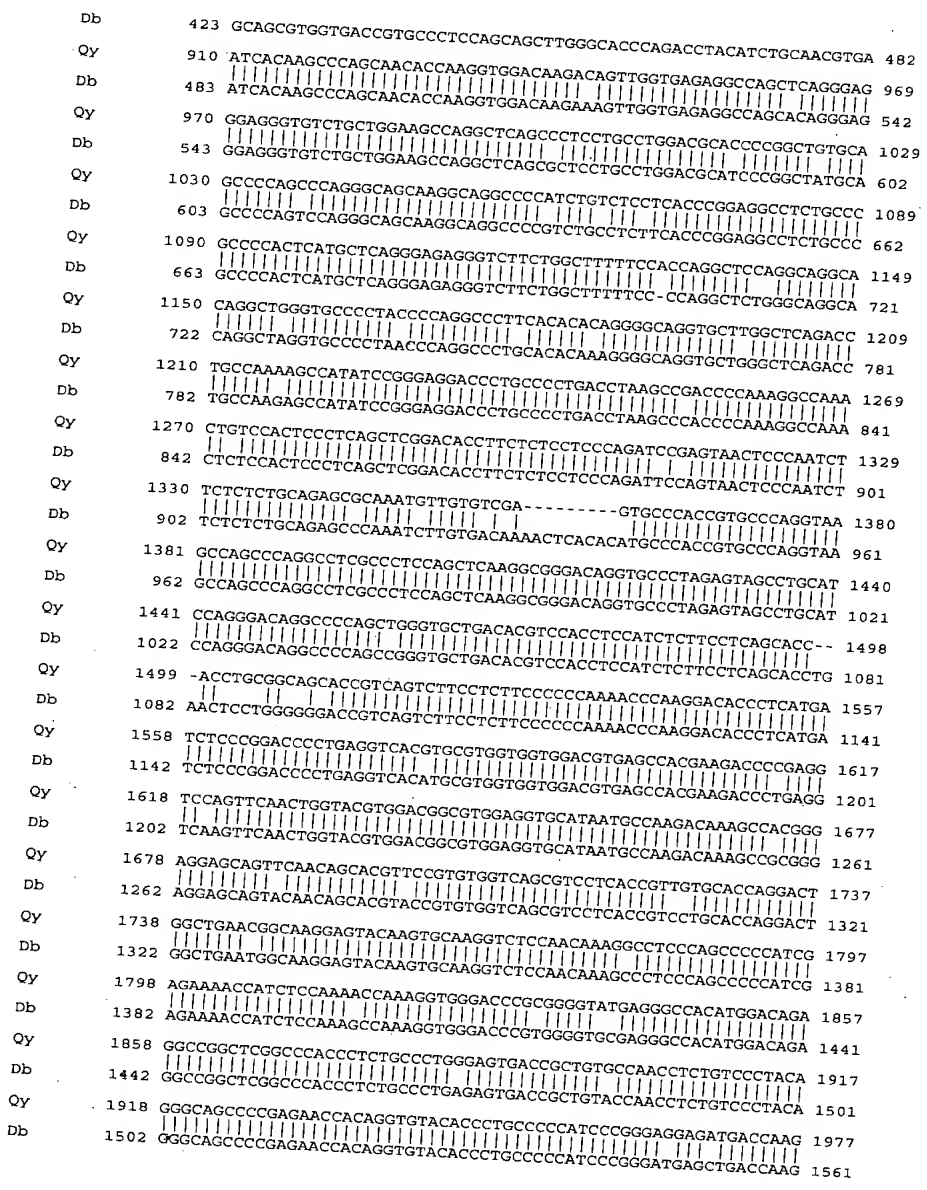

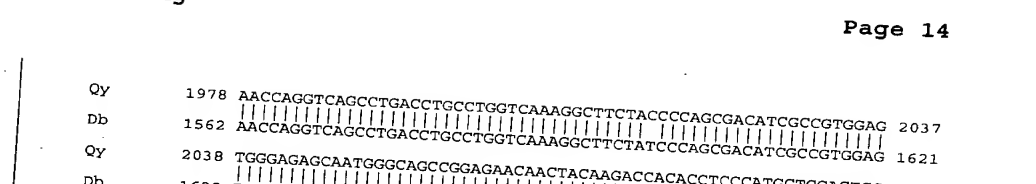

RESULT 10
ABK85576
ID ABK85576 standard; DNA; 4723 BP.
XX
AC ABK85576;
XX
DT 03-SEP-2002 (first entry)
XX
DE Human IgGgamma1 heavy chain plasmid pCG7-96.
XX
KW Transgenic; rodent; immunoglobulin; Ig; transchromosome; B-cell;
KW human antibody display library; immune-related disorder; mutant;
KW immunomodulatory; IgGgamma1 heavy chain; pCG7-96; cyclic;
KW circular; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200243478-A2.
XX
PD 06-JUN-2002.
XX
PF 30-NOV-2001; 2001WO-US45293.
XX
PR 30-NOV-2000; 2000US-250340P.
XX
PA (MEDA-) MEDAREX INC.
PA (KIRI) KIRIN BEER KK.
XX
PI Tomizuka K, Ishida I, Lonberg N, Halk E;
XX
DR WPI; 2002-500300/53.
XX
PT New transgenic nonhuman mammal, useful for generating B-cells
PT expressing human antibody sequences and generating antigen-specific
PT hybridomas secreting human sequence antibody, comprises two human
PT immunoglobulin loci
XX
PS Disclosure; Page 47-48; 110pp; English.
XX
CC The present invention relates to novel transgenic nonhuman mammals,
CC particularly rodents, comprising two human immunoglobulin (Ig) loci,
CC where one of two the human immunoglobulin loci is a human heavy chain
CC locus and the other locus is a human light chain locus, and where
CC only one of the loci is of a transchromosome. The transgenic animals
CC are useful for generating a number of B-cell expressing human
CC antibody sequences. They are also useful for producing rearranged
CC immunoglobulin sequences, producing human antibody display libraries,
CC and generating a human sequence antibody that binds to a predetermined
CC antigen. The produced antibodies are useful for treating immune-related
CC disorders. The present sequence represents a plasmid used in the

```
CC   construction of expression vectors for human IgG.
XX
SQ   Sequence 4723 BP; 1072 A; 1411 C; 1253 G; 987 T; 0 other;

  Query Match             71.7%;  Score 1611.8;  DB 24;  Length 4723;
  Best Local Similarity   94.3%;  Pred. No. 1.7e-313;
  Matches 1722;  Conservative    0;  Mismatches   87;  Indels   18;  Gaps    4;

Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              | |  ||  ||||||||||||  ||| ||||||| |||||||||||||||||| |||
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              |||| ||     || ||||| ||| ||  ||||||| |||||||||||||||||||||||
Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||||||||||||||||| |||| ||||| ||||||||| | | ||||||||||||||||
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              |||||||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db        423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA 482

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              |||||||||||||||||||||||||||||| |||||||||||||||| |||||||
Db        483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||| ||||
Db        543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              ||||||| |||||||||||||||||||||| |||| ||| ||||||||||||||||||||
Db        603 GCCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||| ||||||||  ||||||||
Db        663 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGGCA 721

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||| |||||||||| |||||||||| |||||| |||||||||||| ||||||||||
Db        722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACC 781

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
              |||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 841

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              || |||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db        842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAA 1380
              |||||||||||||| ||||| ||||| | |         ||||||||||||||||||||
Db        902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1022 CCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTG 1081

Qy       1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557
               ||    ||  | ||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1141

Qy       1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||| ||||
Db       1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy       1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
              || ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy       1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
              |||||||| |||||||||| ||||||||||||||||||||||| ||||||||||||
Db       1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
              ||||||| |||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857
              |||||||||||||||| |||||||||||||||| |||||  ||||||||||||||||||
Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917
              |||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
              |||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
              |||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
              |||||||||||| ||||||||||||||
Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828


RESULT 11
AAV39243
ID   AAV39243 standard; DNA; 4723 BP.
XX
AC   AAV39243;
XX
DT   18-DEC-1998  (first entry)
XX
DE   Plasmid pCG7-96 nucleotide sequence.
XX
KW   Transgenic animal; human heterologous antibody; transgene;
KW   isotype switching; neutrophil efflux; reperfusion injury; CD4 binding;
KW   autoimmune reaction; inflammatory response; transplant rejection;
```

KW acid induced lung injury; acute adult respiratory distress syndrome;
KW ARDS; vasculitis; septic shock; allergic reaction; asthma;
KW cystic fibrosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824884-A1.
XX
PD 11-JUN-1998.
XX
PF 01-DEC-1997; 97WO-US21803.
XX
PR 02-DEC-1996; 96US-0758417.
XX
PA (GENP-) GENPHARM INT.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1998-333306/29.
XX
PT Hybridoma producing antibody specific for interleukin-8 - used to
PT prevent efflux of neutrophils from vasculature, and treat
PT reperfusion injury
XX
PS Example 42; Pages 312-315; 452pp; English.
XX
CC The present sequence represents the gamma1 heavy chain plasmid, pCG7-96,
CC which includes the human gamma1 constant region and polyadenylation site.
CC The plasmid is used in the construction of minigenes for expression of
CC IgGkappa anti-CD4 antibodies, in the transgenic mouse of the invention.
CC The specification describes transgenic non-human animals, especially a
CC mouse, which are capable of producing a human heterologous antibodies of
CC multiple isotypes by undergoing isotype switching. The transgenic animals
CC have human heavy and light chain transgenes. The transgenes are capable
CC of functionally rearranging a heterologous diversity (D) gene in a
CC variable-diversity-junction (V-D-J) recombination. The transgenes include
CC a heavy chain transgene comprising at least one V, D and J gene segment,
CC and one constant region gene segment. The immunoglobulin (Ig) light chain
CC transgene comprises at least one V and J gene segment and one constant
CC region gene segment. The gene segments are heterologous to the transgenic
CC animal. The antibody can be used to prevent efflux of neutrophils from
CC vasculature. It can also be used to treat reperfusion injury. CD4 binding
CC antibodies are used to reduce undesirable autoimmune reactions,
CC inflammatory responses and rejection of transplanted organs. The
CC anti-IL-8 antibodies can reduce tissue damage and prolong survival in
CC animal models of acute adult respiratory distress syndrome (ARDS) and
CC acid induced lung injury. The anti-IL-8 antibodies can also be used for
CC the treatment of vasculitis, septic shock, allergic reactions
CC (e.g. asthma) and cystic fibrosis.
XX
SQ Sequence 4723 BP; 1072 A; 1410 C; 1253 G; 988 T; 0 other;

Query Match 71.6%; Score 1610.2; DB 19; Length 4723;
Best Local Similarity 94.2%; Pred. No. 3.6e-313;
Matches 1721; Conservative 0; Mismatches 88; Indels 18; Gaps 4;

```
Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              |  |  ||  ||||||||||||||  ||| ||||||||| ||||||||||||||||||| |||
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              ||||  ||      || ||||| ||| ||  ||||||| |||||||||||||||||||| |
Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCTC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||||||||||||||||||| |||| ||||| ||||||||| | | ||||||||||||||||
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              |||||||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db        423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA 482

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||| |||||||
Db        483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||||| ||||||||||||||| ||||||| ||||
Db        543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              ||||||| |||||||||||||||||||||| |||| ||| |||||||||||||||||||||
Db        603 GCCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||  ||||||||
Db        663 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGGCA 721

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||| |||||||||| |||||||||| |||||| |||||||||||||| ||||||||||
Db        722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACC 781

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
              |||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 841

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              || |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db        842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAA 1380
              ||||||||||||||| ||||| ||||| | |         |||||||||||||||||||||
Db        902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        1022 CCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTG 1081

Qy       1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557
               ||    ||  | ||||||||||||||||||||||||||||||||||||||||||||||
Db        1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1141

Qy       1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||| ||||
Db        1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy       1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
              || |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy       1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
              ||||||||| |||||||||| |||||||||||||||||||||||||||| ||||||||||
Db        1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
```

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Db       1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGACAGA 1857

Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917

Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977

Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037

Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097

Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157

Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217

Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244

Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
```

RESULT 12
AAQ30909
ID AAQ30909 standard; DNA; 2029 BP.
XX
AC AAQ30909;
XX
DT 02-APR-1993 (first entry)
XX
DE pBAG101 insert.
XX
KW Primer; polymerase chain reaction; amplify; IgG4; heavy chain;
KW constant region; human; placenta; EcoR5; pNN03; pBAG101; HIV;
KW antibody; anti-CD4; gp120; ss.
XX
OS Synthetic.
XX
PN WO9209305-A.
XX
PD 11-JUN-1992.
XX
PF 27-NOV-1991; 91WO-US08843.
XX
PR 27-NOV-1990; 90US-0618542.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
XX
DR WPI; 1992-398399/48.
XX
PT New anti-CD4 antibody homolognes - which bind CD4, do not block
PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
PT formation between CD4+ cells
XX
PS Disclosure; Page 149-50; 205pp; English.
XX
CC The sequence given is the insert from the intermediate plasmid pBAG101.
CC pBAG101 was designed to carry genomic DNA encoding the human IgG4
CC heavy chain constant region. The IgG4 DNA was isolated by polymerase
CC chain reaction from human placental DNA using the primer sequences given
CC in AAQ30907-08. The amplification product of this reaction was approx.
CC 2109 bp. This fragment was inserted into EcoR5 linearised pNN03 (see
CC also AAQ30566) to give the intermediate plasmid pBAG101.
XX
SQ Sequence 2029 BP; 423 A; 710 C; 564 G; 331 T; 1 other;

  Query Match   71.6%; Score 1609.2; DB 13; Length 2029;
  Best Local Similarity 94.5%; Pred. No. 5.1e-313;
  Matches 1711; Conservative   0; Mismatches   93; Indels   6; Gaps   4;

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Qy        438 GAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTG 497

Db          2 GAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGC-TGGGGGCAGGGAGGGGGCTAAGGTG 60

Qy        498 AGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTG 557

Db         61 ACGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACCCTG 120

Qy        558 CCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGT 617

Db        121 CATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGT 180

Qy        618 CCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTC 677

Db        181 CCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCCCATCCGTC 240

Qy        678 TTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTG 737

Db        241 TTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTG 300

Qy        738 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGC 797

Db        301 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC 360

Qy        798 GGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG 857

Db        361 GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG 420

Qy        858 GTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAG 917

Db        421 GTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAG 480

Qy        918 CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTG 977

Db        481 CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 540

Qy        978 TCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGC 1037

Db        541 TCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGC 600

Qy       1038 CCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACT 1097

Db        601 CCAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACCACCCCACT 660

Qy       1098 CATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGG 1157

Db        661 CATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCCGGCA-CCACAGGCTGG 719

Qy       1158 GTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAA 1217

Db        720 ATGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAGA 778

Qy       1218 GCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCAC 1277

Db        779 GCCATATCCGGGAGGACCCTGCCCCTGACCTAAHCCCACCCCAAAGGCCAAACTCTCCAC 838

Qy       1278 TCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTG 1337

Db        839 TCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTG 898
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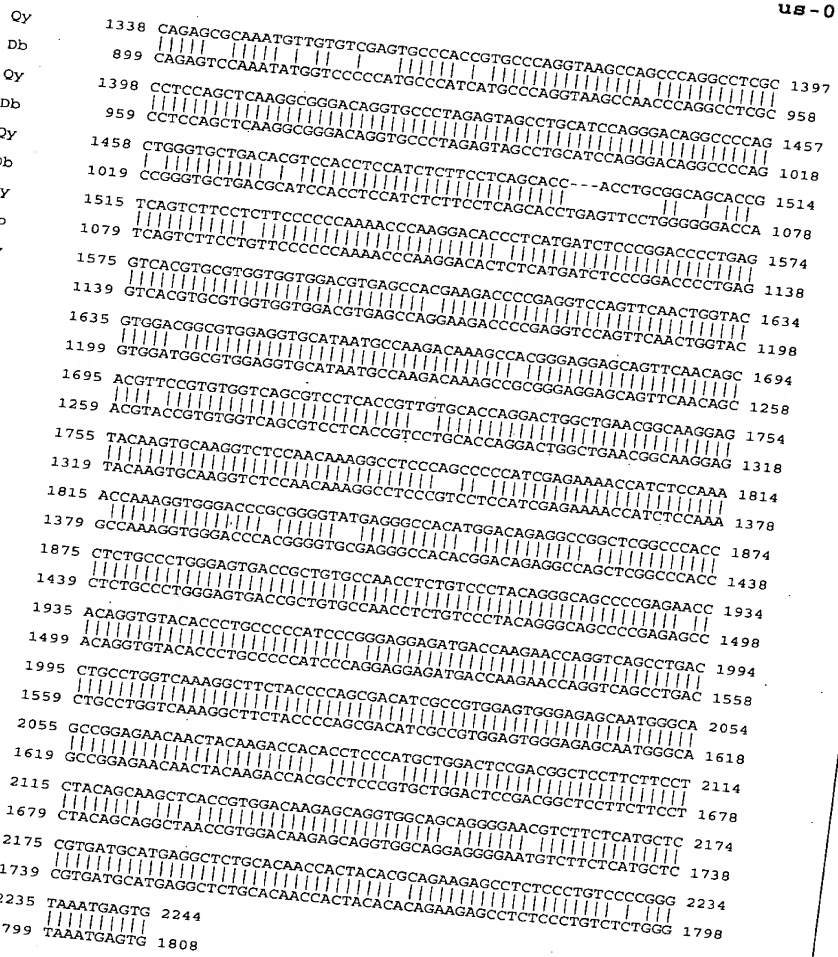
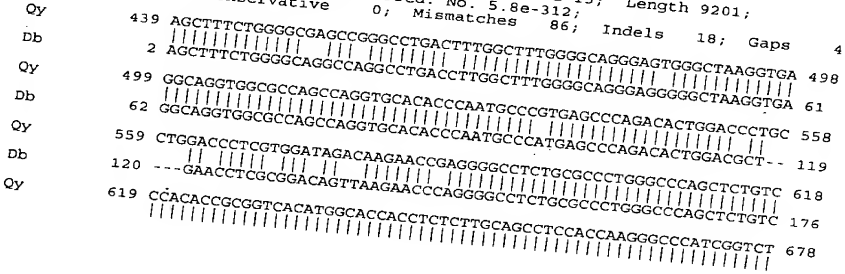


RESULT 13
AAQ55003
ID AAQ55003 standard; DNA; 9201 BP.
XX
AC AAQ55003;
XX
DT 06-JUL-1994 (first entry)
XX
DE Humanised anti-CD18 Ab 60.3 variable heavy chain (pNg1.16(2)).
XX
KW Monoclonal antibody; MAb; heavy chain; light chain;
KW constant region; variable region; amplification; primer;
KW polymerase chain reaction; PCR; chimera; Ig;
KW immunoglobulin; humanised antibody; leucocyte; integrin; ss.
XX
OS Chimeric: Homo sapiens.
OS Chimeric: Mus sp.
XX
PN EP578515-A.
XX
PD 12-JAN-1994.
XX
PF 24-MAY-1993; 93EP-0401328.
XX
PR 26-MAY-1992; 92US-0888233.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Bajorath J, Harris LJ, Hsiao K, Ku-Chuan H;
XX
DR WPI; 1994-010334/02.
XX
PT Humanised monoclonal antibodies prepn. - using comparative model
PT building, by computer database searching
XX
PS Disclosure; Page 22-27; 68pp; English.
XX
CC A humanised monoclonal antibody corresponding to the murine anti-CD18
CC antibody 60.3 was prepared. The variable (V) region sequences from
CC both the heavy (H) and light (L) chains were determined from cDNA
CC (amplified by PCR), and spliced onto human constant (C) regions,
CC resulting in a chimeric 60.3 Ab (IgG1, kappa). The chimeric Ab was
CC expressed in tissue culture (Ag8.653 mouse myeloma cells, detected
CC by ELISA), and examined in binding assays. The results from
CC competition and inhibition assays showed that the chimeric Ab was
CC as effective as the murine 60.3 MAb. The deduced murine VH and VL
CC protein sequences were compared to the protein sequence data base,
CC and two human Ig protein sequences were selected to be used as
CC templates. A murine 60.3 Fv was modeled according to the deduced
CC VH and VL protein sequences. Based on the 60.3 Fv model and the two
CC human template sequences selected from the protein data base, a
CC humanised Fv was modeled. Construction of the humanised 60.3 was
CC done by piecing 5 pairs of complementary oligonucleotides together
CC (spanning the entire V region) to form the VH and VL. These were
CC then attached onto vectors containing genes for appropriate C regions
CC to form humanised Ab (IgG1, kappa). The humanised proteins were again
CC expressed in Ag8.653 cells and binding assays were done. FACS analyses
CC indicated that the humanised Ab recognised cells expressing CD18.
CC About a dozen of the humanised 60.3 Ab master wells were transferred
XX and assayed for Ig.
SQ Sequence 9201 BP; 2280 A; 2558 C; 2319 G; 2044 T; 0 other;

Query Match 71.3%; Score 1604.4; DB 15; Length 9201;
Best Local Similarity 94.3%; Pred. No. 5.8e-312;
Matches 1714; Conservative 0; Mismatches 86; Indels 18; Gaps 4;



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Db        177 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 236

Qy        679 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGG 738
              ||||||||| |||| |||| |||||||| | | ||||||||||||||||||||||||||
Db        237 TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG 296

Qy        739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 798
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        297 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG 356

Qy        799 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 858
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        357 GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 416

Qy        859 TGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC 918
              |||||||||||||||||| ||| |||||||||||||||| |||||||||  |||||||||
Db        417 TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC 476

Qy        919 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGT 978
              ||||||||||||||||||||    |||||||||||||||| ||||||||||||||||||
Db        477 CCAGCAACACCAAGGTGGACAAACGCGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGT 536

Qy        979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 1038
              |||||||||||||||||||| |||||||||||||||| ||||||| |||||||||||  |
Db        537 CTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTC 596

Qy       1039 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 1098
              |||||||||||||||||||| |||| ||| ||||||||||||||||||||||||||||||
Db        597 CAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCCGCCCCACTC 656

Qy       1099 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 1158
              |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||  ||
Db        657 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGGCACAGGCTAGG 715

Qy       1159 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAG 1218
              |||||||| |||||||||| |||||| |||||||||||||| |||||||||||||||  ||
Db        716 TGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAG 775

Qy       1219 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACT 1278
              |||||||||||||||||||||||||||||||| |||||||||||||||| ||||||
Db        776 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACT 835

Qy       1279 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC 1338
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        836 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGC 895

Qy       1339 AGAGCGCAAATGTTGTGTCGAG---------TGCCCACCGTGCCCAGGTAAGCCAGCCCA 1389
              ||||| ||||| ||||| | |          ||||||||||||||||||||||||||||
Db        896 AGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCA 955

Qy       1390 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        956 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1015

Qy       1450 GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGG 1506
              |||||||| |||||||||||||||||||||||||||||||||||||||   ||    ||
Db       1016 GGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGG 1075

Qy       1507 CAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1135

Qy       1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
              |||||||||||| |||||||||||||||||||||||||||||||| |||||| ||||||
Db       1136 CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCA 1195

Qy       1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       1196 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1255

Qy       1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
              |||||||||||| |||||||||||||||||||||||  |||||||||||||||||||| |
Db       1256 ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATG 1315
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Qy       1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
              |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1316 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA 1375

Qy       1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866
              |||||||| |||||||||||||||| |||||   |||||||||||||||||||||||||||
Db       1376 TCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTC 1435

Qy       1867 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1926
              |||||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||
Db       1436 GGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACAGGGCAGCCC 1495

Qy       1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
              |||||||||||||||||||||||||||||||  | ||||||||||||||||||||||||
Db       1496 CGAGAACCACAGGTGTACACCCTGCCCCCATCTAGAGAGGAGATGACCAAGAACCAGGTC 1555

Qy       1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       1556 AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGC 1615

Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
              |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||
Db       1616 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 1675

Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1676 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 1735

Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1736 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 1795

Qy       2227 TCCCCGGGTAAATGAGTG 2244
              || ||||||||||||||
Db       1796 TCTCCGGGTAAATGAGTG 1813
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RESULT 14
AAQ28089
ID   AAQ28089 standard; cDNA; 2482 BP.
XX
AC   AAQ28089;
XX
DT   06-FEB-1993  (first entry)
XX
DE   Encodes CD4-IgG2 chimeric heavy chain.
XX
KW   homodimer; soluble CD4; T cell receptor; CD4 antigen; high recovery;
KW   chimeric; increased serum half life; HIV infection; AIDS; ss.
XX
OS   Homo sapiens chimeric.
XX
FH   Key             Location/Qualifiers
FT   CDS             76..980
FT                   /*tag=  a
FT                   /label= CD4 domain
FT   CDS             1374..1408
FT                   /*tag=  b
FT                   /label= hinge domain
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PN   WO9213947-A.
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PD   20-AUG-1992.
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XX
PF 10-FEB-1992; 92WO-US01143.
XX
PR 08-FEB-1991; 91US-0653684.
XX
PA (PROG-) PROGENICS PHARM INC.
XX
PI Beaudry GA, Maddon PJ;
XX
DR WPI; 1992-300034/36.
DR P-PSDB; AAR26783.
XX
PT CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors - for
PT treatment; prevention and diagnosis of HIV infection
XX
PS Claim 13; Fig 4; 90pp; English.
XX
CC This sequence encodes a CD4-gamma2 chimeric heavy chain homodimer.
CC Human CD4 cDNA was excised from plasmid pSP6T4 as an EcoRI/StuI
CC 0.7 kb fragment, and cloned into M13mp18 forming M13mp18(CD4). This
CC was linearised with Pst1, and the SacII(flush)/Pst1 fragment from pBr
CC gamma2 containing human gamma2 heavy chain (CH1 exon) isolated and
CC ligated to the M13mp18(CD4) vector. Resulting recombinants were then
CC screened by restriction analysis for the presence of both CD4 and
CC CH1 which occur in tandem CD4(EcoRI/StuI)-CH1(SacI(flush)/PstI).
CC Site directed mutagenesis was performed to juxtapose the CD4 and
CC CH1 heavy chain sequences in frame. The resulting chimeric DNA
CC molecule encodes a protein containing the V1V2 domains of CD4 fused
CC to the CH1 domain of heavy chain. Plaques containing the chimeric gene
CC with the correct sequence were then grown in TG1 cells and Rf DNA
CC isolated from the cells.
XX
SQ Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 other;

Query Match 70.5%; Score 1584.6; DB 13; Length 2482;
Best Local Similarity 99.7%; Pred. No. 4.4e-308;
Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
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Db   2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278
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RESULT 15
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AC AAZ98856;
XX
DT 19-JUN-2000 (first entry)
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DE CD4-IgG2 chimeric heterotetramer heavy chain nucleotide sequence.
XX
KW CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment;
KW cytotoxic radionuclide; cell surface glycoprotein; prevent; infection;
KW cellular immune response interaction mediator; HIV interaction;
KW staging; prognosis; envelope glycoprotein burden; human; ds.
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OS Homo sapiens.
XX
PN US6034223-A.
XX
PD 07-MAR-2000.
XX
PF 07-JUN-1995; 95US-0477460.
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PR 07-AUG-1992; 92US-0927931.
PR 06-AUG-1993; 93WO-US07422.
PR 03-FEB-1995; 95US-0379516.
XX
PA (PROG-) PROGENICS PHARM INC.
XX
PI Allaway GP, Maddon PJ;
XX
DR WPI; 2000-269502/23.
DR P-PSDB; AAY85080.
XX
PT New immunoconjugate, used to treat, prevent or image human immune
PT deficiency virus infection, comprises radionuclide attached to
PT heterotetramer of CD4-immunoglobulin chimeras -
XX
PS Disclosure; Fig 4; 58pp; English.
XX
CC This sequence represents the CD4-IgG2 chimeric heavy chain nucleotide
CC sequence from the CD4-IgG2 chimeric heterotetramer. The invention relates
CC to an immunoconjugate comprising a cytotoxic radionuclide and a
CC heterotetramer of two heavy chains and two light chains. The cytotoxic
CC radionuclide is linked to either the heavy chains or the light chains, or
CC to all four chains, directly or through a bifunctional chelator. Both
CC heavy chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by
CC vector CD4-IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric
CC CD4-kappa chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a
CC non-polymorphic cell surface glycoprotein that is expressed on the
CC surface of helper T lymphocytes, cells of the monocyte/macrophage lineage
CC and dendritic cells. CD4 associates with major histocompatibility complex
CC (MHC) class II molecules on the surface of antigen presenting cells to
CC mediate efficient cellular immune response interactions. In humans CD4 is
CC the target of interaction with the human immunodeficiency virus HIV. The
CC immunoconjugate is used to kill cells infected with HIV, and for treating
CC or preventing infection. It is also used for imaging HIV-infected tissues
CC (for staging or prognosis of infection, and for assessing efficacy of
CC treatments). The immunoconjugate is also used to determine the HIV
CC envelope glycoprotein burden, once determined, this information is used
CC in the staging and prognosis of HIV infected patients. The
CC immunoconjugate should be active against all strains of HIV (since the
CC CD4-gp120 interaction is essential for infection). The heterotetramers
CC are assembled intracellularly and secreted efficiently from mammalian
CC cells, allowing high recovery and purification from the culture medium.
CC They have longer half-life in serum and greater avidity than heavy chain
CC dimers.
XX
SQ Sequence 2482 BP; 559 A; 812 C; 676 G; 435 T; 0 other;

Query Match 70.5%; Score 1584.6; DB 21; Length 2482;
Best Local Similarity 99.7%; Pred. No. 4.4e-308;

Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy    714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1787.6	79.5	2009	15	US-10-047-542-55	Sequence 55, Appl
3	1638	72.8	4694	15	US-10-000-433-3	Sequence 3, Appli
4	1613	71.7	2028	15	US-10-047-542-57	Sequence 57, Appl
5	1611.8	71.7	4723	15	US-10-000-433-2	Sequence 2, Appli
6	1584.6	70.5	2482	8	US-08-485-163-4	Sequence 4, Appli
7	1584.6	70.5	2482	10	US-09-766-995-3	Sequence 3, Appli
8	1580.4	70.3	1999	15	US-10-153-382-2	Sequence 2, Appli
9	1548	68.8	2770	15	US-10-027-075-29	Sequence 29, Appl
10	1547.2	68.8	2009	15	US-10-047-542-54	Sequence 54, Appl
11	1463.4	65.1	2071	15	US-10-216-484-116	Sequence 116, App
12	1458.6	64.9	2077	15	US-10-216-484-88	Sequence 88, Appl
13	1455.4	64.7	2073	15	US-10-216-484-142	Sequence 142, App
14	1455.4	64.7	2073	15	US-10-216-484-144	Sequence 144, App
15	1455.4	64.7	2077	15	US-10-216-484-156	Sequence 156, App
16	1453.8	64.6	2073	15	US-10-216-484-146	Sequence 146, App
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18	1093.8	48.6	11265	15	US-10-185-318-1	Sequence 1, Appli
19	1093.8	48.6	11265	15	US-10-185-799-1	Sequence 1, Appli
20	1086.4	48.3	1494	12	US-09-822-851B-4	Sequence 4, Appli
21	1086.4	48.3	1494	15	US-10-119-637A-4	Sequence 4, Appli
22	1042.4	46.3	2590	15	US-10-047-542-56	Sequence 56, Appl
23	901.8	40.1	1796	10	US-09-766-995-1	Sequence 1, Appli
24	898.6	40.0	1796	8	US-08-485-163-2	Sequence 2, Appli
25	815.2	36.2	1394	15	US-10-176-266-1	Sequence 1, Appli
26	807.2	35.9	1747	15	US-10-027-075-27	Sequence 27, Appl
27	806.4	35.9	1705	15	US-10-027-075-23	Sequence 23, Appl
28	804	35.7	1747	15	US-10-027-075-25	Sequence 25, Appl
29	545.4	24.3	1616	11	US-09-859-053-27	Sequence 27, Appl
30	545.4	24.3	1673	11	US-09-859-053-35	Sequence 35, Appl
31	545.4	24.3	1708	11	US-09-859-053-31	Sequence 31, Appl
32	542.4	24.1	1392	15	US-10-153-382-1	Sequence 1, Appli
33	542.4	24.1	1392	15	US-10-153-382-12	Sequence 12, Appl
34	542.4	24.1	1395	15	US-10-153-382-8	Sequence 8, Appli
35	542.4	24.1	1413	15	US-10-153-382-16	Sequence 16, Appl
36	541.8	24.1	1332	12	US-09-932-812-17	Sequence 17, Appl
37	541.8	24.1	1368	12	US-09-968-362-17	Sequence 17, Appl
c 38	540.6	24.0	571	10	US-09-864-761-8612	Sequence 8612, Ap
39	539.4	24.0	978	15	US-10-047-542-21	Sequence 21, Appl
40	539.2	24.0	1392	15	US-10-153-382-4	Sequence 4, Appli
41	539	24.0	1344	10	US-09-822-849A-33	Sequence 33, Appl
42	539	24.0	1539	10	US-09-822-849A-87	Sequence 87, Appl
43	539	24.0	1574	10	US-09-822-849A-82	Sequence 82, Appl
c 44	534.4	23.8	2732	10	US-09-822-849A-154	Sequence 154, App
45	514	22.9	1426	15	US-10-264-634-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-249-011A-23
; Sequence 23, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)..(417)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (655)..(948)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1341)..(1376)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1495)..(1821)

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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1919)..(2238)
US-09-249-011A-23

  Query Match             100.0%;  Score 2249;  DB 11;  Length 2249;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2249;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCTAGACCACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTG 60
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Db          1 TCTAGACCACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTG 60

Qy         61 TGCACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAG 120

Qy        121 TGAAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGAAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGA 180

Qy        181 GACAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATA 240

Qy        241 CAAACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCA 300

Qy        301 CAGCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAA 360

Qy        361 GAGCGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTG 420

Qy        421 AGTCCTTAAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGTCCTTAAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCA 480

Qy        481 GGGAGTGGGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGAGTGGGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGC 540

Qy        541 CCAGACACTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCAGACACTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGC 600

Qy        601 CCTGGGCCCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCTGGGCCCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCA 660

Qy        661 CCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAG 720

Qy        721 CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT 780

Qy        781 CAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCT 840

Qy        841 ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT 900

Qy        901 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAG 960

Qy        961 CTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCC 1020

Qy       1021 GGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGG 1080

Qy       1081 CCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCC 1140

Qy       1141 AGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTG 1200

Qy       1201 GCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCA 1260

Qy       1261 AAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAAC 1320

Qy       1321 TCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAA 1380

Qy       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440

Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCAC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCAC 1500

Qy       1501 CTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 1560

Qy       1561 CCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCC 1620

Qy       1621 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGG 1680

Qy       1681 AGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGC 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 AGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGC 1740

Qy       1741 TGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGA 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGA 1800

Qy       1801 AAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGC 1860
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Qy       1861 CGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGG 1920
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Db       1861 CGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGG 1920

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Db       1921 CAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAAC 1980

Qy       1981 CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG 2040
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Db       1981 CAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGG 2040

Qy       2041 GAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGAC 2100
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Db       2041 GAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGAC 2100

Qy       2101 GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC 2160
Db       2101 GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC 2160

Qy       2161 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC 2220
Db       2161 GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTC 2220

Qy       2221 TCCCTGTCCCCGGGTAAATGAGTGAATTC 2249
Db       2221 TCCCTGTCCCCGGGTAAATGAGTGAATTC 2249


RESULT 2
US-10-047-542-55
; Sequence 55, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
;  APPLICANT: LARRICK, JAMES W.
;  APPLICANT:  WYCOFF, KEITH L.
;  TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
;  TITLE OF INVENTION:  AND BACTERIAL DISEASES
;  FILE REFERENCE: 030905.0004.CIP1
;  CURRENT APPLICATION NUMBER: US/10/047,542
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: PCT/US01/13932
;  PRIOR FILING DATE: 2001-04-28
;  PRIOR APPLICATION NUMBER: 60/200,298
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 2009
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-047-542-55

  Query Match             79.5%;  Score 1787.6;  DB 15;  Length 2009;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1801;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy        439 AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGA 498
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Qy        499 GGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGC 558
Db         61 GGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGC 120

Qy        559 CTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 618
Db        121 CTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTC 179

Qy        619 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 678
Db        180 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 239

Qy        679 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGG 738
Db        240 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGG 299

Qy        739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 798
Db        300 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 359

Qy        799 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 858
Db        360 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 419

Qy        859 TGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC 918
Db        420 TGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC 479

Qy        919 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGT 978
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Qy        979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 1038
Db        540 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 599

Qy       1039 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 1098
Db        600 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 659

Qy       1099 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 1158
Db        660 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 719

Qy       1159 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAG 1218
Db        720 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAG 779

Qy       1219 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACT 1278
Db        780 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACT 839

Qy       1279 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC 1338
Db        840 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC 899

Qy       1339 AGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCC 1398
Db        900 AGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCC 959

Qy       1399 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1458
Db        960 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1019

Qy       1459 TGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCACCTGCGGCAGCACCGTCAG 1518
Db       1020 TGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCACCTGTGGCAGGACCGTCAG 1079

Qy       1519 TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA 1578
Db       1080 TCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA 1139

Qy       1579 CGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGG 1638
Db       1140 CGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGG 1199

Qy       1639 ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGT 1698
Db       1200 ACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGT 1259

Qy       1699 TCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACA 1758
Db       1260 TCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACA 1319

Qy       1759 AGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCA 1818
Db       1320 AGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCA 1379

Qy       1819 AAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCT 1878
Db       1380 AAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCT 1439

Qy       1879 GCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAG 1938
Db       1440 GCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACAG 1499

Qy       1939 GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC 1998
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Db       1500 GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGC 1559

Qy       1999 CTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG 2058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1560 CTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG 1619

Qy       2059 GAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTAC 2118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1620 GAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTAC 1679

Qy       2119 AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG 2178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1680 AGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG 1739

Qy       2179 ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAAA 2238
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1740 ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1799

Qy       2239 TGAGTG 2244
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Db       1800 TGAGTG 1805


RESULT 3
US-10-000-433-3
; Sequence 3, Application US/10000433
; Publication No. US20020199213A1
; GENERAL INFORMATION:
;  APPLICANT: Tomizuka, Kazuma
;  APPLICANT:  Ishida, Isao
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Halk, Ed
;  TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 014643-012110US
;  CURRENT APPLICATION NUMBER: US/10/000,433
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: US 60/250,340
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 4694
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Gamma4 heavy
;   OTHER INFORMATION: chain plasmid
;   OTHER INFORMATION: pG4HE
US-10-000-433-3

  Query Match             72.8%;  Score 1638;  DB 15;  Length 4694;
  Best Local Similarity   94.6%;  Pred. No. 0;
  Matches 1719;  Conservative    0;  Mismatches   95;  Indels    4;  Gaps    2;

Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              | |  ||  |||||||||||||  |||||||||||||||||| | ||||||||||| |||
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCGGGCCTGACTTTGGC-TGGGGGCAGGGAGGGGG 66

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
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Db         67 CTAAGGTGACGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 126

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              ||||||||| |||||| ||| ||||||||||||||||||||||||||||||||||||||||
Db        127 GGACCCTGCATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 186

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        187 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCC 246

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||

Db        247 CATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGG 306

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        307 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 366

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 426

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              |||||||||||||||||||||||||||||| ||| |||||  ||||||||||||||||||||
Db        427 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAG 486

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAG 546

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 606

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||| ||
Db        607 GCCCCAGCCCAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACC 666

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        667 ACCCCACTCATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCGGGCAGCCA 726

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||||| |||||||||||||||||| | || |||||||||||||||  |||||||||
Db        727 CAGGCTGGATGCCCCTACCCCAGGCCCTGCGCATACAGGGGCAGGTGCTGCGCTCAGACC 786

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
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Db        787 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 846

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              || |||||||||||||||| |||||||||||||||||||||||| ||||||||||||||||
Db        847 CTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCT 906

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCA 1389
              |||||||||||||  ||||| | ||  |  ||||||  | ||||||||||||||| ||||
Db        907 TCTCTCTGCAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCA 966

Qy       1390 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1026

Qy       1450 GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGG 1506
              |||||||| |||||||||| | ||||||||||||||||||||||||||         ||
Db        1027 GGCCCCAGCCGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGG 1086

Qy       1507 CAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
              | ||| |||||||||||| |||||||||||||||||||||||| |||||||||||||||||
Db        1087 GGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGA 1146

Qy       1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        1147 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCA 1206

Qy       1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
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Db        1207 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1266

Qy       1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
              |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||||
Db        1267 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1326

Qy       1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
              |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db        1327 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCA 1386
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Qy       1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866
             |||||||| |||||||||||||||| ||||||  |||||||||||||||||||| | ||||
Db       1387 TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACATGGACAGAGGTCAGCTC 1446

Qy       1867 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1926
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1447 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1506

Qy       1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
             |||||  |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db       1507 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC 1566

Qy       1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1567 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 1626

Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
             |||||||||||||||||||||||||||||||| ||||||  ||||||||||||||||||||
Db       1627 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 1686

Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
             ||||||||||||||| ||| ||||||||||||||||||||| ||||||| ||||||
Db       1687 TTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 1746

Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
             |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1747 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTG 1806

Qy       2227 TCCCCGGGTAAATGAGTG 2244
              || | ||||||||||||||
Db       1807 TCTCTGGGTAAATGAGTG 1824
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RESULT 4
US-10-047-542-57
; Sequence 57, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-047-542-57

Query Match 71.7%; Score 1613; DB 15; Length 2028;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 1713; Conservative 0; Mismatches 90; Indels 6; Gaps 4;

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Qy        439 AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGA 498
              |||||||||||||  |||||||||||||||||| | ||||||||||| ||||||||||||
Db          1 AGCTTTCTGGGGCAGGCCGGGCCTGACTTTGGC-TGGGGGCAGGGAGGGGGCTAAGGTGA 59

Qy        499 GGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGC 558
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         60 CGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACCCTGC 119

Qy        559 CTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 618
              ||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 ATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTC 179

Qy        619 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 678
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| ||||
Db        180 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCCCATCCGTCT 239

Qy        679 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGG 738
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        240 TCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTGG 299

Qy        739 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCG 798
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        300 TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCG 359

Qy        799 GCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 858
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        360 GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 419

Qy        859 TGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC 918
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Db        420 TGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAGC 479

Qy        919 CCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGT 978
              |||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        480 CCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGT 539

Qy        979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 1038
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Db        540 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 599

Qy       1039 CAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTC 1098
              |||||||||||||||| ||||||||||||||||||||||||||||||||| || ||||||||
Db        600 CAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACCACCCCACTC 659

Qy       1099 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 1158
              |||||||||||||||||||||| |||||||||||||||| ||||  ||||||||||
Db        660 ATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCCGGCA-CCACAGGCTGGA 718

Qy       1159 TGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAG 1218
              |||||||||||||||||| | || ||| |||||||||||  |||||||||||||||| ||
Db        719 TGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAGAG 777

Qy       1219 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACT 1278
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 CCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACT 837

Qy       1279 CCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGC 1338
              |||||||||| |||||||||||||||||||||| ||||||||||||||||||||||||||
Db        838 CCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTGC 897

Qy       1339 AGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCC 1398
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Db        898 AGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCAGGCCTCGCC 957

Qy       1399 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGC 1017

Qy       1459 TGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGT 1515
              |||||||||| | ||||||||||||||||||||||||||      ||  | ||| |
Db       1018 CGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGGGGGGACCAT 1077

Qy       1516 CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGG 1575
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 CAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGG 1137

Qy       1576 TCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACG 1635
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 TCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACG 1197

Qy       1636 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCA 1695
              |||| |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1198 TGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGCA 1257
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Qy      1696 CGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGT 1755
             ||| ||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db      1258 CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAGT 1317

Qy      1756 ACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAA 1815
             |||||||||||||||||||||||||||||||||  || ||||||||||||||||||||||
Db      1318 ACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAAG 1377

Qy      1816 CCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCC 1875
             |||||||||||||||| ||||||  |||||||||| |||||||||| ||||||||||||
Db      1378 CCAAAGGTGGGACCCACGGGGTGCGAGGGCCACACGGACAGAGGCCAGCTCGGCCCACCC 1437

Qy      1876 TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCA 1935
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db      1438 TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAGCCA 1497

Qy      1936 CAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACC 1995
             |||||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||
Db      1498 CAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGACC 1557

Qy      1996 TGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 2055
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1558 TGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1617

Qy      2056 CCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTC 2115
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Db      1618 CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1677

Qy      2116 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 2175
             |||||||| ||| ||||||||||||||||||||||| ||||||| ||||||||||||||||
Db      1678 TACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTCC 1737

Qy      2176 GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGT 2235
             |||||||||||||||||||||||||||||||| |||||||||||||||||| | ||||
Db      1738 GTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGGT 1797

Qy      2236 AAATGAGTG 2244
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Db      1798 AAATGAGTG 1806
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RESULT 5
US-10-000-433-2
; Sequence 2, Application US/10000433
; Publication No. US20020199213A1
; GENERAL INFORMATION:
;  APPLICANT: Tomizuka, Kazuma
;  APPLICANT:  Ishida, Isao
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Halk, Ed
;  TITLE OF INVENTION: TRANSGENIC TRANSCHROMOSOMAL RODENTS FOR MAKING HUMAN
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 014643-012110US
;  CURRENT APPLICATION NUMBER: US/10/000,433
;  CURRENT FILING DATE:  2001-11-30
;  PRIOR APPLICATION NUMBER: US 60/250,340
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4723
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Gamma1 heavy
;   OTHER INFORMATION: chain plasmid
;   OTHER INFORMATION: pCG7-96
US-10-000-433-2

  Query Match             71.7%;  Score 1611.8;  DB 15;  Length 4723;
  Best Local Similarity   94.3%;  Pred. No. 0;
  Matches 1722;  Conservative    0;  Mismatches   87;  Indels   18;  Gaps    4;
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Qy       430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
             | |  ||  |||||||||||||  ||| ||||||| ||||||||||||||||||| |||
Db         8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy       490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy       550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
             |||| ||     || ||||| ||| ||  ||||||| ||||||||||||||||||||||
Db       128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy       610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy       670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
             |||||||||||||||||| |||| ||||| |||| |||| | | ||||||||||||||||
Db       243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy       730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy       790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy       850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
             |||||||||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db       423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA 482

Qy       910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
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Db       483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy       970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
             |||||||||||||||||||||||||||||||| |||||||||||||||| ||||||| ||||
Db       543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy      1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
             ||||||| |||||||||||||||||||| |||| ||| ||||||||||||||||||||||
Db       603 GCCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662

Qy      1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
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Qy      1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
             |||||| |||||||||| |||||||||| |||||| |||||||||||||| ||||||||||
Db       722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACC 781

Qy      1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
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Db       782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 841

Qy      1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
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Db       842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy      1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAA 1380
             |||||||||||||| ||||| ||||| | |          ||||||||||||||||||||
Db       902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy      1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy      1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1022 CCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTG 1081

Qy      1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557
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Db       1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1141

Qy       1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
             |||||||||||||||||||| |||||||||||||||||||||||||||||||| ||||
Db       1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy       1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy       1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
             ||||||||| |||||||||| |||||||||||||||||||||| ||||||||||||
Db       1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
             ||||||| |||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857
             |||||||||||||||| |||||||||||||||| |||||  ||||||||||||||||||
Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917
             |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||||
Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
             |||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||||
Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828


RESULT 6
US-08-485-163-4
; Sequence 4, Application US/08485163
; Publication No. US20020098191A1
;  GENERAL INFORMATION:
;    APPLICANT:  Beaudry, Gary A.
;    APPLICANT:  Maddon, Paul J.
;    TITLE OF INVENTION:  CD4-GAMMA2 CD4-IgG2 CHIMERAS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,163
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  37690-II-1-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2482 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      CELL TYPE:  lymphocyte
US-08-485-163-4

  Query Match             70.5%;  Score 1584.6;  DB 8;  Length 2482;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy        714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy        774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy        894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy        954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy       1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1107

Qy       1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1167

Qy       1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1227

Qy       1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1287

Qy       1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1313
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1347

Qy       1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373
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Db       1348 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1407

Qy       1374 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1433

Db       1408 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy       1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493

Db       1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

Qy       1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1553

Db       1528 GCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1587

Qy       1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613

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Db       1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

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Qy       1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793

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Qy       1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1853

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Qy       1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913

Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy       1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973

Db       1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy       1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033

Db       2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

Qy       2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093

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Qy       2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153

Db       2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy       2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213

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Qy       2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244

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RESULT 7
US-09-766-995-3
; Sequence 3, Application US/09766995
; Patent No. US20020052481A1
; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway et al.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 2048/41215-CB/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/766,995
; CURRENT FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2482
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-766-995-3

Query Match 70.5%; Score 1584.6; DB 10; Length 2482;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713

Db        688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy        714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773

Db        748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy        774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833

Db        808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893

Db        868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy        894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953

Db        928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy        954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013

Db        988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy       1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073

Db       1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1107

Qy       1074 CCGGAGGCCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133

Db       1108 CCGGAGGCCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1167

Qy       1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193

Db       1168 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1227

Qy       1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253

Db       1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1287

Qy       1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1313

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Qy       1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373

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Qy       1374 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1433

Db       1408 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy       1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493

Db       1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

Qy       1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1553

Db       1528 GCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1587
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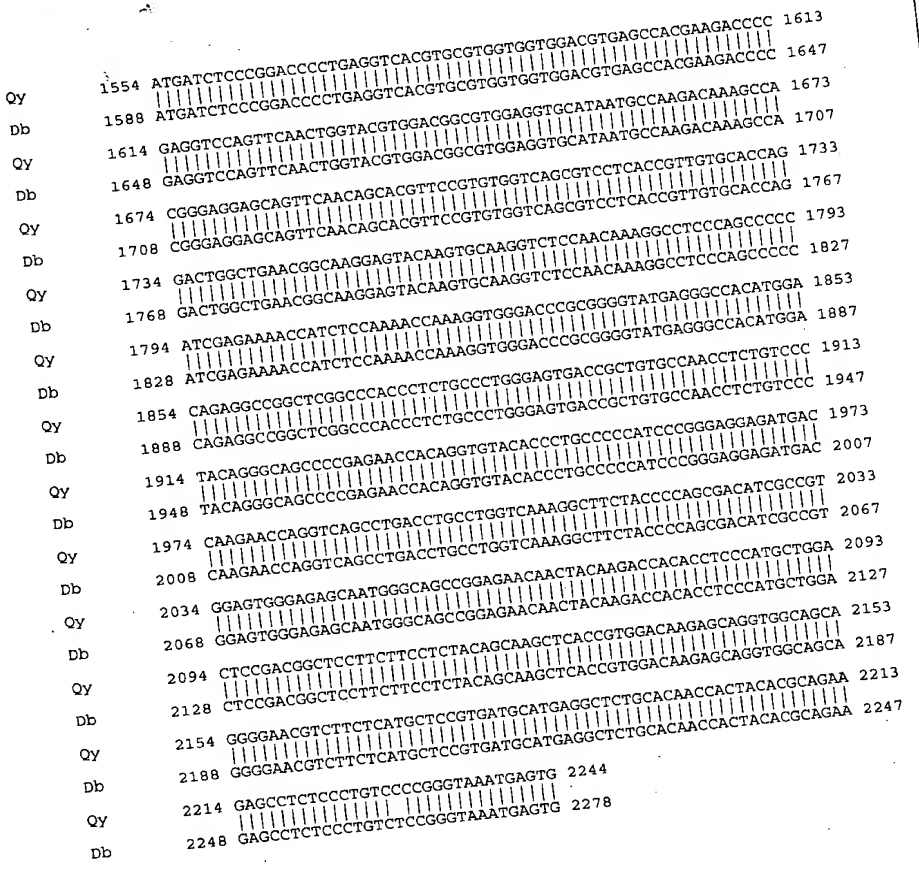
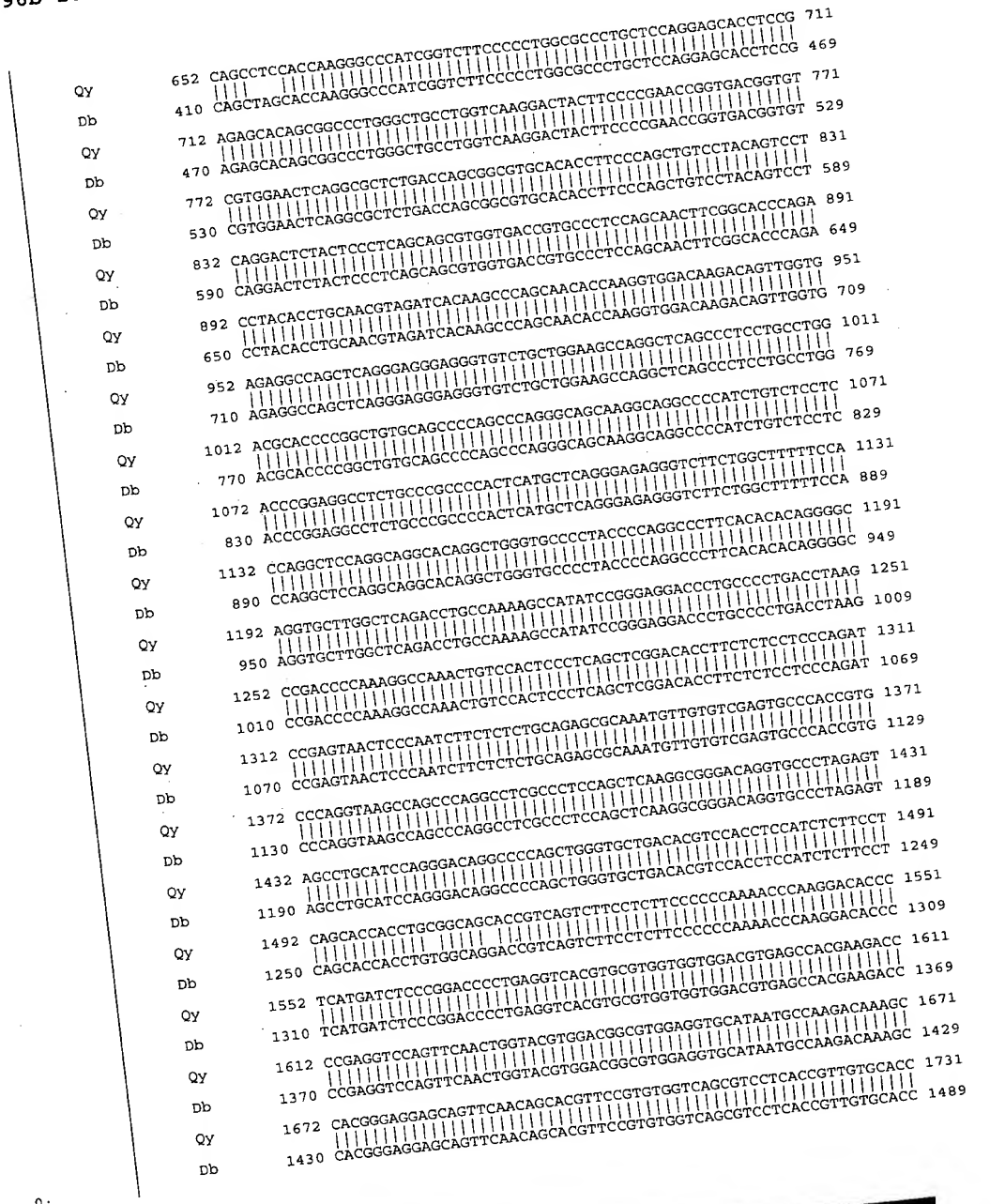


RESULT 8
US-10-153-382-2
; Sequence 2, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER PRODUCTS INC.
; TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
; FILE REFERENCE: PC23019A
; CURRENT APPLICATION NUMBER: US/10/153,382
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293042
; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-153-382-2

Query Match 70.3%; Score 1580.4; DB 15; Length 1999;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1584, Conservative 0; Mismatches 6; Indels 0; Gaps 0;



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Qy       1732 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1791
Db       1490 AGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCC 1549
Qy       1792 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATG 1851
Db       1550 CCATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATG 1609
Qy       1852 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1911
Db       1610 GACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC 1669
Qy       1912 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1971
Db       1670 CCTACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATG 1729
Qy       1972 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 2031
Db       1730 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCC 1789
Qy       2032 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTG 2091
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Qy       2092 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 2151
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Qy       2152 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 2211
Db       1910 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 1969
Qy       2212 AAGAGCCTCTCCCTGTCCCCGGGTAAATGA 2241
Db       1970 AAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1999

RESULT 9
US-10-027-075-29
; Sequence 29, Application US/10027075
; Publication No. US20020114814A1
;   GENERAL INFORMATION:
;        APPLICANT: Gray, Gary S. et al.
;        TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
;                            Having Modified Effector Functions and Uses Therefor
;        NUMBER OF SEQUENCES: 32
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD
;             STREET: 60 State Street, suite 510
;             CITY: Boston
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109-1875
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/027,075
;             FILING DATE: 20-Dec-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/227,595
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Amy E. Mandragouras
;             REGISTRATION NUMBER: 36,207
;             REFERENCE/DOCKET NUMBER: <Unknown>
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)227-7400
;             TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 29:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2770 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-027-075-29

  Query Match             68.8%;  Score 1548;  DB 15;  Length 2770;
  Best Local Similarity   93.8%;  Pred. No. 0;
  Matches 1716;  Conservative    0;  Mismatches   90;  Indels   24;  Gaps    9;

Qy       427 TAAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGT 486
Db       750 TAGAGGATCCCCAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGG 809
Qy       487 GGGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGAC 546
Db       810 GGGCTAAGGTGAGGCAGGTGGCGCCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGAC 868
Qy       547 ACTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGG 606
Db       869 ACTGGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGG 922
Qy       607 CCCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGG 666
Db       923 CCCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGG 982
Qy       667 GCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCC 726
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Db       1043 TGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCG 1102
Qy       787 CTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCC 846
Db       1103 CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCC 1162
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Db       1223 TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGG 1282
Qy       967 GAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGT 1026
Db       1283 GAGGGAGGGTGTCTGCTGGAAG-CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTAT 1341
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Db       1639 TCTTCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGG 1698

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Db       1699 TAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTG 1758

Qy       1438 CATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCAC 1497
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Qy       1555 TGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCG 1614
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Qy       1675 GGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGG 1734
             |||||||||||| |||||||||| ||| |||||||||||||||||||  |||||||||
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Qy       1735 ACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCA 1794
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Qy       1795 TCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGAC 1854
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Qy       1915 ACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACC 1974
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Db       2238 ACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 2297

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Db       2418 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 2477

Qy       2155 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 2214
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Db       2478 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 2537

Qy       2215 AGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db       2538 AGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2567
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RESULT 10
US-10-047-542-54
; Sequence 54, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
;  APPLICANT: LARRICK, JAMES W.
;  APPLICANT:  WYCOFF, KEITH L.
;  TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
;  TITLE OF INVENTION:  AND BACTERIAL DISEASES
;  FILE REFERENCE: 030905.0004.CIP1
;  CURRENT APPLICATION NUMBER: US/10/047,542
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: PCT/US01/13932
;  PRIOR FILING DATE: 2001-04-28
;  PRIOR APPLICATION NUMBER: 60/200,298
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
;   LENGTH: 2009
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-047-542-54

  Query Match             68.8%;  Score 1547.2;  DB 15;  Length 2009;
  Best Local Similarity   94.1%;  Pred. No. 0;
  Matches 1711;  Conservative    0;  Mismatches   83;  Indels   24;  Gaps    9;
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Qy        619 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 678
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Db        174 CCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCT 233

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Db        234 TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG 293

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Db        354 GCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGG 413

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Db        414 TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC 473

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Db        474 CCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGT 533

Qy        979 CTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCC 1038
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Db        593 CAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTC 651

Qy       1099 ATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGG 1158
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Db        710 TGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAG 769

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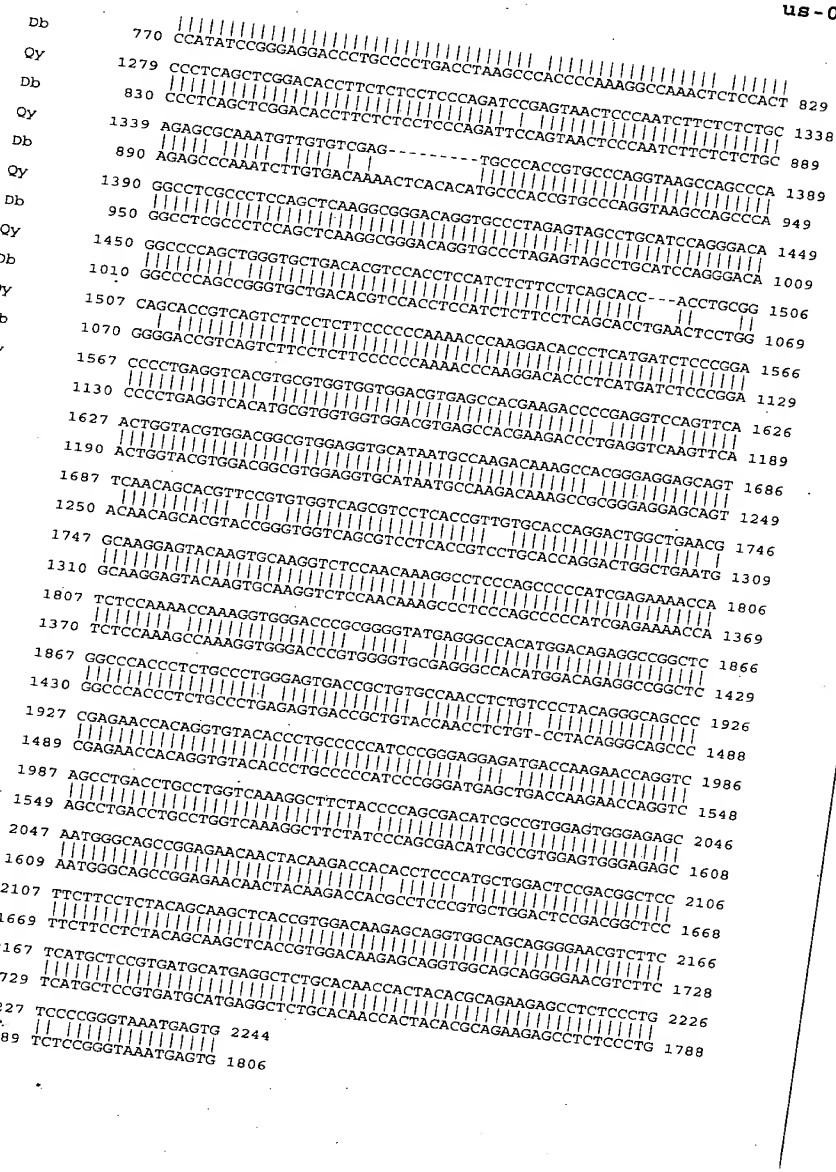

ESULT 11

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US-10-216-484-116
; Sequence 116, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976A1ufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 116
;  LENGTH: 2071
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;  OTHER INFORMATION; encoding the heavy chain of a humanized anti-Fas
;  OTHER INFORMATION: antibody
;  FEATURE:
;  NAME/KEY: sig peptide
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;  LOCATION: (1716)..(2036)
US-10-216-484-116

  Query Match            65.1%;  Score 1463.4;  DB 15;  Length 2071;
  Best Local Similarity  82.2%;  Pred. No. 0;
  Matches 1848;  Conservative    0;  Mismatches  166;  Indels  235;  Gaps    5;

Qy          8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
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Db         17 CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTC 76

Qy         68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
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Db         77 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT 136

Qy        128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
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Db        137 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGGC 196

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Db        257 CAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCACTAGCACAGCCTA 316

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Db        317 CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAAATAG 376

Qy        368 CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTT 427
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Qy        428 AAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTG 487
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Qy        488 GGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACA 547
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Qy        548 CTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC 607
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Db        755 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATG 814

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Db       1234 ATCCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC 1293

Qy       1499 ---ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 1555
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Db       1294 TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 1353

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Qy       1736 CTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCAT 1795
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Db       1534 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1593

Qy       1796 CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGACA 1855
              |||||||||||||||||| |||||||||||||||| |||||  ||||||||||||||||
Db       1594 CGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACA 1653

Qy       1856 GAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTA 1915
              |||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||
Db       1654 GAGGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTA 1713

Qy       1916 CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1773

Qy       1976 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG 2035
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1774 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG 1833

Qy       2036 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACT 2095
              |||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||
Db       1834 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT 1893
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Qy       2096 CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 2155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 1953

Qy       2156 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2013

Qy       2216 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
             |||||||||||||||||||||||||||||
Db       2014 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2042
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RESULT 12
US-10-216-484-88
; Sequence 88, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976A1ufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 88
;   LENGTH: 2077
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;   OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
;   OTHER INFORMATION: antibody
;   FEATURE:
;   NAME/KEY: sig peptide
;   LOCATION:  (27)..(83)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION:  (741)..(1131)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION:  (1177)..(1294)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION:  (1625)..(1721)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION:  (27)..(740)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION:  (1132)..(1176)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION:  (1295)..(1624)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION:  (1722)..(2042)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION:  (84)..(740)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION:  (1132)..(1176)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION:  (1295)..(1624)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION:  (1722)..(2042)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION:  (27)..(740)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION:  (1132)..(1176)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION:  (1295)..(1624)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION:  (1722)..(2042)
US-10-216-484-88
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Query Match 64.9%; Score 1458.6; DB 15; Length 2077;
Best Local Similarity 82.0%; Pred. No. 0;
Matches 1845; Conservative 0; Mismatches 169; Indels 235; Gaps 5;

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Qy         8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
             ||||||||| |||| |||||||||| |||| |||| | ||||||||||||||| |||||
Db        23 CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTC 82

Qy        68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
             |||||||| |||||||||||||||||||||| |||||||||||    |||||||||||
Db        83 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT 142

Qy       128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
             ||||||||| ||||| |||||||| |||||    ||    || |||||||| | ||||||
Db       143 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGGC 202

Qy       188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
             ||||||||| | || |||||||| |||| ||| || ||  ||  |||| ||||||
Db       203 CCCTGGACAGAGGCTTGAGTGGATGGGAGAGATTGATCCTTCTGATAGCTATACTAACTA 262

Qy       248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 307
             ||| || ||||| |||||||||||||| ||||||||||||   || | ||||||||||||
Db       263 CAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCGCTAGCACAGCCTA 322

Qy       308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC 367
             ||||| || ||  ||||||||||||||| ||||| || |||||||||||||||||||
Db       323 CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAAATAG 382

Qy       368 CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTT 427
             ||||   || |||||                                           
Db       383 GGACTATAGTAACAACTGG---------------------------------------- 401

Qy       428 AAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTG 487
             |     | | | ||||||||||    | ||||                          
Db       402 ------TACTTCGATGTCTGGGGCGAAGGGACCCTGG---------------------- 432

Qy       488 GGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACA 547
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       433 ------------------------------------------------------------ 432

Qy       548 CTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC 607
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       433 ------------------------------------------------------------ 432

Qy       608 CCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGG 667
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       433 ------------------------------TCACCGTCTCCTCAGCCTCCACCAAGGG 460

Qy       668 CCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCT 727
             |||||||||||||||||||| |||| |||||||||| | | ||||||||||||||||||
Db       461 CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT 520

Qy       728 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 787
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       521 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 580
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Qy       788 TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 847
Db       581 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 640

Qy       848 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 907
Db       641 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT 700

Qy       908 AGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGG 967
Db       701 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGG 760

Qy       968 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG 1027
Db       761 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATG 820

Qy      1028 CAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGC 1087
Db       821 CAGTCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGC 880

Qy      1088 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG 1147
Db       881 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGG 939

Qy      1148 CACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGA 1207
Db       940 CACAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGA 999

Qy      1208 CCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCA 1267
Db       1000 CCTGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCA 1059

Qy      1268 AACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAAT 1327
Db       1060 AACTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAAT 1119

Qy      1328 CTTCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGT 1378
Db       1120 CTTCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGT 1179

Qy      1379 AAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC 1438
Db       1180 AAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC 1239

Qy      1439 ATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC 1498
Db       1240 ATCCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC 1299

Qy      1499 ---ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 1555
Db       1300 TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 1359

Qy      1556 GATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGA 1615
Db       1360 GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA 1419

Qy      1616 GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG 1675
Db       1420 GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG 1479

Qy      1676 GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGA 1735
Db       1480 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA 1539

Qy      1736 CTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCAT 1795
Db       1540 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1599

Qy      1796 CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGACA 1855
Db       1600 CGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACA 1659

Qy      1856 GAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTA 1915
Db       1660 GAGGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTA 1719

Qy      1916 CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1975
Db       1720 CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1779

Qy      1976 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG 2035
Db       1780 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG 1839

Qy      2036 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACT 2095
Db       1840 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT 1899

Qy      2096 CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 2155
Db       1900 CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 1959

Qy      2156 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2215
Db       1960 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2019

Qy      2216 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
Db       2020 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2048
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RESULT 13
US-10-216-484-142
; Sequence 142, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 142
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
; OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
; OTHER INFORMATION: antibody
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: (23)..(79)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (737)..(1127)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1173)..(1290)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1621)..(1717)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (23)..(736)
; FEATURE:
; NAME/KEY: exon

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;   LOCATION: (1128)..(1172)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1291)..(1620)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1718)..(2038)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (80)..(736)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (1128)..(1172)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (1291)..(1620)
;   FEATURE:
;   NAME/KEY: mat peptide
;   LOCATION: (1718)..(2038)
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;   NAME/KEY: CDS
;   LOCATION: (23)..(736)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1128)..(1172)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1291)..(1620)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1718)..(2038)
US-10-216-484-142

  Query Match             64.7%;  Score 1455.4;  DB 15;  Length 2073;
  Best Local Similarity   81.9%;  Pred. No. 0;
  Matches 1843;  Conservative    0;  Mismatches  171;  Indels  235;  Gaps    5;

Qy          8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
              ||||||||| |||| |||||||||| ||||  |||| | ||||||||||||| || ||
Db         19 CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTC 78

Qy         68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
              |||||||| ||||||||||||||||||||||| |||||||||||    ||||||||||
Db         79 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT 138

Qy        128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
              ||||||||| ||||| |||||||| |||||    ||    || |||||||| | ||||||
Db        139 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGGC 198

Qy        188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
              |||||||||| || |||||||| |||| ||| ||  ||   ||    |||| ||||||
Db        199 CCCTGGACAGGGACTTGAGTGGATGGGAGAGATTGATCCTTCTGATAGCTATACTAACTA 258

Qy        248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 307
              ||| || ||||| |||||||||||||| ||||||||||||  || || ||||||||||||
Db        259 CAATCAAAAGTTCAAGGGCAAGGCCACATTGACTGTAGACACATCCACTAGCACAGCCTA 318

Qy        308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC 367
              |||||  ||  ||     |||||||||||||| ||||| || ||||||||||||||||
Db        319 CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAAATAG 378

Qy        368 CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTT 427
                 ||||   ||  |||||       | |
Db        379 GGACTATAGTAACAACTGGTACTTCGAT---------------------------------- 406

Qy        428 AAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTG 487

Db        407 ------------------------------------------------------------ 406

Qy        488 GGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACA 547

Db        407 ------------------------------------------------------------ 406
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Qy        548 CTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC 607
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Db        407 ----------------------------------------------GTCTGGGGCCAAGGT 421

Qy        608 CCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGG 667
               ||     |  ||  | ||                            ||||||||||||||||
Db        422 ACACTGGTCACCGTCTCC-------------------------TCAGCCTCCACCAAGGG 456

Qy        668 CCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCT 727
              |||||||||||||||||||| |||| ||||| |||||||||  | | ||||||||||||||
Db        457 CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT 516

Qy        728 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 576

Qy        788 TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 847
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        577 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 636

Qy        848 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 907
              |||||||||||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db        637 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT 696

Qy        908 AGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGG 967
              |||||||||||||||||||||||||||||||||| |||||||||||||||||| |||||
Db        697 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGG 756

Qy        968 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG 1027
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||| ||
Db        757 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATG 816

Qy       1028 CAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGC 1087
              ||| ||||| |||||||||||||||||||| |||| ||| ||||||||||||||||||
Db        817 CAGTCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGC 876

Qy       1088 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG 1147
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||  ||||||
Db        877 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGG 935

Qy       1148 CACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGA 1207
              ||||||| |||||||||| |||||||||| |||||| |||||||||||||| ||||||||
Db        936 CACAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGA 995

Qy       1208 CCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCA 1267
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 CCTGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCA 1055

Qy       1268 AACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAAT 1327
              |||| |||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        1056 AACTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAAT 1115

Qy       1328 CTTCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGT 1378
              |||||||||||||| ||||| ||||| | |         ||||||||||||||||||
Db        1116 CTTCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGT 1175

Qy       1379 AAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC 1438
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1176 AAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGC 1235

Qy       1439 ATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC 1498
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        1236 ATCCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC 1295

Qy       1499 ---ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 1555
                 ||    ||  | |||||||||||||||||||||||||||||||||||||||||||||
Db        1296 TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCAT 1355

Qy       1556 GATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGA 1615
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||| ||
Db        1356 GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGA 1415

Qy       1616 GGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG 1675
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Db       1416 GGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG 1475
Qy       1676 GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGA 1735
Db       1476 GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA 1535
Qy       1736 CTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1795
Db       1536 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT 1595
Qy       1796 CGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACA 1855
Db       1596 CGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACA 1655
Qy       1856 GAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTA 1915
Db       1656 GAGGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTA 1715
Qy       1916 CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1975
Db       1716 CAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCA 1775
Qy       1976 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGG 2035
Db       1776 AGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGG 1835
Qy       2036 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT 2095
Db       1836 AGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT 1895
Qy       2096 CCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 2155
Db       1896 CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGG 1955
Qy       2156 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2215
Db       1956 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA 2015
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Db       2016 GCCTCTCCCTGTCCCCGGGTAAATGAGTG 2044
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; Sequence 144, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
;  APPLICANT: Serizawa, No. US20030103976A1ufusa
;  APPLICANT:  Haruyama, Hideyuki
;  APPLICANT:  Nakahara, Kaori
;  APPLICANT:  Tamaki, Ikuko
;  APPLICANT:  Takahashi, Tohru
;  TITLE OF INVENTION: Anti-Fas Antibodies
;  FILE REFERENCE: 980126CIP/HG
;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 144
;    LENGTH: 2073
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;    OTHER INFORMATION: encoding the heavy chain of a humanized anti-Fas
;    OTHER INFORMATION: antibody
;    FEATURE
;    NAME/KEY: sig peptide
;    LOCATION: (23)..(79)
;    FEATURE:
;    NAME/KEY: intron
;    LOCATION: (737)..(1127)
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;    NAME/KEY: intron
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;    FEATURE:
;    NAME/KEY: intron
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;    FEATURE:
;    NAME/KEY: exon
;    LOCATION: (23)..(736)
;    FEATURE:
;    NAME/KEY: exon
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;    NAME/KEY: exon
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;    FEATURE:
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;    FEATURE:
;    NAME/KEY: mat peptide
;    LOCATION: (1718)..(2038)
;    FEATURE:
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;    LOCATION: (23)..(736)
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1128)..(1172)
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;    NAME/KEY: CDS
;    LOCATION: (1291)..(1620)
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1718)..(2038)
US-10-216-484-144

  Query Match           64.7%;  Score 1455.4;  DB 15;  Length 2073;
  Best Local Similarity 81.9%;  Pred. No. 0;
  Matches 1843;  Conservative    0;  Mismatches  171;  Indels  235;  Gaps    5;

Qy         8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
Db        19 CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTC 78
Qy        68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
Db        79 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT 138
Qy       128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
Db       139 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGGC 198
Qy       188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
Db       199 CCCTGGACAGGGACTTGAGTGGATGGGAGAGATTGATCCTTCTGATAGCTATACTAACTA 258
Qy       248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 307
Db       259 CAATCAAAAGTTCAAGGGCAAGGCCACAATAACTGTAGACACATCCACTAGCACAGCCTA 318
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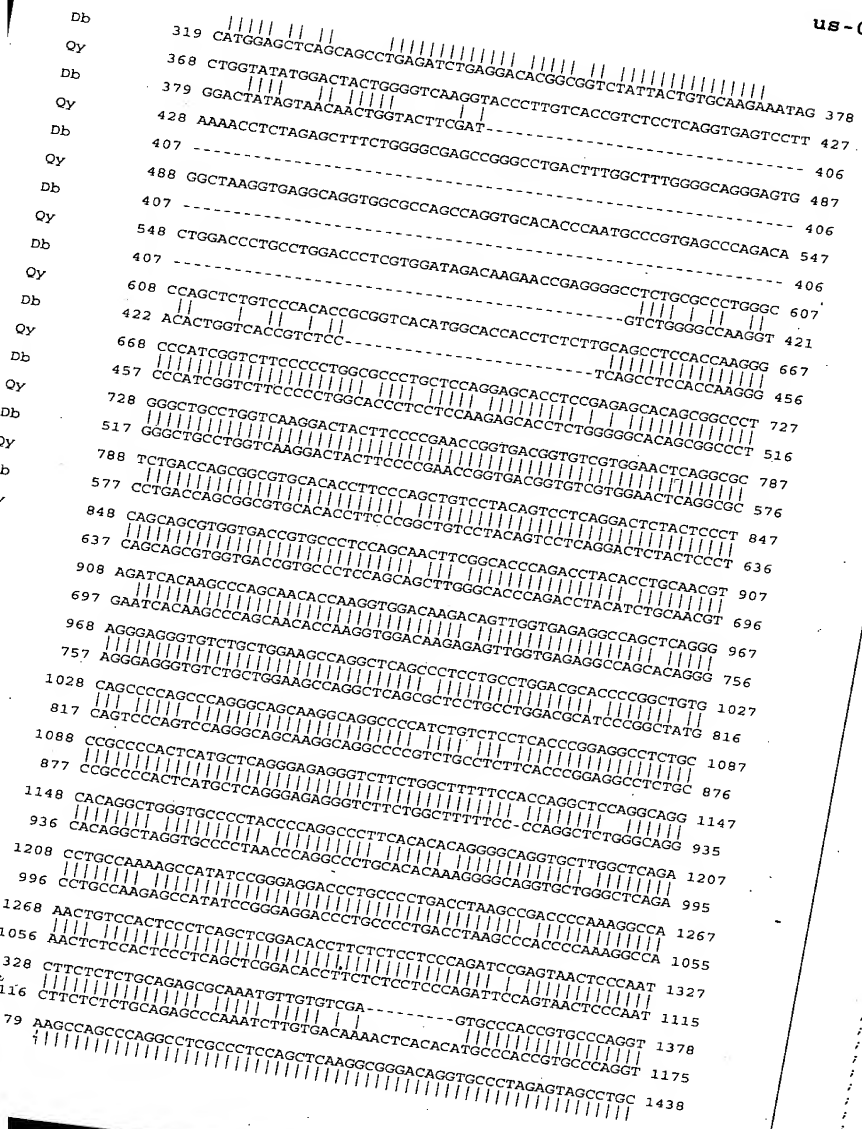

RESULT 15
US-10-216-484-156
; Sequence 156, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER US/10/216,484
; CURRENT FILING DATE 2002-08-09

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;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 156
;   LENGTH: 2077
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: sig peptide
;   LOCATION: (27)..(83)
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (741)..(1131)
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;   FEATURE:
;   NAME/KEY: exon
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;   LOCATION: (1132)..(1176)
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;   NAME/KEY: exon
;   LOCATION: (1295)..(1624)
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (1722)..(2042)
;   FEATURE:
;   NAME/KEY: mat peptide
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;   NAME/KEY: mat peptide
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;   NAME/KEY: mat peptide
;   LOCATION: (1722)..(2042)
;   FEATURE:
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;   LOCATION: (27)..(740)
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;   NAME/KEY: CDS
;   LOCATION: (1722)..(2042)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Designed DNA
;   OTHER INFORMATION: encoding the heavy chain of humanized anti-Fas
;   OTHER INFORMATION: antibody
US-10-216-484-156

  Query Match            64.7%;  Score 1455.4;  DB 15;  Length 2077;
  Best Local Similarity  81.9%;  Pred. No. 0;
  Matches 1843;  Conservative    0;  Mismatches  171;  Indels  235;  Gaps    5;

Qy          8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
              ||||||||| |||| |||||||||| ||||  ||||  | ||||||||||||||| |||||
Db         23 CACCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCACTC 82

Qy         68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
              ||||||||| |||||||||||||||||||||||| |||||||||||   ||||||||||

Db         83 TCAGGTCCAACTGGTGCAGTCTGGGGCTGAGGTCAAGAAGCCTGGGGCTTCAGTGAAGGT 142

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              ||||||||| ||||| |||||||| ||||    ||    || ||||||||  |||||||
Db        143 GTCCTGCAAGGCTTCTGGCTACACCTTCACCAGCTACTGGATGCAGTGGGTACGACAGGC 202

Qy        188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
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Db        203 CCCTGGACAGGGCCTTGAGTGGATGGGAGAGATTGATCCTTCTGATAGCTATACTAACTA 262

Qy        248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 307
              ||| || ||||| ||||||  || ||||||  |||  |||||  || || ||||||||||||
Db        263 CAATCAAAAGTTCAAGGGCCGGGTCACAATCACTCGAGACACATCCACTAGCACAGCCTA 322

Qy        308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAGCGGC 367
              ||||| || ||      |||||||||||||| ||||| || ||||||||||||||||
Db        323 CATGGAGCTCAGCAGCCTGAGATCTGAGGACACGGCGGTCTATTACTGTGCAAGAAATAG 382

Qy        368 CTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTT 427
              ||||   || |||||
Db        383 GGACTATAGTAACAACTGG---------------------------------------- 401

Qy        428 AAAACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTG 487
                  |    | | ||||||||||   |  ||||
Db        402 ------TACTTCGATGTCTGGGGCGAAGGGACCCTGGT---------------------- 433

Qy        488 GGCTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACA 547
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 ------------------------------------------------------------ 433

Qy        548 CTGGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGC 607
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 ------------------------------------------------------------ 433

Qy        608 CCAGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGG 667
                                                  ||||       ||||||||||||||||
Db        434 --------------------------------CACCGTCTCCTCAGCCTCCACCAAGGG 460

Qy        668 CCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCT 727
              |||||||||||||||||||| |||| ||||| ||||||||| | | ||||||||||||||
Db        461 CCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCT 520

Qy        728 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 787
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        521 GGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC 580

Qy        788 TCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 847
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        581 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT 640

Qy        848 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGT 907
              |||||||||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db        641 CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGT 700

Qy        908 AGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGG 967
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Db        701 GAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGG 760

Qy        968 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG 1027
              |||||||||||||||||||||||||||||||| |||||||||||||||| ||||||| ||
Db        761 AGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATG 820

Qy       1028 CAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGC 1087
              ||| ||||| |||||||||||||||||||| |||| ||| ||||||||||||||||||
Db        821 CAGTCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGC 880

Qy       1088 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGG 1147
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||  ||||||
Db        881 CCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGG 939

Qy       1148 CACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGA 1207
              |||||||| |||||||||| |||||||||| |||||| |||||||||||||| ||||||||
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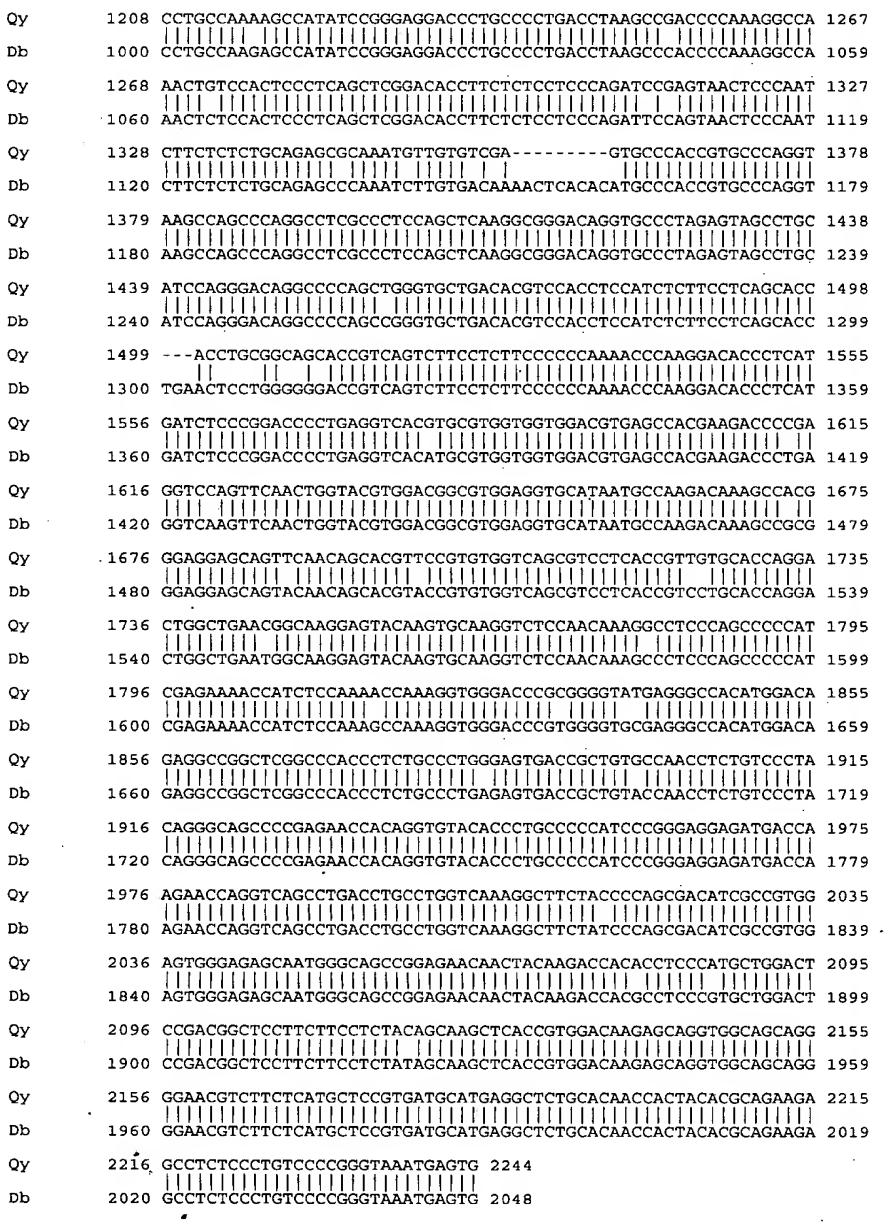

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Sat Jul 19 10:01:51 2003

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 09:26:19 ; Search time 119.256 Seconds
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5783.490 Million cell updates/sec

Title: US-09-627-896B-23
Perfect score: 2249
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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1804	80.2	2560	2	US-07-916-098A-44	Sequence 44, Appl
	2	1742.6	77.5	2287	5	PCT-US96-10043-8	Sequence 8, Appli
	3	1651.6	73.4	2287	1	US-08-480-036-1	Sequence 1, Appli
	4	1651.6	73.4	2287	1	US-08-461-968A-1	Sequence 1, Appli
	5	1651.6	73.4	2287	2	US-08-462-571-1	Sequence 370, App
	6	1611.8	71.7	4723	4	US-09-042-353-370	Sequence 218, App
	7	1611.8	71.7	4723	4	US-08-758-417A-218	Sequence 43, Appl
	8	1610.8	71.6	2029	2	US-07-916-098A-43	Sequence 3, Appli
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	10	1584.6	70.5	2482	4	US-08-379-516-3	Sequence 3, Appli
	11	1584.6	70.5	2482	4	US-09-329-916-3	Sequence 3, Appli
	12	1584.6	70.5	2482	4	US-08-485-372A-3	Sequence 3, Appli
	13	1584.6	70.5	2482	4	US-09-409-006A-3	Sequence 3, Appli
	14	1584.6	70.5	2482	4	US-08-484-681-3	Sequence 3, Appli
	15	1584.6	70.5	2482	5	PCT-US93-07422-3	Sequence 29, Appl
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c	27	1438.6	64.0	3282	5	PCT-US95-08743-169	Sequence 169, App
c	28	1438.6	64.0	13254	1	US-08-276-852-156	Sequence 156, App
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c	30	1438.6	64.0	13254	1	US-08-899-575-156	Sequence 156, App
c	31	1438.6	64.0	13254	1	US-08-899-575-170	Sequence 170, App
c	32	1438.6	64.0	13254	1	US-08-899-575-156	Sequence 156, App
c	33	1438.6	64.0	13254	1	US-08-899-575-170	Sequence 170, App
c	34	1438.6	64.0	13254	5	PCT-US95-08743-156	Sequence 418, App
c	35	1438.6	64.0	13254	5	PCT-US95-08743-170	Sequence 268, App
c	36	1438.6	64.0	13254	4	US-09-042-353-418	Sequence 5, Appli
	37	1437	63.9	4926	4	US-08-758-417A-268	Sequence 5, Appli
	38	1437	63.9	4926	4	US-09-247-352-5	Sequence 1, Appli
	39	1435.8	63.8	8614	4	US-09-466-635-5	Sequence 41, Appl
	40	1435.8	63.8	8614	4	US-08-070-116A-1	Sequence 41, Appl
	41	1426.4	63.4	2399	2	US-08-444-644-41	Sequence 18, Appl
	42	1410.4	62.7	10844	3	US-08-232-246A-41	Sequence 18, Appl
	43	1410.4	62.7	10844	4	US-08-444-644-18	
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ALIGNMENTS

RESULT 1
US-07-916-098A-44
; Sequence 44, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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;    ANTI-SENSE:  NO
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;      NAME/KEY:  intron
;      LOCATION:  1432..1549
;    FEATURE:
;      NAME/KEY:  intron
;      LOCATION:  1880..1976
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pMDR1002 insert: pre-5A8
;      OTHER INFORMATION:  humanized heavy chain"
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  12..435
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  712..1005
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1396..1431
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1550..1879
;    FEATURE:
;      NAME/KEY:  exon
;      LOCATION:  1977..2296
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(12..435, 712..1005, 1396..1431, 1550..1879,
;      LOCATION:  1977..2296)
US-07-916-098A-44

  Query Match          80.2%;  Score 1804;  DB 2;  Length 2560;
  Best Local Similarity  89.2%;  Pred. No. 0;
  Matches 2049;  Conservative    0;  Mismatches  185;  Indels   64;  Gaps    7;

Qy          8 CACCATGGGTTGGAACTGTATCATCTTCTTTCTGGTTACCACAGCTACAGGTGTGCACTC 67
              ||||||||  |||| ||| |  ||||||   ||  |  |   |||  ||||||  |||||
Db          8 CACCATGGACTGGACCTGGAGGGTCTTCTGCTTGCTGGCTGTAGCACCAGGTGCCCACTC 67

Qy         68 CCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTGAAGGT 127
              |||||||||  |||  | |||||||  |||||  |||||  |||||||||    ||||||||||
Db         68 CCAGGTCCAACTGCAGGAGTCTGGAGCTGAAGTGAAAAAGCCTGGGGCTTCAGTGAAGGT 127

Qy        128 GTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGACAGGC 187
              |||||||||  |||||  ||  ||||||||||||    ||||  ||||||  ||||||||  |||||
Db        128 GTCCTGCAAGGCTTCTGGATACACATTCACTAGCTATGTTATACACTGGGTGAGGCAGGC 187

Qy        188 TCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACAAACTA 247
               |||||  ||||||||  ||||||||||  |||||||  ||||  |||||  |||  ||||
Db        188 GCCTGGGCAGGGCCTTGAGTGGATTGGATATATTAATCCTTACAATGATGGTACTGACTA 247

Qy        248 CAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACAGCCTA 307
              |  |  |||||||  ||  ||||||||||||  |||||  |||||    ||  ||  |  |||||||||
Db        248 CGATGAGAAGTTCAAAGGCAAGGCCACAGTGACTTTAGACCCATCCACCAACACAGCCTA 307

Qy        308 TATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGAG---- 363
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                ||||| ||  ||     ||||  ||||||||  ||  ||  ||  ||||||||||||||||
Db        308 CATGGAGCTCAGCAGCCTGAGGTCTGAGGACACTGCGGTCTATTACTGTGCAAGAGAGAA 367

Qy        364 --------------CGGCCTGGTATATGGACTACTGGGGTCAAGGTACCCTTGTCACCGT 409
                           |||    |   | |  ||||||||  |||||  |||||  ||||||||
Db        368 GGATAACTACGCGACGGGGGCCTGGTTTGCTTACTGGGGCCAAGGGACCCTGGTCACCGT 427

Qy        410 CTCCTCAGGTGAGTCCTTAAA----------------------------------ACCT 434
              ||||||||||||||||  |                                    |  ||
Db        428 CTCCTCAGGTGAGTCCTAAGCTTGGTACCCGGGAATTCAGATCTGCAGCATGCTCGAGCT 487

Qy        435 CTAG-----AGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              ||||     ||||||||||||  ||||||||||||||||||  ||||||||||  |||
Db        488 CTAGATATCAGCTTTCTGGGGCAGGCCGGGCCTGACTTTGGCTG-GGGGCAGGGAGGGGG 546

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              |||||||||  |||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        547 CTAAGGTGACGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 606

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              |||||||||  |||||  |||  ||||||||||||||||||||||||||||||||||||||
Db        607 GGACCCTGCATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 666

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||
Db        667 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCC 726

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              ||||  |||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        727 CATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGG 786

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        787 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 846

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        847 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 906

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              |||||||||||||||||||||||||||||||  |||  |||||  ||||||||||||||||||||
Db        907 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAG 966

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||  |||||||
Db        967 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAG 1026

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1086

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              |||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||  ||
Db       1087 GCCCCAGCCCAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACC 1146

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||||||||||||  ||||  ||
Db       1147 ACCCCACTCATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCCGGCA-CCA 1205

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              ||||||||  |||||||||||||||||||  |  ||  |||  ||||||||||  |||||||||
Db       1206 CAGGCTGGATGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACC 1264

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
              ||||||  ||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db       1265 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 1324

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              ||  ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1325 CTCTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCT 1384

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCAGGTAAGCCAGCCCA 1389
              |||||||||||||  |||||  |  ||  |  ||||||  |  ||||||||||||||||  ||||
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Db       1385 TCTCTCTGCAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCA 1444

Qy       1390 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1445 GGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACA 1504

Qy       1450 GGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGG 1506
             |||||||| ||||||||| | ||||||||||||||||||||||||||     ||
Db       1505 GGCCCCAGCCGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGG 1564

Qy       1507 CAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGA 1566
                | ||| |||||||||| |||||||||||||||||||||| ||||||||||||||||
Db       1565 GGGGACCATCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGA 1624

Qy       1567 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCA 1626
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Db       1625 CCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCA 1684

Qy       1627 ACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGT 1686
             |||||||||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db       1685 ACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT 1744

Qy       1687 TCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACG 1746
             |||||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db       1745 TCAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACG 1804

Qy       1747 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCA 1806
             |||||||||||||||||||||||||||||||||||||||  || ||||||||||||||||
Db       1805 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCA 1864

Qy       1807 TCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTC 1866
             |||||||| |||||||||||||| ||||||  |||||||||| |||||||||| ||||
Db       1865 TCTCCAAAGCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACACGGACAGAGGCCAGCTC 1924

Qy       1867 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1926
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1925 GGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCC 1984

Qy       1927 CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTC 1986
             ||||| |||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1985 CGAGAGCCACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTC 2044

Qy       1987 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2046
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2045 AGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGC 2104

Qy       2047 AATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCC 2106
             |||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||||
Db       2105 AATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC 2164

Qy       2107 TTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC 2166
             ||||||||||||||| ||| |||||||||||||||||||| ||||||| ||||||||||||
Db       2165 TTCTTCCTCTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTC 2224

Qy       2167 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTG 2226
             |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       2225 TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTG 2284

Qy       2227 TCCCCGGGTAAATGAGTG 2244
             || | ||||||||||||||
Db       2285 TCTCTGGGTAAATGAGTG 2302


RESULT 2
PCT-US96-10043-8
; Sequence 8, Application PC/TUS9610043
;  GENERAL INFORMATION:
;    APPLICANT:  The General Hospital Corporation
;    TITLE OF INVENTION:  P-SELECTIN LIGANDS AND RELATED MOLECULES
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,213
;      FILING DATE:  14-JUN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  00786/284001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US96-10043-8

  Query Match           77.5%;  Score 1742.6;  DB 5;  Length 2287;
  Best Local Similarity  89.1%;  Pred. No. 0;
  Matches 2038;  Conservative    0;  Mismatches  184;  Indels   65;  Gaps   12;

Qy          6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACAGCTACAGGTGTG 62
              ||||||||||  |||| ||| |   || |||||||| ||||  |  ||||||||||||
Db          7 ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTGTGGTGGCAGCAGCTACAGGTGTC 66

Qy         63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
              || |||||||| ||||||||||||||||||||||||||||||||||||  ||| |||
Db         67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG 126

Qy        123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
              ||||| |||||||| ||||| ||   ||| ||||      ||||||||    |||||| ||
Db        127 AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy        183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
              ||||| |||||||| || || |||||||| ||||  || |   |  || || ||   ||
Db        187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCA 246

Qy        243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302
              ||||||   |||||||  ||||||  | ||| || || |  ||| | || |||||||||
Db        247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA 306

Qy        303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA 362
              ||||| ||||| || ||     |||||||||||| |||||||| |||||||||| |||
Db        307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 366

Qy        363 GCGG----------------------------------CCTGGTATATGGACTACTGGGGT 389
              |                                  | | |   | |||  ||||||
Db        367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGC 426

Qy        390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
              || || ||||| |||||||||| |||||||||| || ||  |      ||||||||||
Db        427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT-----AGCTTTCTGGG 481

Qy        450 GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
              ||  ||| |||||||| |||||||||||||||||| ||||||||||||||||||||||
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Db        482 GCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 541

Qy        510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGCCTGGACCCTCG 569
              |||| |||||||||||||||||||| |||||||||||||||||| ||      || |||||
Db        542 CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT-----GAACCTCG 595

Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
              ||| ||  |||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Db        596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCACACCGCGG 654

Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714

Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
              |||| ||||| ||||||||| | | ||||||||||||||||||||||||||||||||||||
Db        715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy        750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy        810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy        870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
              ||||||| ||| |||||||||||||| |||||||||  ||||||||||||||||||||||
Db        895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy        930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC 989
              |||||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db        955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAG- 1013

Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049
              |||||||||| |||||||||||||||| ||||||| |||||||||| ||||||||||||
Db       1014 CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAA 1073

Qy       1050 GGCAGGCCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109
              |||||||||| |||| ||| |||||||| ||||||||||||||||||||||||||||||
Db       1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA 1132

Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169
              |||||||||||||||||||  ||||||||  |||||||||||||| |||||||||| ||
Db       1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190

Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
              |||||||| |||||| |||||||||||||| |||||||||||||||| ||||||||||||
Db       1191 CAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG 1250

Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
              |||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||||
Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
              |||||||||||||||||||| | |||||||||||||||||||||||||||||| |||||
Db       1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370

Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
              |||||  | |         ||||||||||||||||||||||||||||||||||||||||
Db       1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy       1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGTCA 1517
              |||||||||||||||||||||||||||||||||||||    ||    ||  | |||||||
Db       1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA 1550

Qy       1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1610

Qy       1578 ACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTG 1637
              || |||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Db       1611 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 1670

Qy       1638 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACG 1697
              |||||||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db       1671 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 1730

Qy       1698 TTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTAC 1757
              | ||| |||||||||||||||||||  |||||||||||||||||||| ||||||||||||
Db       1731 TACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 1790

Qy       1758 AAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACC 1817
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1791 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 1850

Qy       1818 AAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTC 1877
              |||||||||||||| |||||  |||||||||||||||||||||||||||||||||||||||
Db       1851 AAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTC 1910

Qy       1878 TGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACCACA 1937
              ||||||| |||||||||||||| |||||||||| |||||||||||||||||||||||||||
Db       1911 TGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAACCACA 1969

Qy       1938 GGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTG 1997
              |||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||
Db       1970 GGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTG 2029

Qy       1998 CCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC 2057
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       2030 CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCC 2089

Qy       2058 GGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCTCTA 2117
              |||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db       2090 GGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTA 2149

Qy       2118 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT 2177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2150 CAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT 2209

Qy       2178 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTAA 2237
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       2210 GATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAA 2269

Qy       2238 ATGAGTG 2244
              |||||||
Db       2270 ATGAGTG 2276
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RESULT 3
US-08-480-036-1
; Sequence 1, Application US/08480036
; Patent No. 5723583
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian et al.
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE
;    TITLE OF INVENTION:  INTERACTIONS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.00)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
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;      APPLICATION NUMBER:  US/08/480,036
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/618,314C
;      FILING DATE:  No. 5723583ember 23, 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  00786/067001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-480-036-1

  Query Match             73.4%;  Score 1651.6;  DB 1;  Length 2287;
  Best Local Similarity   87.2%;  Pred. No. 0;
  Matches 1998;  Conservative    0;  Mismatches  219;  Indels   75;  Gaps   14;

Qy          6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACAGCTACAGGTGTG 62
              |||||||||  |||| ||| |    || |||||||| ||||  |  ||||||||||||
Db          7 ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTGTGGTGGCAGCAGCTACAGGTGTC 66

Qy         63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
              || ||||||||  |||||||||||||||||||||||||||||||||||||||  ||| |||
Db         67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG 126

Qy        123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
              |||||  ||||||||  |||||  ||   |||  ||||      ||||||||     ||||||  ||
Db        127 AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy        183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
              |||||  ||||||||  ||  ||  ||||||||  ||||   ||  |      |  ||  ||    ||
Db        187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCA 246

Qy        243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302
              ||||||   ||||||||  ||||||  | |||  ||  ||  |  |||  |  ||  |||||||||
Db        247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA 306

Qy        303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA 362
              |||||  |||||  ||  ||      ||||||||||||  ||||||||  ||||||||||  |||
Db        307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 366

Qy        363 GCGG---------------------------------CCTGGTATATGGACTACTGGGGT 389
              |                                     |  |  |   |  |||  ||||||
Db        367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGC 426

Qy        390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
              ||  ||  |||||  ||||||||||  |||||||||  ||  ||      ||||||||||
Db        427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT-----AGCTTTCTGGG 481

Qy        450 GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
              ||  |||  ||||||||  ||||||||||||||||||  ||||||||||||||||||||||
Db        482 GCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 541

Qy        510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGCCTGGACCCTCG 569
              ||||  ||||||||||||||||||  ||||||||||||||||||  ||      ||  |||||
Db        542 CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT-----GAACCTCG 595

Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
               |||  ||  |||||||  |||||||||||||  |||||||||||||||||||||||||||||
Db        596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCACACCGCGG 654

Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714

Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
              ||||  |||||  |||||||||  |  |  ||||||||||||||||||||||||||||||||
Db        715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy        750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy        810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy        870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
              |||||||  |||  ||||||||||||||||  |||||||||  ||||||||||||||||||||
Db        895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy        930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC 989
              |||||||||||||  ||||||||||||||||||  ||||||||||||||||||||||||||
Db        955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAG- 1013

Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049
              |||||||||  ||||||||||||||||  |||||||  ||||||||||  ||||||||||||
Db       1014 CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAA 1073

Qy       1050 GGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109
              |||||||||  ||||  |||  ||||||||  ||||||||||||||||||||||||||||||
Db       1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA 1132

Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169
              |||||||||||||||||||  ||||||||  ||||||||||||||  ||||||||||  ||
Db       1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190

Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229
              |||||||  ||||||  ||||||||||||  ||||||||||||||||  ||||||||||||
Db       1191 CAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG 1250

Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289
              |||||||||||||||||||||  ||||||||||||||||  ||||||||||||||||||||
Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349
              |||||||||||||||||||||||||  |||||||||||||||||||||||||||  |||||
Db       1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370

Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400
              |||||  | |         ||||||||||||||||||||||||||||||||||||||||||
Db       1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy       1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGTCA 1517
              |||||||||||||||||||||||||||||||||||||||  ||    ||  |  |||||||
Db       1491 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCA 1550

Qy       1518 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 1577
              |||||||||                 ||  ||    ||  |  |    |||| || |
Db       1551 GTCTTCCTCT-----AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGAC 1605

Qy       1578 ACGTGCGT-----GGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGT 1632
                |  ||       |||||||||||||||||||||||||  ||||||  ||||||||||||
Db       1606 TCCAGTGTACGCACCTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT 1665

Qy       1633 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACA 1692
              |||||||||||||||||||||||||||||||||||||||||  ||||||||||||  |||||
Db       1666 ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA 1725

Qy       1693 GCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGG 1752
              ||||||  |||  ||||||||||||||||||  ||||||||||||||||||  |||||||
Db       1726 GCACGTACCGGGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG 1785
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Qy       1753 AGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1812
             ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1786 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1845

Qy       1813 AAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1872
             || ||||||||||||||| |||||  ||||||||||||||||||||||||||||||||||||
Db       1846 AAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCA 1905

Qy       1873 CCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA 1932
             |||||||||||| |||||||||||| |||||||||| ||||||||||||||||||||||||
Db       1906 CCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAA 1964

Qy       1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG 1992
             |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db       1965 CCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTG 2024

Qy       1993 ACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2052
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       2025 ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGG 2084

Qy       2053 CAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTC 2112
             |||||||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||
Db       2085 CAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC 2144

Qy       2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2145 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2204

Qy       2173 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCG 2232
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       2205 TCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG 2264

Qy       2233 GGTAAATGAGTG 2244
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Db       2265 GGTAAATGAGTG 2276
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RESULT 4
US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
; GENERAL INFORMATION:
; APPLICANT: Seed et al., Brian
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 0210-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,968A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/618,314
; FILING DATE: 23-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/067003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-968A-1

Query Match 73.4%; Score 1651.6; DB 1; Length 2287;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14;

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Qy          6 ACCACCATGGGTTGGAACTGTA---TCATCTTCTTTCTGGTTACCACAGCTACAGGTGTG 62
              |||||||||| |||| ||| |   || |||||||| |||| |  ||||||||||||||
Db          7 ACCACCATGGACTGGACCTGGAGGTTCCTCTTCTTTGTGGTGGCAGCAGCTACAGGTGTC 66

Qy         63 CACTCCCAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGAGCTCAGTG 122
              || |||||||| |||||||||||||||||||||||||||||||||||||  ||| |||
Db         67 CAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTG 126

Qy        123 AAGGTGTCCTGCAAAGCTTCCGGCTACACATTCACTGATTATGCTATACAGTGGGTGAGA 182
              ||||| |||||||| ||||| ||   ||| ||||      ||||||||    |||||| ||
Db        127 AAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGA 186

Qy        183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
              ||||| |||||||| || || |||||||| |||| || |     | || || ||   ||
Db        187 CAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCA 246

Qy        243 AACTACAACCAGAAGTTTAAGGGCAAGGCCACAATGACTGTAGACAAGTCGACGAGCACA 302
              ||||||   |||||||  ||||||  | ||| || || |  ||| | || |||||||||
Db        247 AACTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACA 306

Qy        303 GCCTATATGGAACTTAGTTCTTTGAGATCTGAGGATACGGCCGTTTATTACTGTGCAAGA 362
              ||||| ||||| || ||     |||||||||||| |||||||| |||||||||| |||
Db        307 GCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 366

Qy        363 GCGG----------------------------------CCTGGTATATGGACTACTGGGGT 389
              |                                  | | | | | |||  ||||||
Db        367 GATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGC 426

Qy        390 CAAGGTACCCTTGTCACCGTCTCCTCAGGTGAGTCCTTAAAACCTCTAGAGCTTTCTGGG 449
              || || ||||| |||||||||| |||||||||| || ||   |       ||||||||||
Db        427 CAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCT-----AGCTTTCTGGG 481

Qy        450 GCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTGAGGCAGGTGGCG 509
              ||  ||| |||||||| |||||||||||||||||| |||||||||||||||||||||||
Db        482 GCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGCG 541

Qy        510 CCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTGCCTGGACCCTCG 569
              |||| |||||||||||||||||| |||||||||||||||||| ||      || |||||
Db        542 CCAG-CAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCT-----GAACCTCG 595

Qy        570 TGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGTCCCACACCGCGG 629
              ||| ||  ||||||| |||||||||||||| |||||||||||||||||||||||||||||
Db        596 CGGACAGTTAAGAACCCAGGGGCCTCTGCG-CCTGGGCCCAGCTCTGTCCCACACCGCGG 654

Qy        630 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCG 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 TCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 714

Qy        690 CCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 749
              |||| ||||| |||||||||  | | ||||||||||||||||||||||||||||||||||
Db        715 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 774

Qy        750 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACC 809
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        775 TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 834

Qy        810 TTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 869
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        835 TTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC 894

Qy        870 TCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCAGCAACACC 929
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Db        895 TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC 954

Qy        930 AAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGC 989

Db        955 AAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAG- 1013

Qy        990 CAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAA 1049

Db       1014 CAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAA 1073

Qy       1050 GGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGA 1109

Db       1074 GGCAGGCCCCGTCTGCCTCTTCACCCGGA-GCCTCTGCCCGCCCCACTCATGCTCAGGGA 1132

Qy       1110 GAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCC 1169

Db       1133 GAGGGTCTTCTGGCTTTTTC--CCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCTAACC 1190

Qy       1170 CAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGG 1229

Db       1191 CAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGG 1250

Qy       1230 AGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCG 1289

Db       1251 AGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCG 1310

Qy       1290 GACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAAT 1349

Db       1311 GACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAAT 1370

Qy       1350 GTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1400

Db       1371 CTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCT 1430

Qy       1401 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCTG 1460

Db       1431 CCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCG 1490

Qy       1461 GGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCGTCA 1517

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Db       1786 AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA 1845

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Qy       1933 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG 1992

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Qy       2113 CTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGC 2172

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Qy       2233 GGTAAATGAGTG 2244

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RESULT 5
US-08-462-571-1
; Sequence 1, Application US/08462571
; Patent No. 5858983
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian et al.
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,571
; FILING DATE: 05 June 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/618,314
; FILING DATE: 23 No. 5858983ember 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/067002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-462-571-1

Query Match 73.4%; Score 1651.6; DB 2; Length 2287;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1998; Conservative 0; Mismatches 219; Indels 75; Gaps 14;

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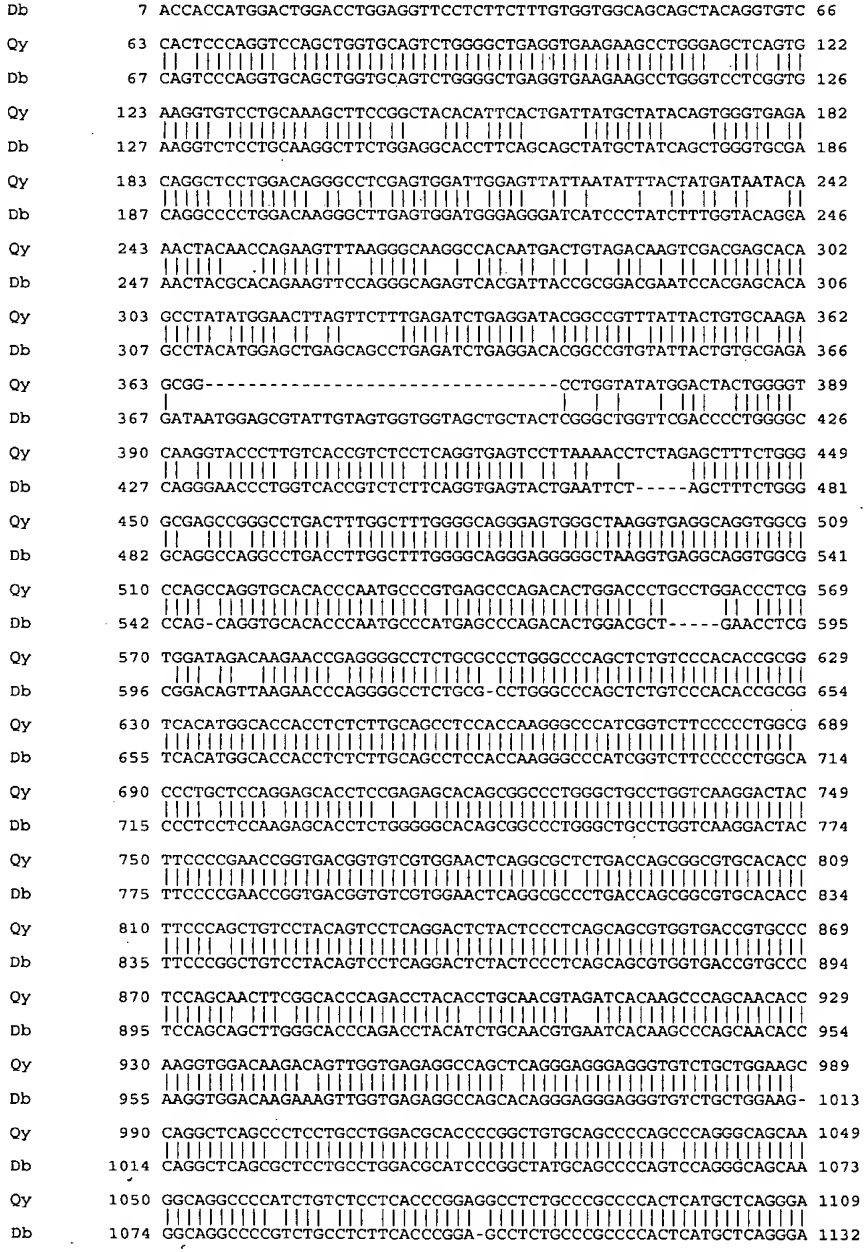
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Qy 183 CAGGCTCCTGGACAGGGCCTCGAGTGGATTGGAGTTATTAATATTTACTATGATAATACA 242
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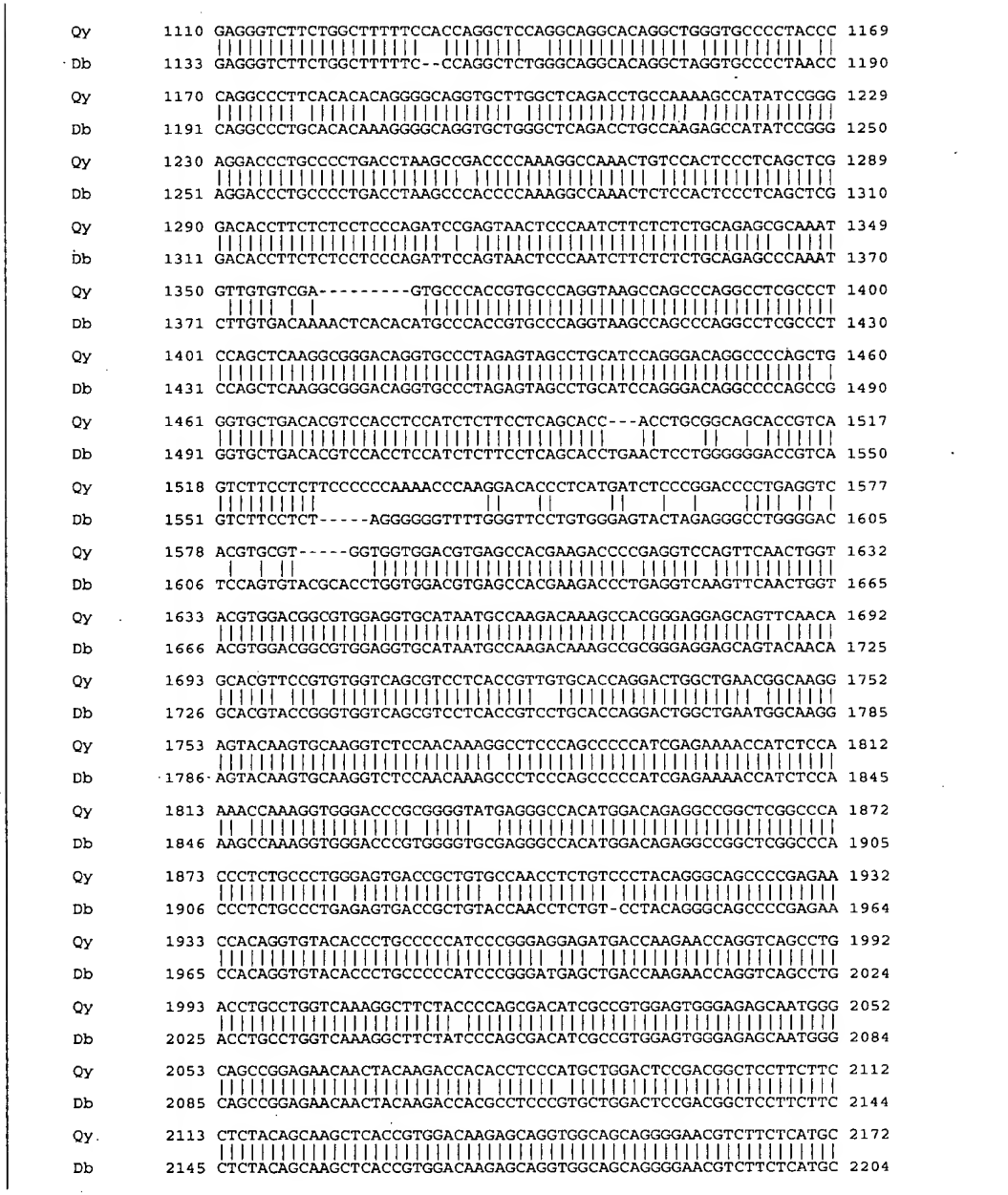
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Qy 1873 CCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAA 1932
Db 1906 CCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGT-CCTACAGGGCAGCCCCGAGAA 1964
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Db 1965 CCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTG 2024
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RESULT 6
US-09-042-353-370
; Sequence 370, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  370:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4723 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-370

  Query Match             71.7%;  Score 1611.8;  DB 4;  Length 4723;
  Best Local Similarity   94.3%;  Pred. No. 0;
  Matches 1722;  Conservative    0;  Mismatches   87;  Indels   18;  Gaps    4;

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Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857
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Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917
             |||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||
Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
             |||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
             |||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
             |||||||||| ||||||||||||||||
Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828
```

RESULT 7
US-08-758-417A-218
; Sequence 218, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-08-758-417A-218

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  Query Match             71.7%;  Score 1611.8;  DB 4;  Length 4723;
  Best Local Similarity   94.3%;  Pred. No. 0;
  Matches 1722;  Conservative    0;  Mismatches   87;  Indels   18;  Gaps    4;

Qy        430 AACCTCTAGAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGG 489
              | |  ||  |||||||||||||  ||| ||||||||| |||||||||||||||||||| |||
Db          8 AGCAGCTGAAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGG 67

Qy        490 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACT 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CTAAGGTGAGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACT 127

Qy        550 GGACCCTGCCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCC 609
              |||| ||      || ||||| ||| ||  ||||||| ||||||||||||||||||||||||
Db        128 GGACGCT-----GAACCTCGCGGACAGTTAAGAACCCAGGGGCCTCTGCGCCCTGGGCCC 182

Qy        610 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AGCTCTGTCCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCC 242

Qy        670 CATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGG 729
              |||||||||||||||||| |||| ||||| ||||||||| | | ||||||||||||||||
Db        243 CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGG 302

Qy        730 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTC 789
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        303 GCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCC 362

Qy        790 TGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 849
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        363 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA 422

Qy        850 GCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAG 909
              |||||||||||||||||||||||||||| ||| ||||||||||||||| |||||||||
Db        423 GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA 482

Qy        910 ATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAG 969
              |||||||||||||||||||||||||||||||| |||||||||||||||| |||||||
Db        483 ATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAG 542

Qy        970 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCA 1029
              |||||||||||||||||||||||||||||| |||||||||||||||| ||||||| ||||
Db        543 GGAGGGTGTCTGCTGGAAGCCAGGCTCAGCGCTCCTGCCTGGACGCATCCCGGCTATGCA 602

Qy       1030 GCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCC 1089
              ||||||| |||||||||||||||||||||| |||| ||| ||||||||||||||||||||
Db        603 GCCCCAGTCCAGGGCAGCAAGGCAGGCCCCGTCTGCCTCTTCACCCGGAGGCCTCTGCCC 662

Qy       1090 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCA 1149
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
Db        663 GCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCC-CCAGGCTCTGGGCAGGCA 721

Qy       1150 CAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACC 1209
              |||||| |||||||||| |||||||||| |||||| |||||||||||||| ||||||||||
Db        722 CAGGCTAGGTGCCCCTAACCCAGGCCCTGCACACAAAGGGGCAGGTGCTGGGCTCAGACC 781

Qy       1210 TGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAA 1269
              |||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        782 TGCCAAGAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAA 841

Qy       1270 CTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCT 1329
              || |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        842 CTCTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATTCCAGTAACTCCCAATCT 901

Qy       1330 TCTCTCTGCAGAGCGCAAATGTTGTGTCGA---------GTGCCCACCGTGCCCAGGTAA 1380
              |||||||||||||| ||||| ||||| | |          ||||||||||||||||||||
Db        902 TCTCTCTGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGGTAA 961

Qy       1381 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 GCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCAT 1021

Qy       1441 CCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC-- 1498
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       1022 CCAGGGACAGGCCCCAGCCGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACCTG 1081

Qy       1499 -ACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1557
               ||    ||  | ||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 1141

Qy       1558 TCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGG 1617
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| ||||
Db       1142 TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG 1201

Qy       1618 TCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGG 1677
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1202 TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 1261

Qy       1678 AGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACT 1737
              |||||||| |||||||||| |||||||||||||||||||||||  ||||||||||||
Db       1262 AGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACT 1321

Qy       1738 GGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCG 1797
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCG 1381

Qy       1798 AGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGA 1857
              |||||||||||||||||||||||||||||||| |||||  ||||||||||||||||||
Db       1382 AGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGTGGGGTGCGAGGGCCACATGGACAGA 1441

Qy       1858 GGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACA 1917
              |||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||||
Db       1442 GGCCGGCTCGGCCCACCCTCTGCCCTGAGAGTGACCGCTGTACCAACCTCTGTCCCTACA 1501

Qy       1918 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAG 1977
              |||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||
Db       1502 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1561

Qy       1978 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAG 2037
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1562 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1621

Qy       2038 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCC 2097
              |||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db       1622 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1681

Qy       2098 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 2157
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1682 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1741

Qy       2158 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 2217
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1742 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1801

Qy       2218 CTCTCCCTGTCCCCGGGTAAATGAGTG 2244
              |||||||||| ||||||||||||||||
Db       1802 CTCTCCCTGTCTCCGGGTAAATGAGTG 1828


RESULT 8
US-07-916-098A-43
; Sequence 43, Application US/07916098A
; Patent No. 5871732
;  GENERAL INFORMATION:
;    APPLICANT:  BURKLY, LINDA C.
;    APPLICANT:  CHISHOLM, PATRICIA L.
;    APPLICANT:  THOMAS, DAVID W.
;    APPLICANT:  ROSA, MARGARET D.
;    APPLICANT:  ROSA, JOSEPH J.
;    TITLE OF INVENTION:  ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
;    TITLE OF INVENTION:  PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ALLEGRETTI & WITCOFF, LTD.
;      STREET:  10 SOUTH WACKER DRIVE
;      CITY:  CHICAGO
```

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;      STATE:  ILLINOIS
;      COUNTRY:  U.S.A.
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/916,098A
;      FILING DATE:  July 24, 1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08843
;      FILING DATE:  No. 5871732ember 27, 1991
;      CLASSIFICATION:  424
;      APPLICATION NUMBER:  07/618,542
;      FILING DATE:  No. 5871732ember 27, 1990
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  JOHN J. MC DONNELL
;      REGISTRATION NUMBER:  26,949
;      REFERENCE/DOCKET NUMBER:  92,310-G
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;      TELEX:  910/221-5317
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2029 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "pBAG101 insert"
US-07-916-098A-43

  Query Match             71.6%;  Score 1610.8;  DB 2;  Length 2029;
  Best Local Similarity   94.6%;  Pred. No. 0;
  Matches 1712;  Conservative    0;  Mismatches   92;  Indels    6;  Gaps    4;

Qy        438 GAGCTTTCTGGGGCGAGCCGGGCCTGACTTTGGCTTTGGGGCAGGGAGTGGGCTAAGGTG 497
              ||||||||||||||  ||| ||||||| ||||| | |||||||||| ||||||||||
Db          2 GAGCTTTCTGGGGCAGGCCAGGCCTGACCTTGGC-TGGGGGCAGGGAGGGGGCTAAGGTG 60

Qy        498 AGGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCGTGAGCCCAGACACTGGACCCTG 557
              | |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 ACGCAGGTGGCGCCAGCCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACCCTG 120

Qy        558 CCTGGACCCTCGTGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGT 617
              | |||||| ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        121 CATGGACCATCGCGGATAGACAAGAACCGAGGGGCCTCTGCGCCCTGGGCCCAGCTCTGT 180

Qy        618 CCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTC 677
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Db        181 CCCACACCGCGGTCACATGGCACCACCTCTCTTGCAGCTTCCACCAAGGGCCCATCCGTC 240

Qy        678 TTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTG 737
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        241 TTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCCGCCCTGGGCTGCCTG 300

Qy        738 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGC 797
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        301 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC 360

Qy        798 GGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG 857
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        361 GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG 420

Qy        858 GTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAG 917
              |||||||||||||||||| ||| |||||  |||||||||||||||||||||||||||||
Db        421 GTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAACGTAGATCACAAG 480

Qy        918 CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGGGTG 977
              |||||||||||||||||||||||| |||||||||||||||| ||||||||||||||||
Db        481 CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTG 540

Qy        978 TCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGC 1037
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTGCAGCCCCAGC 600

Qy       1038 CCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGCCCGCCCCACT 1097
              |||||||||||||||| |||||||||||||||||||||||||||||| || |||||||
Db        601 CCAGGGCAGCAAGGCATGCCCCATCTGTCTCCTCACCCGGAGGCCTCTGACCACCCCACT 660

Qy       1098 CATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACCAGGCTCCAGGCAGGCACAGGCTGG 1157
              |||||||||||||||||||||||| |||||||||||||||| ||||  ||||||||||
Db        661 CATGCTCAGGGAGAGGGTCTTCTGGATTTTTCCACCAGGCTCCCGGCA-CCACAGGCTGG 719

Qy       1158 GTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAGGTGCTTGGCTCAGACCTGCCAAAA 1217
              |||||||||||||||||| | || ||| |||||||||| ||||||||||||||||| |
Db        720 ATGCCCCTACCCCAGGCCCTGCGCATACA-GGGCAGGTGCTGCGCTCAGACCTGCCAAGA 778

Qy       1218 GCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCAC 1277
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||||
Db        779 GCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCAC 838

Qy       1278 TCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTG 1337
              |||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||
Db        839 TCCCTCAGCTCAGACACCTTCTCTCCTCCCAGATCTGAGTAACTCCCAATCTTCTCTCTG 898

Qy       1338 CAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCCCCAGGTAAGCCAGCCCAGGCCTCGC 1397
              |||||  |||||| | ||  |   |||||| | |||||||||||||| ||||||||||||
Db        899 CAGAGTCCAAATATGGTCCCCCATGCCCATCATGCCCAGGTAAGCCAACCCAGGCCTCGC 958

Qy       1398 CCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAG 1457
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 CCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAG 1018

Qy       1458 CTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCAGCACC---ACCTGCGGCAGCACCG 1514
              | |||||||||| | |||||||||||||||||||||||||      ||  | |||
Db        1019 CCGGGTGCTGACGCATCCACCTCCATCTCTTCCTCAGCACCTGAGTTCCTGGGGGGACCA 1078

Qy       1515 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 1574
              |||||||||| |||||||||||||||||||||||| |||||||||||||||||||||||
Db        1079 TCAGTCTTCCTGTTCCCCCCAAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAG 1138

Qy       1575 GTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTAC 1634
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1139 GTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTAC 1198

Qy       1635 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGC 1694
              ||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        1199 GTGGATGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTTCAACAGC 1258

Qy       1695 ACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAG 1754
              |||| |||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        1259 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAACGGCAAGGAG 1318

Qy       1755 TACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 1814
              |||||||||||||||||||||||||||||||||  || ||||||||||||||||||||||
Db        1319 TACAAGTGCAAGGTCTCCAACAAAGGCCTCCCGTCCTCCATCGAGAAAACCATCTCCAAA 1378

Qy       1815 ACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACC 1874
              |||||||||||||| ||||||  |||||||||| |||||||||| ||||||||||||||
Db        1379 GCCAAAGGTGGGACCCACGGGGTGCGAGGGCCACACGGACAGAGGCCAGCTCGGCCCACC 1438

Qy       1875 CTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAACC 1934
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        1439 CTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCGAGAGCC 1498
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Qy       1935 ACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC 1994
             ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1499 ACAGGTGTACACCCTGCCCCCATCCCAGGAGGAGATGACCAAGAACCAGGTCAGCCTGAC 1558

Qy       1995 CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA 2054
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1559 CTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA 1618

Qy       2055 GCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTTCCT 2114
             |||||||||||||||||||||||| |||||| ||||||||||||||||||||||||||||
Db       1619 GCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT 1678

Qy       2115 CTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC 2174
             |||||||| ||| ||||||||||||||||||||| ||||||| ||||||||||||||
Db       1679 CTACAGCAGGCTAACCGTGGACAAGAGCAGGTGGCAGGAGGGGAATGTCTTCTCATGCTC 1738

Qy       2175 CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGG 2234
             |||||||||||||||||||||||||||||||| |||||||||||||||||| | |||
Db       1739 CGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCTGGG 1798

Qy       2235 TAAATGAGTG 2244
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Db       1799 TAAATGAGTG 1808
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RESULT 9
US-08-477-460B-3
; Sequence 3, Application US/08477460B
; Patent No. 6034223
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,460B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-477-460B-3

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  Query Match             70.5%;  Score 1584.6;  DB 3;  Length 2482;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy        714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy        774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy        894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy        954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy       1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073
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Db       1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1107

Qy       1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1167

Qy       1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193
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Db       1168 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1227

Qy       1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253
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Db       1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1287

Qy       1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1347

Qy       1314 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1373
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Db       1348 GAGTAACTCCCAATCTTCTCTCTGCAGAGCGCAAATGTTGTGTCGAGTGCCCACCGTGCC 1407

Qy       1374 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1408 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy       1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

Qy       1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1553
              |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1528 GCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1587

Qy       1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1647

Qy       1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy       1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733
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Db       1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1767

Qy       1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827

Qy       1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1853
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Db       1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1887

Qy       1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy       1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy       1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

Qy       2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2127

Qy       2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153
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Db       2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy       2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy       2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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Db       2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278


RESULT 10
US-08-379-516-3
; Sequence 3, Application US/08379516
; Patent No. 6083478
; GENERAL INFORMATION:
;  APPLICANT: Allaway, Graham P.
;  APPLICANT: Maddon, Paul J.
;  TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
;  TITLE OF INVENTION: Immunoconjugates and Uses Thereof
;  FILE REFERENCE: 41215-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/08/379,516
;  CURRENT FILING DATE: 1996-06-10
;  EARLIER APPLICATION NUMBER: PCT/US93/07422
;  EARLIER FILING DATE: 1993-08-06
;  EARLIER APPLICATION NUMBER: 07/927,931
;  EARLIER FILING DATE: 1992-08-07
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 2482
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-379-516-3

  Query Match           70.5%;  Score 1584.6;  DB 3;  Length 2482;
  Best Local Similarity  99.7%;  Pred. No. 0;
  Matches 1587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy        714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773

Db        748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy        774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy        894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy        954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy       1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073
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Db       1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1107

Qy       1074 CCGGAGGCCTCTGCCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1167

Qy       1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193
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Db       1168 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1227

Qy       1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493
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Db       1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

Qy       1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1553
              |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1528 GCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1587

Qy       1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1647

Qy       1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673
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Db       1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy       1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1767

Qy       1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827

Qy       1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1853
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Db       1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1887

Qy       1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913

Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy       1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973

Db       1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy       1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033

Db       2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

Qy       2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093

Db       2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2127

Qy       2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153

Db       2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy       2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213

Db       2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy       2214 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2244

Db       2248 GAGCCTCTCCCTGTCTCCGGGTAAATGAGTG 2278


RESULT 11
US-09-329-916-3
; Sequence 3, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
;   APPLICANT:  Progenics Pharmaceuticals, Inc.
;   TITLE OF INVENTION:  NON-PEPTIDYL MOIETY-CONJUGATED
;   TITLE OF INVENTION:  CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
;   NUMBER OF SEQUENCES:  9
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Cooper & Dunham
;     STREET:  30 Rockefeller Plaza
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  USA
;     ZIP:  10112
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/329,916
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/477,460
;     FILING DATE:  07-JUN-1995
;     APPLICATION NUMBER:  US 07/927,931
;     FILING DATE:  07-AUG-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  White, John P.
;     REGISTRATION NUMBER:  28,678
;     REFERENCE/DOCKET NUMBER:  41215-A-PCT/JPW/AJM
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (212) 977-9550
;     TELEFAX:  (212) 977-9809
;     TELEX:  422523 COOP UI
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH  2482 base pairs
;       TYPE  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;       MOLECULE TYPE:  cDNA
;       ORIGINAL SOURCE:
;       ORGANISM:  homo sapien
;       CELL TYPE:  lymphocyte
US-09-329-916-3

 Query Match             70.5%;  Score 1584.6;  DB 4;  Length 2482;
 Best Local Similarity   99.7%;  Pred. No. 0;
 Matches 1587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713

Db       688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

Qy       714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773

Db       748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy       774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833

Db       808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy       834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893

Db       868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy       894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953

Db       928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy       954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013

Db       988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy      1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073

Db      1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1107

Qy      1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133

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Qy      1194 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1253

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Qy      1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1313

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Qy      1374 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1433

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Qy      1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493

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Qy      1494 GCACCACCTGCGGCAGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1553

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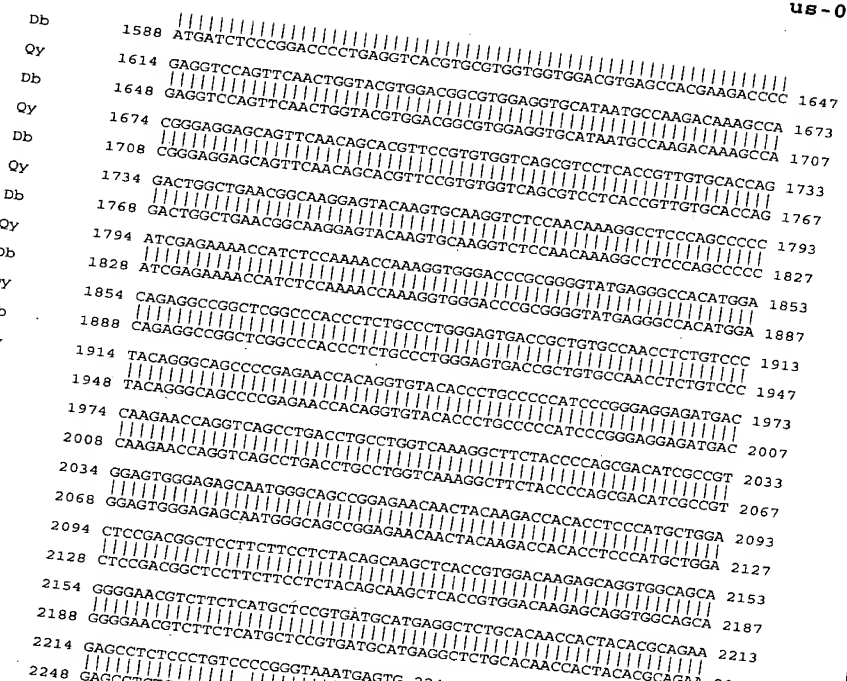
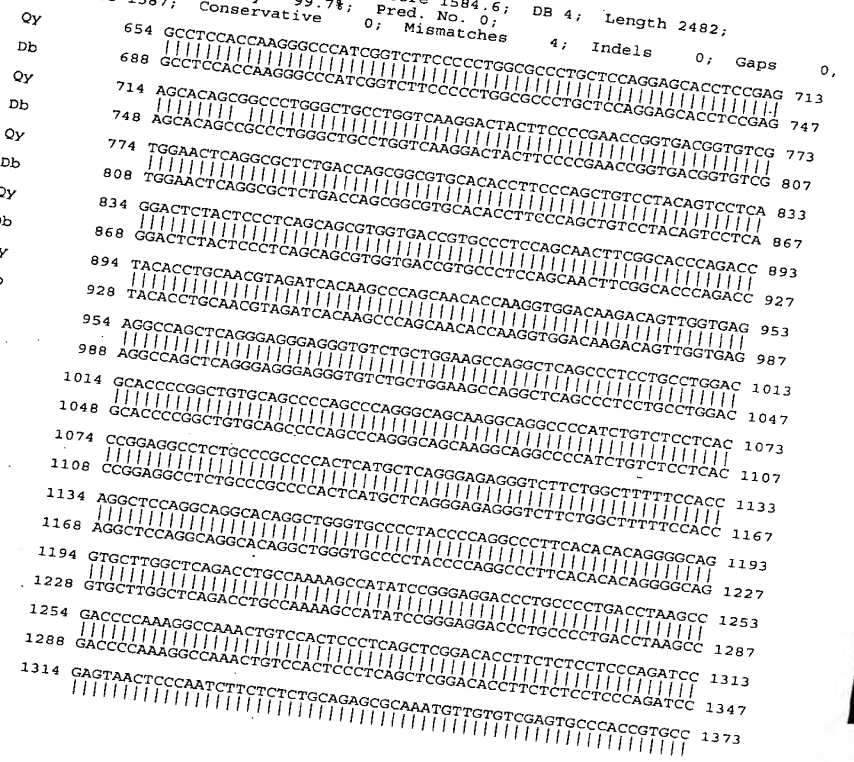


RESULT 12
US-08-485-372A-3
; Sequence 3, Application US/08485372A
; Patent No. 6187748
; GENERAL INFORMATION:
; APPLICANT: Beaudry, Gary A.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,372A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,227
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37690-II-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-485-372A-3

Query Match
Best Local Similarity 70.5%; Score 1584.6; DB 4; Length 2482;
Matches 1587; Conservative 99.7%; Pred. No. 0;
0; Mismatches 4; Indels 0; Gaps 0;



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Db       1408 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy       1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493
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Db       1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

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Db       1528 GCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 1587

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Db       1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1647

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Db       1648 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1707

Qy       1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733
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Db       1708 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1767

Qy       1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793
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Db       1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827

Qy       1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGA 1853
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Db       1828 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGTATGAGGGCCACATGGA 1887

Qy       1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913
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Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy       1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy       1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Db       2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

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Db       2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2127

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Db       2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy       2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Db       2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy       2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 13
US-09-409-006A-3
; Sequence 3, Application US/09409006A
; Patent No. 6342586
;  GENERAL INFORMATION:
;    APPLICANT:  Progenics Pharmaceuticals, Inc.
;    TITLE OF INVENTION:  NON-PEPTIDYL MOIETY-CONJUGATED
;    TITLE OF INVENTION:  CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/409,006A
;      FILING DATE:  29-SEP-1999
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/927,931
;      FILING DATE:  07-AUG-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  41215-A-PCT/JPW/AJM
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 977-9809
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2482 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      CELL TYPE:  lymphocyte
US-09-409-006A-3

  Query Match           70.5%;  Score 1584.6;  DB 4;  Length 2482;
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  Matches 1587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
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Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy       1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy       1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Db       2008 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2067

Qy       2034 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2093
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Qy       2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153
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Db       2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy       2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213
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Qy       2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 14
US-08-484-681-3
; Sequence 3, Application US/08484681
; Patent No. 6451313
;  GENERAL INFORMATION:
;    APPLICANT:  Beaudry, Gary A.
;    APPLICANT:  Maddon, Paul J.
;    TITLE OF INVENTION:  CD4-GAMMA2 CD4-IgG2 CHIMERAS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,681
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  37690-II-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2482 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      CELL TYPE:  lymphocyte
US-08-484-681-3

  Query Match             70.5%;  Score 1584.6;  DB 4;  Length 2482;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1587;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        654 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 713
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Qy        714 AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 773
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 AGCACAGCCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG 807

Qy        774 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893
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Db        868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy        894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987
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Qy        954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy       1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073
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Db       1048 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1107

Qy       1074 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1133
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Db       1108 CCGGAGGCCTCTGCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCCACC 1167

Qy       1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193
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Qy       1794 ATCGAGAAAACCATCTCCAAAACCAAAGGTGGGACCCGCGGGGGTATGAGGGCCACATGGA 1853
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Qy       1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913
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Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

Qy       1914 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 1973
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Db       1948 TACAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGAC 2007

Qy       1974 CAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGCCGT 2033
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Qy       2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244
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RESULT 15
PCT-US93-07422-3
; Sequence 3, Application PC/TUS9307422
; GENERAL INFORMATION:
; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES, AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07422
; FILING DATE: 19930806
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/927,931
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9809
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2482 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
PCT-US93-07422-3

Query Match 70.5%; Score 1584.6; DB 5; Length 2482;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1587; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db        688 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAG 747

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Db        808 TGGAACTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCAGCTGTCCTACAGTCCTCA 867

Qy        834 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 893

Db        868 GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACC 927

Qy        894 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 953

Db        928 TACACCTGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAG 987

Qy        954 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1013

Db        988 AGGCCAGCTCAGGGAGGGAGGGTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGAC 1047

Qy       1014 GCACCCCGGCTGTGCAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCAC 1073

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Qy       1134 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCCTACCCCAGGCCCTTCACACACAGGGGCAG 1193

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Db       1228 GTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCCTGCCCCTGACCTAAGCC 1287

Qy       1254 GACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGACACCTTCTCTCCTCCCAGATCC 1313

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Qy       1374 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1433

Db       1408 CAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAG 1467

Qy       1434 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1493

Db       1468 CCTGCATCCAGGGACAGGCCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCCTCA 1527

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Qy       1554 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1613

Db       1588 ATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCC 1647

Qy       1614 GAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCA 1673

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Qy       1674 CGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAG 1733

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Qy       1734 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1793

Db       1768 GACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCC 1827

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Qy       1854 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1913

Db       1888 CAGAGGCCGGCTCGGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC 1947

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Db       2068 GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGA 2127

Qy       2094 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2153

Db       2128 CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA 2187

Qy       2154 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2213

Db       2188 GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA 2247

Qy       2214 GAGCCTCTCCCTGTCCCCGGGTAAATGAGTG 2244

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Job time : 124.256 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:46:48 ; Search time 915.261 Seconds
(without alignments)
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Title: US-09-627-896B-25
Perfect score: 327
Sequence: 1 gacatccagatgacccagtc.....ccaaggtggaaatcaaacgt 327

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	327	100.0	327	9	HSVK1I2RM	X70459 H.sapiens D
2	304.8	93.2	743	6	AX258853	AX258853 Sequence
3	300.4	91.9	338	9	HSU86803	U86803 Human Ig ka
4	300.4	91.9	395	9	HSIGKLV41	X72462 H.sapiens m
5	298.4	91.3	761	6	AX258845	AX258845 Sequence
6	298.2	91.2	447	9	HUMIGHGQ	L03152 Homo sapien
7	297.2	90.9	324	9	AB063945	AB063945 Homo sapi
8	296	90.5	328	9	AY043160	AY043160 Homo sapi
9	295.6	90.4	324	9	AF035044	AF035044 Homo sapi
10	295.2	90.3	752	6	AX258847	AX258847 Sequence
11	295.2	90.3	752	6	AX258851	AX258851 Sequence
12	295.2	90.3	761	6	AX258895	AX258895 Sequence
13	290.2	88.7	450	9	HUMIGHGU	L03156 Homo sapien
14	289.2	88.4	390	9	AF103772	AF103772 Homo sapi
15	289	88.4	316	9	AF193852	AF193852 Homo sapi
16	289	88.4	321	9	HSIGKVBAC	Z18827 Homo sapien
17	288	88.1	1073	9	HSIKLVA20	X63398 H.sapiens D
18	288	88.1	36886	9	AP001238	AP001238 Homo sapi
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20	287	87.8	287	9	HSIGDPK4	X93622 H.sapiens g
21	285.4	87.3	330	9	AF103536	AF103536 Homo sapi
22	284.6	87.0	312	9	AF103486	AF103486 Homo sapi
23	284.6	87.0	332	9	AF103489	AF103489 Homo sapi
24	284	86.9	321	9	HSIGKLV55	X72476 H.sapiens m
25	284	86.9	324	9	AF099196	AF099196 Homo sapi
26	283.4	86.7	325	9	AY043164	AY043164 Homo sapi
27	282.8	86.5	372	9	HSIGKLV25	X72446 H.sapiens m
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34	278.6	85.2	322	9	AY043138	AY043138 Homo sapi
35	278	85.0	342	9	HSU97250	U97250 Homo sapien
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37	277.4	84.8	320	9	HUMFRAQ	L08900 Homo sapien
38	277.4	84.8	329	9	HUMFRBJ	L09085 Homo sapien
39	276.4	84.5	327	9	AF107244	AF107244 Homo sapi
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41	275.8	84.3	324	9	AF146408	AF146408 Homo sapi
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ALIGNMENTS

RESULT 1
HSVK1I2RM
LOCUS HSVK1I2RM 327 bp DNA linear PRI 17-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody light chain variable region,subgroup V(K)1 (III-2R IgM line).
ACCESSION X70459
VERSION X70459.1 GI:38436
KEYWORDS anti-DNA antibody; complementarity determining region; Ig kappa light chain; Ig light chain; Ig variable region; IgM; immunoglobulin; systemic lupus erythematosus.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)

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  AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
            and Diamond,B.
  TITLE     Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype
  JOURNAL   J. Exp. Med. 174 (6), 1639-1652 (1991)
  MEDLINE   92078875
   PUBMED   1660528
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     misc_feature    71. .102
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BASE COUNT       84 a     89 c     77 g     77 t
ORIGIN

  Query Match             100.0%;  Score 327;  DB 9;  Length 327;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-94;
  Matches  327;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300

Qy        301 CAAGGGACCAAGGTGGAAATCAAACGT 327
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Db        301 CAAGGGACCAAGGTGGAAATCAAACGT 327


RESULT 2
AX258853
LOCUS       AX258853                743 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 2352 from Patent WO0172771.
ACCESSION   AX258853
VERSION     AX258853.1  GI:16508406
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
            Hansen,P.H., Ravera,M. and Hsiao,K.C.
  TITLE     Insulin and igf-1 receptor agonists and antagonists
  JOURNAL   Patent: WO 0172771-A 2352 04-OCT-2001;
            DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
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     CDS             <19. .>735
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                     /db_xref="GI:16508407"
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                     LEWVSAIGTGGGTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMAVYYCAREGELG
                     VTSFWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQG
                     ISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATY
                     YCQKYNSAPWTFGQGTKVEIK"
BASE COUNT      163 a    195 c    218 g    167 t
ORIGIN

  Query Match             93.2%;  Score 304.8;  DB 6;  Length 743;
  Best Local Similarity   98.5%;  Pred. No. 2.6e-87;
  Matches  319;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 474

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 534

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 594

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 654

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||    | |||||||||
Db        655 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TGGACGTTCGGC 711

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              |||||||||||||||||||||||||
Db        712 CAAGGGACCAAGGTGGAAATCAAA 735


RESULT 3
HSU86803
LOCUS       HSU86803                338 bp    mRNA    linear   PRI 04-MAR-1997
DEFINITION  Human Ig kappa chain V-region (VL-COL) mRNA, partial cds.
ACCESSION   U86803
VERSION     U86803.1  GI:1864136
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 338)
  AUTHORS   Pritsch,O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
  TITLE     V gene usage by seven hybrids derived from CD5+ B-cell chronic
            lymphocytic leukemia and displaying autoantibody activity
  JOURNAL   Blood 82 (10), 3103-3112 (1993)
  MEDLINE   94033522
   PUBMED   7693035
REFERENCE   2  (bases 1 to 338)
  AUTHORS   Pritsch,O., Magnac,C., Dumas,G., Egile,C. and Dighiero,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-1997) Unite d'Immunohematologie et
            d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
            75724, France
FEATURES             Location/Qualifiers
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     source          1. .338
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2p11-p12"
                     /cell_type="B cells"
                     /note="patient with chronic lymphocytic leukemia"
     gene            1. .338
                     /gene="VL-COL"
     CDS             <1. .>338
                     /gene="VL-COL"
                     /note="rearranged"
                     /codon_start=1
                     /product="Ig kappa chain V-region"
                     /protein_id="AAB48616.1"
                     /db_xref="GI:1864137"
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                     KLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPPLFGGGT
                     KVEIKRIRARA"
BASE COUNT       84 a     92 c     81 g     81 t
ORIGIN

  Query Match             91.9%;  Score 300.4;  DB 9;  Length 338;
  Best Local Similarity   97.2%;  Pred. No. 7.2e-86;
  Matches  317;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||    |  ||||||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCACTT---TTCGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||| ||||||||
Db        298 GGAGGGACCAAGGTGGAGATCAAACG 323


RESULT 4
HSIGKLV41
LOCUS       HSIGKLV41                 395 bp    mRNA    linear   PRI 31-JAN-1994
DEFINITION  H.sapiens mRNA for rearranged Ig kappa light chain variable region
            (I.40).
ACCESSION   X72462
VERSION     X72462.1  GI:441392
KEYWORDS    C-region; immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 395)
  AUTHORS   Zachau,H.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische
            Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2,
            FRG
REFERENCE   2  (bases 1 to 395)
  AUTHORS   Klein,R., Jaenichen,R. and Zachau,H.G.
  TITLE     Expressed human immunoglobulin kappa genes and their hypermutation
  JOURNAL   Eur. J. Immunol. 23 (12), 3248-3262 (1993)
    MEDLINE   94080891
     PUBMED   8258341
FEATURES             Location/Qualifiers
     source          1. .395
                     /organism="Homo sapiens"
                     /isolate="M.L."
                     /db_xref="taxon:9606"
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                     /clone_lib="lambda zap II phage library"
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                     /partial
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                     /db_xref="GI:441393"
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                     ASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFSLTISSLQPED
                     VATYYCQKYNSVPRTFGQGTKVEIKRTVL"
     V_region        1. .395
                     /product="Ig kappa light chain (VJC)"
     V_segment       61. .345
     J_segment       346. .384
                     /note="J-Kappa 1"
     C_region        385. .395
BASE COUNT       95 a    109 c     96 g     95 t
ORIGIN

  Query Match             91.9%;  Score 300.4;  DB 9;  Length 395;
  Best Local Similarity   97.2%;  Pred. No. 7.1e-86;
  Matches  317;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db         61 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGAACAGAGTCACC 120

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 180

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db        181 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCGTCCACTTTGCAATCAGGGGTCCCATCT 240

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        241 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCTCTCTCACCATCAGCAGCCTGCAGCCT 300

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||| |||||   | |||||||||
Db        301 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGTCCCTC---GAACGTTCGGC 357

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        358 CAAGGGACCAAGGTGGAAATCAAACG 383


RESULT 5
AX258845
LOCUS       AX258845                  761 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 2344 from Patent WO0172771.
ACCESSION   AX258845
VERSION     AX258845.1  GI:16508398
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
            Hansen,P.H., Ravera,M. and Hsiao,K.C.
  TITLE     Insulin and igf-1 receptor agonists and antagonists
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  JOURNAL   Patent: WO 0172771-A 2344 04-OCT-2001;
            DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .761
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"
     CDS             <19. .>753
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD10171.1"
                     /db_xref="GI:16508399"
                     /translation="QMQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKG
                     LEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTWG
                     SVDTDNYARFWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT
                     CRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQP
                     EDVATYYCQKYNSAPLTFGGGTKVEIK"
BASE COUNT      179 a    201 c    219 g    162 t
ORIGIN

  Query Match           91.3%;  Score 298.4;  DB 6;  Length 761;
  Best Local Similarity   97.2%;  Pred. No. 3.1e-85;
  Matches  315;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 492

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db        493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 552

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db        553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 612

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        613 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 672

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||     || ||||||
Db        673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---TCACTTTCGGC 729

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
                |||||||||||||| ||||||
Db        730 GGAGGGACCAAGGTGGAGATCAAA 753


RESULT 6
HUMIGHGQ
LOCUS       HUMIGHGQ                447 bp    mRNA    linear   PRI 03-MAY-2000
DEFINITION  Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
            (IGHV@) mRNA, partial cds.
ACCESSION   L03152
VERSION     L03152.1  GI:185387
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   Collet,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.
            and Lerner,R.A.
  TITLE     A binary plasmid system for shuffling combinatorial antibody
            libraries
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
  MEDLINE   93066172
   PUBMED   1438192
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="14q32.33"
                     /cell_type="T-cell"
                     /tissue_type="bone marrow"
                     /dev_stage="adult"
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     gene            <1. .>447
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     CDS             <1. .>447
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                     /protein_id="AAA52924.1"
                     /db_xref="GI:567146"
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                     EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPERTKVQWKVV"
     V_region        <1. .>447
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                     /note="G00-128-528"
BASE COUNT      110 a    119 c    108 g    110 t
ORIGIN

  Query Match           91.2%;  Score 298.2;  DB 9;  Length 447;
  Best Local Similarity   98.1%;  Pred. No. 3.6e-85;
  Matches  313;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    1;

Qy          8 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67
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Db          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 61

Qy         68 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121

Qy        128 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCA 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCA 181

Qy        188 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 247
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Db        182 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 241

Qy        248 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGGGA 307
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Db        242 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GGACGTTCGGCCAAGGGA 298

Qy        308 CCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||
Db        299 CCAAGGTGGAAATCAAACG 317


RESULT 7
AB063945
LOCUS       AB063945                324 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
            region, partial cds, clone:K118.
ACCESSION   AB063945
VERSION     AB063945.1  GI:21669096
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:K118.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
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REFERENCE   2  (bases 1 to 324)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1. .324
                     /gene="IGK"
     CDS             <1. .>324
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                     /codon_start=1
                     /product="immunoglobulin kappa light chain VLJ region"
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                     /db_xref="GI:21669097"
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                     KVDIER"
BASE COUNT       80 a     89 c     76 g     79 t
ORIGIN

  Query Match             90.9%;  Score 297.2;  DB 9;  Length 324;
  Best Local Similarity   96.6%;  Pred. No. 7.8e-85;
  Matches  315;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTTTTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||-|||||||||||||||||||||||||||||||||||    | || ||||||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GGACTTTCGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |  |||||||| ||||| ||| ||||
Db        298 CCTGGGACCAAAGTGGATATCGAACG 323


RESULT 8
AY043160
LOCUS       AY043160                328 bp    mRNA    linear   PRI 31-DEC-2001
DEFINITION  Homo sapiens MCLL141 immunoglobulin light chain variable region
            mRNA, partial cds.
ACCESSION   AY043160
VERSION     AY043160.1  GI:18025709
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 328)
  AUTHORS   Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,
            Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.
  TITLE     Ig VL gene repertoire in B cell type chronic lymphocytic leukemia
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 328)
  AUTHORS   Ghiotto,F., Fais,F., Valetto,A., Albesiano,E., Allen,S.,
            Schulman,P., Vinciguerra,V., Rai,K., Ferrarini,M. and Chiorazzi,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-2001) North Shore-LIJ Research Institute, 350
            Community Drive, Manhasset, NY 11030, USA
FEATURES             Location/Qualifiers
     source          1. .328
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                     /isolate="MCLL141"
                     /db_xref="taxon:9606"
                     /cell_type="B lymphocyte from patient with IgM+ chronic
                     lymphocytic leukemia (CLL)"
     CDS             <1. .>328
                     /codon_start=1
                     /product="immunoglobulin light chain variable region"
                     /protein_id="AAK94864.1"
                     /db_xref="GI:18025710"
                     /translation="DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
                     KLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRMYTFGQ
                     GTKLEIK"
BASE COUNT       83 a     90 c     76 g     79 t
ORIGIN

  Query Match             90.5%;  Score 296;  DB 9;  Length 328;
  Best Local Similarity   96.0%;  Pred. No. 1.9e-84;
  Matches  315;  Conservative    0;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---CGAGTACGTTC 297
              |||||||||||||||||||||||||||||||||||||||||||||    |   || ||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCGTATGTACACTTTT 300

Qy        298 GGCCAAGGGACCAAGGTGGAAATCAAAC 325
              ||||| ||||||||| |||| |||||||
Db        301 GGCCAGGGGACCAAGCTGGAGATCAAAC 328


RESULT 9
AF035044
LOCUS       AF035044                324 bp    mRNA    linear   PRI 24-SEP-1999
DEFINITION  Homo sapiens clone FD2K myosin-reactive immunoglobulin light chain
            variable region mRNA, partial cds.
ACCESSION   AF035044
VERSION     AF035044.1  GI:5921640
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Wu,X., Liu,B., Van der Merwe,P.L., Kalis,N.N., Berney,S.M. and
            Young,D.C.
  TITLE     Myosin-reactive autoantibodies in rheumatic carditis and normal
```

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  JOURNAL   fetus
  MEDLINE   Clin. Immunol. Immunopathol. 87 (2), 184-192 (1998)
    PUBMED  98277139
REFERENCE   9614934
  AUTHORS   2  (bases 1 to 324)
  TITLE     Young,D.C.
  JOURNAL   Direct Submission
            Submitted (19-NOV-1997) Department of Pathology and Laboratory
            Medicine, University of Texas Health Science Center, 6431 Fannin,
            Houston, TX 77030, USA
FEATURES
     source          Location/Qualifiers
                     1. .324
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="FD2K"
     CDS             <1. .>324
                     /note="autoantibody"
                     /codon_start=1
                     /product="myosin-reactive immunoglobulin light chain
                     variable region"
                     /protein_id="AAD56280.1"
                     /db_xref="GI:5921641"
                     /translation="DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
                     KSLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGT
                     KLEIKR"
BASE COUNT       82 a       89 c       75 g       78 t
ORIGIN
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Query Match             90.4%;  Score 295.6;  DB 9;  Length 324;
Best Local Similarity   96.3%;  Pred. No. 2.6e-84;
Matches  314;  Conservative    0;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
            |||||||||||||||||||||||||||||||||||||||||||||| ||| || |||||||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GCACTTTTGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
            | |||||||||| |||| |||||||||
Db        298 CCAGGGACCAAGCTGGAGATCAAACG 323
```

```
RESULT 10
AX258847
LOCUS
DEFINITION  AX258847
ACCESSION   Sequence 2346 from Patent WO0172771.
VERSION     AX258847                    752 bp    DNA     linear   PAT 26-OCT-2001
KEYWORDS    AX258847.1  GI:16508400
SOURCE      .
  ORGANISM  synthetic construct.
            synthetic construct
REFERENCE   artificial sequences.
  AUTHORS   1
            Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
            Hansen,P.H., Ravera,M. and Hsiao,K.C.
  TITLE     Insulin and igf-1 receptor agonists and antagonists
  JOURNAL   Patent: WO 0172771-A 2346 04-OCT-2001;
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FEATURES    DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
     source          Location/Qualifiers
                     1. .752
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             /note="synthetic DNA"
                     <19. .>744
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD10172.1"
                     /db_xref="GI:16508401"
                     /translation="QMQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKG
                     LEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTPG
                     SQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDV
                     ATYYCQKYNSAPFTFGPGTKVDIK"
BASE COUNT      177 a      196 c      217 g      162 t
ORIGIN
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Query Match             90.3%;  Score 295.2;  DB 6;  Length 752;
Best Local Similarity   96.6%;  Pred. No. 3.3e-84;
Matches  313;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 603

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
            |||||||||||||||||||||||||||||||||||||||||||||| ||| || |||||||
Db        664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TTCACTTTCGGC 720

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
            | |||||||||| |||| |||||||
Db        721 CCTGGGACCAAAGTGGATATCAAA 744
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RESULT 11
AX258851
LOCUS
DEFINITION  AX258851
ACCESSION   Sequence 2350 from Patent WO0172771.
VERSION     AX258851                    752 bp    DNA     linear   PAT 26-OCT-2001
KEYWORDS    AX258851.1  GI:16508404
SOURCE      .
  ORGANISM  synthetic construct.
            synthetic construct
REFERENCE   artificial sequences.
  AUTHORS   1
            Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
            Hansen,P.H., Ravera,M. and Hsiao,K.C.
  TITLE     Insulin and igf-1 receptor agonists and antagonists
  JOURNAL   Patent: WO 0172771-A 2350 04-OCT-2001;
FEATURES    DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
     source          Location/Qualifiers
                     1. .752
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             /note="synthetic DNA"
                     <19. .>744
                     /note="unnamed protein product"
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                /codon_start=1
                /transl_table=11
                /protein_id="CAD10174.1"
                /db_xref="GI:16508405"
                /translation="QMQLVQSGGGLVQPGGSLRLSCAGSGFTFSSYAMHWVRQAPGKG
                LEWVSAIGTGGGTYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMAVYYCARWGHVG
                LWVADVYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRA
                SQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDV
                ATYYCQKYNSAPYTFGQGTKLEIK"
BASE COUNT      162 a    195 c    221 g    174 t
ORIGIN

  Query Match             90.3%;  Score 295.2;  DB 6;  Length 752;
  Best Local Similarity   96.6%;  Pred. No. 3.3e-84;
  Matches  313;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 603

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TACACTTTTGGC 720

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              || |||||||||| |||| ||||||
Db        721 CAGGGGACCAAGCTGGAGATCAAA 744


RESULT 12
AX258895
LOCUS       AX258895                761 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 2394 from Patent WO0172771.
ACCESSION   AX258895
VERSION     AX258895.1  GI:16508408
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beasley,J., Blume,A.J., Schaeffer,L., Pillutla,R., Brandt,J.,
            Brissette,R., Spetzler,J., Cheng,W., Stergaard,S., Mandecki,W.S.,
            Hansen,P.H., Ravera,M. and Hsiao,K.C.
  TITLE     Insulin and igf-1 receptor agonists and antagonists
  JOURNAL   Patent: WO 0172771-A 2394 04-OCT-2001;
            DGI BioTechnologies, L.L.C. (US) ; Novo Nordisk A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .761
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"
     CDS             <19. .>753
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD10176.1"
                     /db_xref="GI:16508409"
                     /translation="EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKG
                     LEWVGRIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTTYG
                     DVYDRDYDGRWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTIT
                     CRASQGISNYLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQP
                     EDVATYYCQKYNSAPFTFGPGTKVDIK"
BASE COUNT      179 a    200 c    217 g    165 t
ORIGIN

  Query Match             90.3%;  Score 295.2;  DB 6;  Length 761;
  Best Local Similarity   96.6%;  Pred. No. 3.3e-84;
  Matches  313;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 492

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 552

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 612

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 672

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TTCACTTTCGGC 729

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              |  |||||||| ||||| ||||||
Db        730 CCTGGGACCAAAGTGGATATCAAA 753


RESULT 13
HUMIGHGU
LOCUS       HUMIGHGU                450 bp    mRNA    linear   PRI 03-MAY-2000
DEFINITION  Homo sapiens cell-type T-cell immunoglobulin gamma-chain, V region
            (IGHV@) mRNA, partial cds.
ACCESSION   L03156
VERSION     L03156.1  GI:185391
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Collet,T.A., Roben,P., O'Kennedy,R., Barbas,C.F. III, Burton,D.R.
            and Lerner,R.A.
  TITLE     A binary plasmid system for shuffling combinatorial antibody
            libraries
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (21), 10026-10030 (1992)
  MEDLINE   93066172
   PUBMED   1438192
FEATURES             Location/Qualifiers
     source          1. .450
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="14q32.33"
                     /cell_type="T-cell"
                     /tissue_type="bone marrow"
                     /dev_stage="adult"
                     /lab_host="XL1-Blue"
                     /tissue_lib="BMHIV"
     gene            <1. .>450
                     /gene="IGHV@"
     CDS             <1. .>450
                     /gene="IGHV@"
                     /codon_start=1
                     /product="immunoglobulin gamma-chain, V region"
                     /protein_id="AAA52928.1"
                     /db_xref="GI:567150"
                     /translation="ELTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPRL
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                     EIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPERPKYSGRWIT"
     V_region        <1. .>450
                     /gene="IGHV@"
                     /note="G00-128-528"
BASE COUNT      110 a    120 c    110 g    110 t
ORIGIN

  Query Match             88.7%;  Score 290.2;  DB 9;  Length 450;
  Best Local Similarity   96.6%;  Pred. No. 1.4e-82;
  Matches  308;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          8 AGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTT 67
              || | |||||||||||||||||||||||||| ||||||||||||| ||||||||||||
Db          2 AGCTCACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTAGGAGACAGGGTCACCATCACTT 61

Qy         68 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAG 121

Qy        128 TTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCA 187
              ||||||  |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        122 TTCCTAGACTCCTGATCTATGCTGCATCCACTTTGCAACCAGGGGTCCCATCTCGGTTCA 181

Qy        188 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATG 241

Qy        248 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGGGA 307
              |||||||||||||||||||||||||||||||||||||    | ||||||||||||||||
Db        242 TTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---GGACGTTCGGCCAAGGGA 298

Qy        308 CCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||
Db        299 CCAAGGTGGAAATCAAACG 317


RESULT 14
AF103772
LOCUS       AF103772                390 bp    mRNA    linear   PRI 03-NOV-1999
DEFINITION  Homo sapiens clone B22 anti-phospholipid immunoglobulin light chain
            VL-J-C region mRNA, partial cds.
ACCESSION   AF103772
VERSION     AF103772.1  GI:6179863
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 390)
  AUTHORS   Chukwuocha,R.U., Hfiao,E., Shaw,P., Witztum,J.L. and Chen,P.P.
  TITLE     Isolation, characterization and sequence analysis of five IgG
            monoclonal anti-phospholipid Fab fragments generated by phage
            display
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 390)
  AUTHORS   Chukwuocha,R.U., Hfiao,E., Shaw,P., Witztum,J.L. and Chen,P.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-NOV-1998) Medicine/Rheumatology, UCLA, 32-59
            Rehabilitation Center, 1000 Veteran Avenue, Los Angeles, CA
            90095-1670, USA
FEATURES             Location/Qualifiers
     source          1. .390
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="B22"
                     /cell_type="lymphocyte"
                     /tissue_type="blood"
                     /note="patient with oxidized low density lipoproteins"
     CDS             <1. .>390
                     /codon_start=1
                     /product="anti-phospholipid immunoglobulin light chain
                     VL-J-C region"
                     /protein_id="AAF05689.1"
                     /db_xref="GI:6179864"
                     /translation="ELQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVP
                     NLLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYDSAPRTFGPGT
                     KVDIKRTVAAPSVFIFPPSDEQVEIGQC"
BASE COUNT       93 a    111 c     91 g     95 t
ORIGIN

  Query Match             88.4%;  Score 289.2;  DB 9;  Length 390;
  Best Local Similarity   95.1%;  Pred. No. 3e-82;
  Matches  310;  Conservative    0;  Mismatches   13;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||
Db        121 GGGAAAGTTCCTAACCTCCTGATCTATGGTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTTCAGTGGCAGTGGATCCGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||| |||||||||||||||||||| ||||||||||||   | || ||||||
Db        241 GAAGATGTTGCGACTTATTACTGTCAAAAGTATGACAGTGCCCCTC---GCACTTTCGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db        298 CCTGGGACCAAAGTGGATATCAAACG 323


RESULT 15
AF193852
LOCUS       AF193852                316 bp    mRNA    linear   PRI 21-FEB-2000
DEFINITION  Homo sapiens clone 11LC immunoglobulin light chain variable region
            mRNA, partial cds.
ACCESSION   AF193852
VERSION     AF193852.1  GI:7012709
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 316)
  AUTHORS   Choi,I.H., Park,S.G., Chung,J.H., Kim,I.J. and Hong,H.J.
  TITLE     Generation of human Fab monoclonal antibodies against preS1 of
            hepatitis B virus using repertoire cloning
  JOURNAL   Hybridoma 17 (6), 535-540 (1998)
  MEDLINE   99105715
   PUBMED   9890709
REFERENCE   2  (bases 1 to 316)
  AUTHORS   Choi,I.H., Park,S.G., Chung,J.H., Kim,I.J. and Hong,H.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-OCT-1999) Microbiology, College of Medicine, INJE
            University, 633-165 Gaegum-Dong Jin-GU, Pusan 614-735, South Korea
FEATURES             Location/Qualifiers
     source          1. .316
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                     /db_xref="taxon:9606"
                     /clone="11LC"
     CDS             <1. .>316
                     /note="Fab monoclonal antibody against preS1 of hepatitis
                     B virus"
                     /codon_start=1
                     /product="immunoglobulin light chain variable region"
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ETK"
BASE COUNT 80 a 88 c 76 g 72 t
ORIGIN

Query Match 88.4%; Score 289; DB 9; Length 316;
Best Local Similarity 95.7%; Pred. No. 3.5e-82;
Matches 311; Conservative 0; Mismatches 5; Indels 9; Gaps 1;

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Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||||||          |||||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---------TCGGC 291

Qy        301 CAAGGGACCAAGGTGGAAATCAAAC 325
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Db        292 GGAGGGACCAAGGTGGAGACCAAAC 316
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Search completed: July 18, 2003, 13:47:34
Job time : 917.261 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:16:54 ; Search time 566.66 Seconds
(without alignments)
9345.860 Million cell updates/sec

Title: US-09-627-896B-25
Perfect score: 327
Sequence: 1 gacatccagatgacccagtc.....ccaaggtggaaatcaaacgt 327

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	302	92.4	826	12	BG684416	BG684416 602636169
2	302	92.4	957	12	BG341934	BG341934 602463276
3	302	92.4	959	12	BG341941	BG341941 602463283
4	290.8	88.9	888	14	BQ881840	BQ881840 AGENCOURT
5	286	87.5	626	13	BM509065	BM509065 ih16b08.x
6	278.2	85.1	358	10	AW404145	AW404145 UI-HF-BL0
7	276.4	84.5	935	12	BG342083	BG342083 602463029
8	274.8	84.0	773	13	BM007845	BM007845 603617528
9	271.6	83.1	928	14	BQ707369	BQ707369 AGENCOURT
10	270	82.6	493	10	AW405753	AW405753 UI-HF-BL0
11	268.4	82.1	422	10	AW407904	AW407904 UI-HF-BL0
12	268.4	82.1	921	12	BG758398	BG758398 602712592
13	265.2	81.1	422	10	AV733746	AV733746 AV733746
14	265.2	81.1	1153	13	BM543718	BM543718 AGENCOURT
15	263.6	80.6	391	10	AW404992	AW404992 UI-HF-BL0
16	263.6	80.6	608	10	AW406562	AW406562 UI-HF-BL0
17	263.6	80.6	891	12	BG540787	BG540787 602570674
18	263.6	80.6	1006	14	BQ706213	BQ706213 AGENCOURT
19	263.2	80.5	358	10	AW408194	AW408194 UI-HF-BL0
20	262	80.1	631	14	BM818943	BM818943 K-EST0086
21	262	80.1	742	12	BG756519	BG756519 602715662
22	262	80.1	776	12	BG684027	BG684027 602635634
23	262	80.1	923	14	BQ882857	BQ882857 AGENCOURT
24	262	80.1	945	14	BQ707400	BQ707400 AGENCOURT
25	261	79.8	768	12	BG685552	BG685552 602637525
26	260.8	79.8	378	10	AW405241	AW405241 UI-HF-BL0
27	260.4	79.6	867	12	BG754732	BG754732 602714301
28	258.8	79.1	417	10	AW406228	AW406228 UI-HF-BL0
29	258.8	79.1	471	10	AW406294	AW406294 UI-HF-BL0
30	258.8	79.1	686	12	BG686745	BG686745 602650714
31	258.8	79.1	886	12	BG756818	BG756818 602710291
32	258.8	79.1	943	12	BF976230	BF976230 602245105
33	258.8	79.1	1100	12	BF663472	BF663472 602144635
34	257.2	78.7	426	10	AW405900	AW405900 UI-HF-BL0
35	257.2	78.7	903	12	BG756188	BG756188 602713490
36	257.2	78.7	943	14	BQ707106	BQ707106 AGENCOURT
37	256.2	78.3	813	12	BG431143	BG431143 602498773
38	256	78.3	655	10	AV731325	AV731325 AV731325
39	255.6	78.2	867	12	BG539961	BG539961 602567476
40	254.8	77.9	712	12	BG538665	BG538665 602566902
41	254.4	77.8	1011	14	BM914591	BM914591 AGENCOURT
42	254	77.7	418	10	AW404507	AW404507 UI-HF-BL0
43	254	77.7	431	10	AW406886	AW406886 UI-HF-BL0
44	254	77.7	447	10	AW405752	AW405752 UI-HF-BL0
45	254	77.7	453	10	AW383563	AW383563 PM4-HT034

ALIGNMENTS

RESULT 1
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LOCUS BG684416 826 bp mRNA linear EST 01-MAY-2001
DEFINITION 602636169F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763993 5', mRNA sequence.
ACCESSION BG684416
VERSION BG684416.1 GI:13915813
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1620 row: i column: 18
High quality sequence stop: 826.
FEATURES Location/Qualifiers
source 1. .826

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4763993"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 199 a 253 c 191 g 183 t
ORIGIN

Query Match 92.4%; Score 302; DB 12; Length 826;
Best Local Similarity 97.5%; Pred. No. 1.6e-86;
Matches 318; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

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Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db         54 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 113

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db        114 ATCACTTGCCGGGCGAGTCAGGGCATTAACAATTTTTTAGCCTGGTATCAGCAGAAACTA 173

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 233

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db        294 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC 350

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        351 CAAGGGACCAAGGTGGAAATCAAACG 376
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RESULT 2
BG341934
LOCUS BG341934 957 bp mRNA linear EST 27-FEB-2001
DEFINITION 602463276F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576170 5', mRNA sequence.
ACCESSION BG341934
VERSION BG341934.1 GI:13148372
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 957)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1288 row: g column: 19
High quality sequence stop: 673.

FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4576170"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 242 a 266 c 231 g 217 t 1 others
ORIGIN

Query Match 92.4%; Score 302; DB 12; Length 957;
Best Local Similarity 97.5%; Pred. No. 1.8e-86;
Matches 318; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

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Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db         53 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 112

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||| ||||| |||||||||||||||||||||| |
Db        113 ATCACTTGCCGGGCGAGTCAGGGCATTAACAATTTTTTAGCCTGGTATCAGCAGAAACTA 172

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        173 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 232

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        233 CGGTTCAGTGGCAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 292

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||| |    |||||||||
Db        293 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC 349

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db        350 CAAGGGACCAAGGTGGAAATCAAACG 375
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RESULT 3
BG341941
LOCUS BG341941 959 bp mRNA linear EST 27-FEB-2001
DEFINITION 602463283F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576124 5', mRNA sequence.
ACCESSION BG341941
VERSION BG341941.1 GI:13148379
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

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          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM1288  row: e  column: 21
          High quality sequence stop: 616.
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      244 a    265 c    232 g    218 t
ORIGIN

  Query Match             92.4%;  Score 302;  DB 12;  Length 959;
  Best Local Similarity   97.5%;  Pred. No. 1.8e-86;
  Matches  318;  Conservative    0;  Mismatches    5;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db         54 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 113

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||| ||||| ||||||||||||||||||||||||| |
Db        114 ATCACTTGCCGGGCGAGTCAGGGCATTAACAATTTTTTAGCCTGGTATCAGCAGAAACTA 173

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db        174 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 233

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        234 CGGTTCAGTGGCAGTGGCTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 293

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||||| |   |||||||||
Db        294 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC 350

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        351 CAAGGGACCAAGGTGGAAATCAAACG 376


RESULT 4
BQ881840
LOCUS       BQ881840                888 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8642888 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295725
            5', mRNA sequence.
ACCESSION   BQ881840
VERSION     BQ881840.1  GI:22273848
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2502  row: g  column: 22
            High quality sequence stop: 655.
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      212 a    274 c    200 g    202 t
ORIGIN

  Query Match             88.9%;  Score 290.8;  DB 14;  Length 888;
  Best Local Similarity   95.4%;  Pred. No. 7.2e-83;
  Matches  311;  Conservative    0;  Mismatches   12;  Indels    3;  Gaps    1;

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Db         76 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 135

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        136 ATCACTTGCCGGGCGAGTCAGGACATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 195

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        196 GGTAAAGTTCCTAACCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 255

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        256 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGACTGCAGCCT 315

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||| ||||||||||||||||||||||||     || ||||||
Db        316 GAAGATGTTGCAACTTATTATTGTCAAAAGTATAACAGTGCCCCTC---ACACTTTCGGC 372

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |  |||||||| ||||| ||||||||
Db        373 CCTGGGACCAAAGTGGATATCAAACG 398


RESULT 5
BM509065
LOCUS       BM509065                626 bp    mRNA    linear   EST 15-FEB-2002
DEFINITION  ih16b08.x1 Human insulinoma Homo sapiens cDNA 3' similar to
            SW:KV1W_HUMAN P04431 IG KAPPA CHAIN V-I REGION WALKER PRECURSOR. ;,
            mRNA sequence.
ACCESSION   BM509065
VERSION     BM509065.1  GI:18680208
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 626)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
```

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  TITLE     , Jackson,Y. and Bowers,Y.
  JOURNAL   Endocrine Pancreas Consortium
            Unpublished (2000)
COMMENT     Other_ESTs: ih16b08.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Possible reversed clone: similarity on wrong strand
            Seq primer: -40UP from Gibco
            High quality sequence stop: 481.
FEATURES              Location/Qualifiers
     source           1. .626
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="Human insulinoma"
                      /tissue_type="insulinoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                      XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                      (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                      pBluescript SK- by Dr. H. Inoue following the Washington
                      University protocol
                      (http://genome.wustl.edu/est/lambda_protocol.shtml).
                      Please contact Hiroshi Inoue, MD/PhD for further
                      information on this library (Metabolism Division, Permutt
                      Laboratory, Washington University School of Medicine, Box
                      8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                      is a Washington University Pancreas EST project library. "
BASE COUNT       156 a    183 c    153 g    134 t
ORIGIN
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  Query Match             87.5%;  Score 286;  DB 13;  Length 626;
  Best Local Similarity   94.5%;  Pred. No. 2.1e-81;
  Matches  308;  Conservative    0;  Mismatches   15;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 113

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||||
Db        114 ATCACTTGCCGGGCGAGTCAGGGCATTAGAAATTATGTAGCCTGGTATCAGCAGAAACCA 173

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||| |||||||||| |||||||||||||||||||| | ||||||||||||||||||||||
Db        174 GGGCAAGTTCCTAAGGTCCTGATCTATGCTGCATCCGCCTTGCAATCAGGGGTCCCATCT 233

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 293

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||  ||| ||||| ||    || ||||||
Db        294 GAAGATGTTGCAACTTATTACTGTCAAAAGTATGCCAGCGCCCCCCC---CACTTTCGGC 350

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||| ||||||||
Db        351 GGAGGGACCAAGGTGGAGATCAAACG 376
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RESULT 6
AW404145
LOCUS       AW404145                 358 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-abu-e-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3057865 5', mRNA sequence.
ACCESSION   AW404145
VERSION     AW404145.1  GI:6923202
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES              Location/Qualifiers
     source           1. .358
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:3057865"
                      /clone_lib="NIH_MGC_37"
                      /tissue_type="lymph"
                      /cell_type="germinal center B cells"
                      /cell_line="MGC85"
                      /lab_host="DH10B (LTI)"
                      /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                      Constructed from size fractionated cytoplasmic mRNA
                      (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                      M. Staudt, Ph.D. Library preparation by Maria de Fatima
                      Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT        80 a    107 c     83 g     88 t
ORIGIN
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  Query Match             85.1%;  Score 278.2;  DB 10;  Length 358;
  Best Local Similarity   97.3%;  Pred. No. 5e-79;
  Matches  283;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 123

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        124 ATCACTTGCCGGGCGAGTCAGGGCATTAGCCATTATTTAGCCTGGTATCAGCAGAAACCA 183

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 243

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CGCTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 303

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGT 291
              |||||||||||||||||||||||||||||||||||||||||||| ||| | | | |
Db        304 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGTCCCGCTCACT 354
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RESULT 7
BG342083
LOCUS       BG342083                 935 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602463029F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575847 5',
            mRNA sequence.
ACCESSION   BG342083
VERSION     BG342083.1  GI:13148509
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KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1287  row: j  column: 08
            High quality sequence stop: 673.
FEATURES             Location/Qualifiers
     source          1. .935
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4575847"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      235 a    260 c    247 g    191 t      2 others
ORIGIN

  Query Match             84.5%;  Score 276.4;  DB 12;  Length 935;
  Best Local Similarity   92.6%;  Pred. No. 3.4e-78;
  Matches  302;  Conservative    0;  Mismatches   21;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         86 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTTTAGGAGACAGAGTCACC 145

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||| | | ||||||||||||||||||||||||||
Db        146 ATCACTTGCCGGGCGAGTCAGGGCATTAGGAGTGATTTAGCCTGGTATCAGCAGAAACCA 205

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GGAAAAGTTCCTGAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 265

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| |||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        266 CGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGCCTGCAGCCT 325

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||| ||||| |||| |   ||    || ||||||
Db        326 GAAGATGTTGCAACTTATTACTGTCAAAACTATAAGAGTGGC---CCCTTCACTTTCGGC 382

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |  |||||||| |||||  |||||||
Db        383 CCTGGGACCAAAGTGGATCTCAAACG 408


RESULT 8
BM007845
LOCUS       BM007845                773 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603617528F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450551 5',
            mRNA sequence.
ACCESSION   BM007845
VERSION     BM007845.1  GI:16522199
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939  row: h  column: 08
            High quality sequence stop: 722.
FEATURES             Location/Qualifiers
     source          1. .773
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5450551"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      193 a    227 c    192 g    161 t
ORIGIN

  Query Match             84.0%;  Score 274.8;  DB 13;  Length 773;
  Best Local Similarity   92.3%;  Pred. No. 9.9e-78;
  Matches  301;  Conservative    0;  Mismatches   22;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 142

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||  |||||||||||||||||||| |  |||||||||||||||||||||| |||||||||
Db        143 ATTGCTTGCCGGGCGAGTCAGGGCTTCGGCAATTATTTAGCCTGGTATCATCAGAAACCA 202

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 262

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 CGATTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 322

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              || |||||||| || |||||| |||||||||||||||| |||||    ||||  || ||||||
Db        323 GAGGATGTTGGAAATTATTATTGTCAAAAGTATAACCGTGCC---CCGATCACCTTCGGC 379

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||     |||| || |||||
Db        380 CAAGGGACGCGACTGGAGATTAAACG 405


RESULT 9
BQ707369
LOCUS       BQ707369                928 bp    mRNA    linear   EST 16-JUL-2002
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DEFINITION  AGENCOURT_8475108 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301597
            5', mRNA sequence.
ACCESSION   BQ707369
VERSION     BQ707369.1  GI:21846268
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: 1  column: 14
            High quality sequence stop: 651.
FEATURES             Location/Qualifiers
     source          1. .928
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301597"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      219 a    284 c    224 g    201 t
ORIGIN

  Query Match           83.1%;  Score 271.6;  DB 14;  Length 928;
  Best Local Similarity 89.6%;  Pred. No. 1.2e-76;
  Matches  292;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCAAC 128

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||
Db        129 ATCACTTGCCGGGCGAGTCAGGTCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA 188

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||| |||||||||| ||| |||||||||| ||| ||  ||||||||||
Db        189 GGGAAAGCCCCTAAGCTCCTACTCTCTGCTGCATCCAGATTGGAAAGTGGGGTCCCATCC 248

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||
Db        249 AGGTTCAGTGGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGCCT 308

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||||||||||| ||||| | ||  |||  ||  ||  ||||||
Db        309 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGAACCCTCGCGCTCACTTTCGGC 368

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||| |||||||
Db        369 GGAGGGACCAAGGTGGAGATCAAACG 394


RESULT 10
AW405753
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LOCUS       AW405753                 493 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-abp-a-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3057290 5', mRNA sequence.
ACCESSION   AW405753
VERSION     AW405753.1  GI:6924810
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 493)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .493
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3057290"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      117 a    138 c    119 g    119 t
ORIGIN

  Query Match           82.6%;  Score 270;  DB 10;  Length 493;
  Best Local Similarity 91.4%;  Pred. No. 2.7e-76;
  Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         72 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 131

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||| ||||| |||||||||  |||||  ||||||||||||||||||||
Db        132 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 191

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||| |||||||    ||||||||||
Db        192 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 251

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db        252 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 311

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| |||||||| ||  | ||||| ||||||  | ||||||||||
Db        312 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GGACGTTCGGC 368

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db        369 CAAGGGACCAAGGTGGAAATCAAACG 394


RESULT 11
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AW407904
LOCUS       ÁW407904                 422 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3061128 5', mRNA sequence.
ACCESSION   AW407904
VERSION     AW407904.1  GI:6926961
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3061128"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      106 a    110 c    105 g    101 t
ORIGIN

  Query Match          82.1%;  Score 268.4;  DB 10;  Length 422;
  Best Local Similarity   91.1%;  Pred. No. 8.2e-76;
  Matches  297;  Conservative    0;  Mismatches   26;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 82

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| ||||||||| ||||||   ||||||||||||||||||
Db         83 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 142

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||||| |||||||   ||||||||||
Db        143 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 202

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        203 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 262

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||  | ||||| ||   ||| | |||||||||
Db        263 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CCGTGGACGTTCGGC 319

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db        320 CAAGGGACCAAGGTGGAAATCAAACG 345
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RESULT 12
BG758398
LOCUS       BG758398                 921 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602712592F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852678 5',
            mRNA sequence.
ACCESSION   BG758398
VERSION     BG758398.1  GI:14069051
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1697  row: h  column: 23
            High quality sequence stop: 848.
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4852678"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      236 a    264 c    219 g    202 t
ORIGIN

  Query Match          82.1%;  Score 268.4;  DB 12;  Length 921;
  Best Local Similarity   89.0%;  Pred. No. 1.3e-75;
  Matches  290;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 146

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| ||||| ||| ||||||   ||||||||||||||||||
Db        147 ATCACTTGCCGGGCAAGTCAGAGCATTCGCAGCTATTTAAATTGGTATCAGCAGAAACCA 206

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||||| |||||||   ||||||||||
Db        207 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 266

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        267 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT 326

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db        327 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTATCCCTCCGGAGACTTTCGGC 386

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db        387 CCCGGGACCAAACTGGATATCAAACG 412


RESULT 13
AV733746
LOCUS       AV733746                422 bp    mRNA    linear   EST 17-OCT-2000
DEFINITION  AV733746 cdA Homo sapiens cDNA clone cdAATB08 5', mRNA sequence.
ACCESSION   AV733746
VERSION     AV733746.1  GI:10851291
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   Yang,Y., Song,H., Peng,Y., Gu,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
            Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
            ,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Chen,J.,
            Chen,Z. and Han,Z.
  TITLE     Homo sapiens cDNA cdA clones
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="cdAATB08"
                     /clone_lib="cdA"
                     /tissue_type="pheochromocytoma"
                     /dev_stage="Adult"
                     /lab_host="BM25.8"
                     /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
BASE COUNT       88 a    118 c    117 g     99 t
ORIGIN

  Query Match             81.1%;  Score 265.2;  DB 10;  Length 422;
  Best Local Similarity   89.6%;  Pred. No. 8.9e-75;
  Matches  285;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db         91 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 150

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||| | | ||||||||||||||||||||||||||
Db        151 ATCACTTGCCGGGCGAGTCAGGGCATTAGCGAGTCTTTAGCCTGGTATCAGCAGAAACCA 210

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||| |||||| ||||||||  |||  |   ||||||||| |
Db        211 GGGAAAGCCCCTAAGCTCCTGGTCTATGGTGCATCCAGATTGGGAAGTGGGGTCCCAGCC 270

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        271 AGGTTCAGTGGCAGTGGATCTGGGACGGACTACAGTCTCACCATCAGTAGTCTGCAGCCT 330

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              || ||| |||||| |||||||||||| ||||| | ||| ||||||||   |||||||||
Db        331 GACGATTTTGCAATTTATTACTGTCAACAGTATTATAGTTCCCCTCCGGTGACGTTCGGC 390

Qy        301 CAAGGGACCAAGGTGGAA 318
              ||||||||||||||||||
Db        391 CAAGGGACCAAGGTGGAA 408


RESULT 14
BM543718
LOCUS       BM543718                1153 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6492277 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5589037
            5', mRNA sequence.
ACCESSION   BM543718
VERSION     BM543718.1  GI:18774347
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1153)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12361  row: b  column: 14
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FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_125"
                     /lab_host="DH10B"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
BASE COUNT      295 a    334 c    272 g    246 t      6 others
ORIGIN

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  Matches  288;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 GGCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 156

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
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Db        157 ATCACTTGCCAGGCGAGTCAGGGCTTCGGCAACTATTTAAATTGGTATCAGCAAAAACCA 216

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
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Db        217 GGGAAAGCCCCCACCCTCCTGATCTACGAGGCATCCAATTTGCAACCAGGGGTCCCATCA 276

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        277 AGGTTCAGTGGGAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCT 336

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| ||||||| |||||||||||| ||| | | | || |||  || | |||||||||
Db        337 GAAGATATTGCAACATATTACTGTCAACAGTTTGATACTGTCCCCTCGTGGACGTTCGGC 396

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              | |||||||||||||||||||||||||
Db        397 CGAGGGACCAAGGTGGAAATCAAACG 422
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RESULT 15
AW404992
LOCUS       AW404992                391 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-abx-a-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3058060 5', mRNA sequence.
ACCESSION   AW404992
VERSION     AW404992.1  GI:6924049
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:3058060"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
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                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT       98 a    108 c     94 g     91 t
ORIGIN

  Query Match             80.6%;  Score 263.6;  DB 10;  Length 391;
  Best Local Similarity   90.2%;  Pred. No. 2.8e-74;
  Matches  294;  Conservative    0;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 124

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| ||||||||  ||||||   |||||||||||||| ||
Db        125 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAATCA 184

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||| |||||||   ||||||||||
Db        185 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 244

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||| || || |||
Db        245 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 304

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
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Db        305 GAAGATTTTGCAATTTACTACTGTCAGCAGAGTTACAGTATCCCTCC---TACGTTCGGC 361

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
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Db        362 CAAGGGACCAAGGTGGAAATCAAACG 387
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	304.8	93.2	743	24	ABK47275	Insulin/insulin-li
	2	298.4	91.3	761	24	ABK47271	Insulin/insulin-li
	3	295.2	90.3	752	24	ABK47272	Insulin/insulin-li
	4	295.2	90.3	752	24	ABK47274	Insulin/insulin-li
	5	295.2	90.3	761	24	ABK47276	Insulin/insulin-li
	6	279.2	85.4	321	18	AAT88403	cDNA for anti-TNF-
	7	278	85.0	632	24	ABK40186	Human/rabbit Ckapp
	8	276.4	84.5	565	24	ABQ58923	Human colon cancer
	9	274.8	84.0	737	24	AAD31829	Human pancreatic t
	10	274.4	83.9	306	24	ABA94230	CB2iE7 kappa light
	11	271.6	83.1	936	21	AAA27390	Human IGFAM-10 imm
	12	270	82.6	396	18	AAT75423	Human anti-tumour
	13	270	82.6	720	20	AAX36070	DNA encoding a sin
	14	270	82.6	729	21	AAA11630	Human immunoglobul
	15	270	82.6	729	24	ABL46009	Humanised anti-Fas
	16	270	82.6	917	21	AAA27381	Human IGFAM-1 immu
	17	270	82.6	1106	24	ABQ54241	Human ovarian anti
	18	269.6	82.4	318	19	AAV19745	Antibody LD1-117-V
	19	269.4	82.4	324	22	AAH42395	Nucleotide sequenc
	20	269	82.3	322	22	AAF55231	Nucleotide sequenc
	21	269	82.3	322	22	AAF55238	DNA sequence of li
	22	268.4	82.1	684	22	AAH30051	TRO005 kappa chain
	23	268.4	82.1	702	14	AAQ43773	Sequence encoding
	24	266.2	81.4	730	21	AAZ29000	Anti-murine CTLA-4
	25	264.8	81.0	321	24	ABA06023	Human monoclonal a
	26	263.8	80.7	341	18	AAT60117	Coding sequence fo
	27	263.6	80.6	974	24	AAS99473	Anti-human AILIM m
	28	263.4	80.6	324	22	AAH68646	Human anti-Rh(D) c
	29	263.4	80.6	324	22	AAH68657	Human anti-Rh(D) c
	30	263.2	80.5	758	24	ABK47277	Insulin/insulin-li
	31	262	80.1	672	22	AAH30049	TRO005 kappa chain
	32	261.8	80.1	324	22	AAH68655	Human anti-Rh(D) c
	33	261.8	80.1	324	22	AAH68712	Human anti-Rh(D) a
	34	261.4	79.9	333	22	AAH74684	Nucleotide sequenc
	35	261.4	79.9	900	22	AAH74688	Nucleotide sequenc
	36	260.4	79.6	324	24	ABK24411	Light chain DNA fr
	37	260.4	79.6	326	22	AAD18149	Human antibody CAT
	38	260.4	79.6	333	15	AAX79686	Human cancer cell
	39	260.4	79.6	438	22	AAH41157	Human coding seque
	40	260.4	79.6	497	24	ABL38222	Human colon tumour
	41	260.4	79.6	714	21	AAA46899	DNA encoding the k
	42	260.2	79.6	321	24	AAL45699	Human endoglin (CD
	43	260.2	79.6	723	20	AAX86938	Antibody ITA7 enco
c	44	260.2	79.6	723	20	AAX86939	Antibody ITA7 comp
	45	260.2	79.6	921	24	AAL45702	Human endoglin (CD

ALIGNMENTS

RESULT 1
ABK47275
ID ABK47275 standard; DNA; 743 BP.
XX
AC ABK47275;
XX
DT 18-JUN-2002 (first entry)
XX
DE Insulin/insulin-like growth factor receptor, DNA sequence #29.
XX
KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW ophthalmological; insulin; receptor; gene therapy; diabetes;
KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW diabetic retinopathy; neurological diseases; stroke;
KW diabetic neuropathy; gene; ss.
XX
OS Synthetic.
XX
PN WO200172771-A2.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2000; 2000WO-US08528.
XX
PR 29-MAR-2000; 2000WO-US08528.
XX
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA (NOVO) NOVO NORDISK AS.
XX
PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI Hansen PH, Ravera M, Hsiao K;

```
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors  -
XX
PS   Disclosure; Figure 39; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research reagents. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 743 BP; 163 A; 195 C; 218 G; 167 T; 0 other;

  Query Match             93.2%;  Score 304.8;  DB 24;  Length 743;
  Best Local Similarity   98.5%;  Pred. No. 4.5e-87;
  Matches  319;  Conservative    0;  Mismatches    2;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        415 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 474

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        475 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 534

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 594

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        595 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 654

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||||||||     | |||||||||
Db        655 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TGGACGTTCGGC 711

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              |||||||||||||||||||||||||
Db        712 CAAGGGACCAAGGTGGAAATCAAA 735


RESULT 2
ABK47271
ID   ABK47271 standard; DNA; 761 BP.
XX
AC   ABK47271;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #25.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Beasley J,  Blume AJ,  Schaeffer L,  Pillutla R,  Brandt J;
PI   Brissette R,  Spetzler J,  Cheng W,  Ostergaard S,  Mandecki WS;
PI   Hansen PH,  Ravera M,  Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors  -
XX
PS   Example 1; Figure 19; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research reagents. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 761 BP; 179 A; 201 C; 219 G; 162 T; 0 other;

  Query Match             91.3%;  Score 298.4;  DB 24;  Length 761;
  Best Local Similarity   97.2%;  Pred. No. 5e-85;
  Matches  315;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 492

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 552

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 612

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 672

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||||||||     || ||||||
Db        673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTC---TCACTTTCGGC 729

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              |||||||||||||||| ||||||
Db        730 GGAGGGACCAAGGTGGAGATCAAA 753


RESULT 3
ABK47272
ID   ABK47272 standard; DNA; 752 BP.
XX
AC   ABK47272;
XX
```

```
DT   18-JUN-2002  (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #26.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI   Hansen PH, Ravera M, Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors
XX
PS   Disclosure; Figure 36; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research that bind to IR or IGF-1 receptor. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 752 BP; 177 A; 196 C; 217 G; 162 T; 0 other;

Query Match             90.3%;  Score 295.2;  DB 24;  Length 752;
Best Local Similarity   96.6%;  Pred. No. 5.2e-84;
Matches  313;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 603

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TTCACTTTCGGC 720

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
            |||||||||||||||||||||||||
Db        721 CCTGGGACCAAAGTGGATATCAAA 744


RESULT 4
ABK47274
ID   ABK47274 standard; DNA; 752 BP.
XX
AC   ABK47274;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #28.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
PI   Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;
PI   Hansen PH, Ravera M, Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors
XX
PS   Disclosure; Figure 38; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research that bind to IR or IGF-1 receptor. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 752 BP; 162 A; 195 C; 221 G; 174 T; 0 other;

Query Match             90.3%;  Score 295.2;  DB 24;  Length 752;
Best Local Similarity   96.6%;  Pred. No. 5.2e-84;
Matches  313;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 483

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 603

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TTCACTTTCGGC 720

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
            |||||||||||||||||||||||||
Db        721 CCTGGGACCAAAGTGGATATCAAA 744
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 543

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 603

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 663

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TACACTTTTGGC 720

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
                || |||||||| |||| ||||||
Db        721 CAGGGGACCAAGCTGGAGATCAAA 744


RESULT 5
ABK47276
ID   ABK47276 standard; DNA; 761 BP.
XX
AC   ABK47276;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Insulin/insulin-like growth factor receptor, DNA sequence #30.
XX
KW   Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
KW   ophthalmological; insulin; receptor; gene therapy; diabetes;
KW   insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
KW   diabetic retinopathy; neurological diseases; stroke;
KW   diabetic neuropathy; gene; ss.
XX
OS   Synthetic.
XX
PN   WO200172771-A2.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2000; 2000WO-US08528.
XX
PR   29-MAR-2000; 2000WO-US08528.
XX
PA   (DGIB-) DGI BIOTECHNOLOGIES LLC.
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Beasley J,  Blume AJ,  Schaeffer L,  Pillutla R,  Brandt J;
PI   Brissette R,  Spetzler J,  Cheng W,  Ostergaard S,  Mandecki WS;
PI   Hansen PH,  Ravera M,  Hsiao K;
XX
DR   WPI; 2002-025774/03.
XX
PT   Modulating insulin activity in mammalian cells, for treating e.g.
PT   diabetes and tumours, comprises using peptides that bind to insulin or
PT   insulin-like growth factor receptors
XX
PS   Disclosure; Figure 57; 390pp; English.
XX
CC   The invention relates to a method of modulating insulin activity in
CC   mammalian cells by administering a peptide that binds the insulin
CC   receptor (IR). A composition containing a peptide, optionally expressed
CC   from gene therapy vectors, that binds to Site 1 of IR and an insulin
CC   agonist are useful for treating diabetes. Also, peptides that are
CC   antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
CC   useful for treating insulin-like growth factor (IGF)-sensitive tumours
CC   (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1
CC   receptor agonists are useful for treating neurological diseases,
CC   including stroke and diabetic neuropathy. The peptides are also useful in
CC   screening for compounds that bind to IR or IGF-1 receptor, potential
CC   therapeutics and research reagents. ABK47246-ABK47277 represent IR
CC   and/or IGF-1 receptor DNA sequences of the invention.
XX
SQ   Sequence 761 BP; 179 A; 200 C; 217 G; 165 T; 0 other;

  Query Match             90.3%;  Score 295.2;  DB 24;  Length 761;
  Best Local Similarity   96.6%;  Pred. No. 5.2e-84;
  Matches  313;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 492

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 552

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 612

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 672

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||      || ||||||
Db        673 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCT---TTCACTTTCGGC 729

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
                |  |||||||| ||||| ||||||
Db        730 CCTGGGACCAAAGTGGATATCAAA 753


RESULT 6
AAT88403
ID   AAT88403 standard; cDNA; 321 BP.
XX
AC   AAT88403;
XX
DT   19-MAR-1998  (first entry)
XX
DE   cDNA for anti-TNF-alpha antibody light chain variable region.
XX
KW   Human; tumour necrosis factor-alpha; TNF-alpha; antibody;
KW   light chain; variable region; inhibition;
KW   treatment; sepsis; disease; autoimmune disease; infectious disease;
KW   malignancy; pulmonary disorder; intestinal disorder; hepatitis;
KW   cardiac disorder; inflammatory bone disorder; reperfusion injury;
KW   bone resorption disease; coagulation disturbance; burn; ELAM-1;
KW   keloid formation; scar tissue formation; pyrexia; HUVEC;
KW   periodontal disease; obesity; radiation toxicity;
KW   endothelial cell leukocyte adhesion molecule-1;
KW   human umbilical vein endothelial cell; ds.
XX
OS   Homo sapiens.
XX
PN   WO9729131-A1.
XX
PD   14-AUG-1997.
XX
PF   10-FEB-1997;   97WO-US02219.
XX
PR   25-NOV-1996;   96US-0031476.
PR   09-FEB-1996;   96US-0599226.
XX
PA   (BADI ) BASF AG.
XX
PI   Allen DJ,  Hoogenboom HRJM,  Kaymakcalan Z,  Labkovsky B;
PI   Mankovich JA,  McGuiness BT,  Roberts AJ,  Sakorafas P;
PI   Salfeld JG,  Schoenhaut D,  Vaughan TJ,  White M,  Wilton AJ;
XX
DR   WPI; 1997-415302/38.
DR   P-PSDB; AAW27568.
```

XX
PT High affinity antibodies against human TNF alpha - useful to inhibit
PT TNF alpha activity, e.g. to treat autoimmune diseases and cancer
XX
PS Disclosure; Page 75; 102pp; English.
XX
CC The present sequence encodes a novel anti-human tumour necrosis
CC factor-alpha (TNF-alpha) antibody (Ab) light chain variable region.
CC The Ab dissociates from TNF-alpha with a Kd of 1x10 power -8 M or
CC less and has a Koff rate constant of 1x10 power -3 s power -1 or
CC less (both determined by surface plasmon resonance), and
CC neutralises human TNF-alpha cytotoxicity in a standard in vitro
CC L929 assay with an IC50 of 1x10 power -7 M or less. The Ab, which
CC inhibits TNF-alpha activity, can be used to treat sepsis,
CC autoimmune diseases, e.g. rheumatoid arthritis, rheumatoid
CC spondylitis, osteoarthritis, gouty arthritis, allergy, multiple
CC sclerosis, autoimmune diabetes, autoimmune uveitis or nephrotic
CC syndrome, infectious diseases, malignancy, pulmonary, intestinal,
CC cardiac or inflammatory bone disorders, bone resorption disease,
CC alcoholic, viral or fulminant hepatitis, coagulation disturbances,
CC burns, reperfusion injury, keloid formation, scar tissue formation,
CC pyrexia, periodontal disease, obesity and radiation toxicity. The
CC Ab also inhibits TNF-alpha induced expression of endothelial cell
CC leukocyte adhesion molecule-1 (ELAM-1) on human umbilical vein
CC endothelial cells (HUVEC).
XX
SQ Sequence 321 BP; 85 A; 87 C; 74 G; 75 T; 0 other;

Query Match 85.4%; Score 279.2; DB 18; Length 321;
Best Local Similarity 93.5%; Pred. No. 4.8e-79;
Matches 303; Conservative 0; Mismatches 18; Indels 3; Gaps 1;

```
Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||||||| || ||||| |||||||||||||||||| ||||||
Db         61 ATCACTTGTCGGGCAAGTCAGGGCATCAGAAATTACTTAGCCTGGTATCAGCAAAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||| ||||||| |||   | |||  ||| || |||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAGGTATAACCGTG---CACCGTATACTTTTGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              || ||||||||||||||||||||||
Db        298 CAGGGGACCAAGGTGGAAATCAAA 321
```

RESULT 7
ABK40186
ID ABK40186 standard; DNA; 632 BP.
XX
AC ABK40186;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human/rabbit Ckappa chimaeric DNA sequence.
XX
KW Antibody; Cgamma; Ckappa; Clambda2; ds; transgenic; vector;
KW infectious disease; malignancy; cancer; tumour; autoimmune disease;
KW humanised immunoglobulin; cytostatic; antibacterial; virucide;
KW fungicide; light chain variable region; heavy chain variable region;
KW Ig.
XX
OS Chimeric - Oryctolagus cuniclus.
OS Chimeric - Homo sapiens.
XX
PN WO200212437-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-US24348.
XX
PR 03-AUG-2000; 2000US-222872P.
PR 15-MAR-2001; 2001US-276156P.
XX
PA (SCHO/) SCHOOTEN W.
PA (BUEL/) BUELOW R.
PA (PLAT/) PLATZER J.
PA (BUEL/) BUELOW J.
XX
PI Schooten W, Buelow R, Platzer J, Buelow J;
XX
DR WPI; 2002-217188/27.
XX
PT Novel humanised antibodies useful for treating diseases caused by
PT bacterial, viral, fungal infection and cancer, are derived from
PT transgenic non-human animals engineered to contain humanised
PT immunoglobulin loci -
XX
PS Claim 12; Fig 11; 81pp; English.
XX
CC The invention relates to a humanised immunoglobulin derived from a
CC transgenic animal, comprising a portion of a human immunoglobulin
CC polypeptide sequence (e.g. form immunoglubulin Cgamma, Ckappa or
CC Clambda2). Also included are 1) nucleic acid molecules comprising the
CC 3' flanking regions of cow, sheep and rabbit Cgamma, the 3' flanking
CC region of rabbit Ckappa and the 5' flanking region of rabbit Cgamma,
CC 2) a recombination vector for replacing an Ig gene segment from
CC a non-human animal with a human immunoglobulin (Ig) gene segment,
CC comprising from 5' to 3', a 5' nucleotide sequence, the human Ig gene
CC segment, and a 3' nucleotide sequence, where the 5' and 3' nucleotide
CC sequences are homologous to the 5' and 3' flanking sequences of the Ig
CC gene segment from the non-human animal, 3) a transgenic vector comprising
CC a humanised Ig locus derived from an Ig locus or a portion of an Ig locus
CC of a non-human animal, where the locus comprises multiple Ig gene
CC segments, where at least one of the gene segments is a human Ig gene
CC segment, and the gene segments are juxtaposed in an unrearranged,
CC partially or fully rearranged configuration, and the locus is capable of
CC undergoing gene conversion and producing a repertoire of humanised Igs in
CC the non-human animal and 3) a transgenic animal comprising a humanised
CC Ig locus. The antibody is useful for treating a disease caused by
CC bacterial, fungal or viral infection, cancer or an autoimmune disease in
CC a human. The vector is useful for replacing rabbit light or heavy chain
CC constant or variable region gene, or a chicken light chain constant
CC region gene. The transgenic vector is useful for making a transgenic
CC non-human animal capable of producing a functional repertoire of
CC humanised antibodies, by introducing the construct into a recipient cell
CC of a non-human animal and integrating the humanised Ig loci in the
CC transgenic construct into the genome of the recipient cell. The animal
CC is rabbit having an impaired expression of endogenous Ig molecules, and
CC the recipient cell is a cell in an early embryo, or is a chicken and
CC the recipient cell is a fertilised egg. Alternatively, transgenic
CC non-human animals capable of producing a functional repertoire of
CC humanised heavy or light chains, respectively are mated and an
CC offspring is selected which produces both humanised heavy and light
CC chains. The Cgamma DNA is useful for creating a humanised Ig locus
CC and making transgenic animals capable of producing humanised Ig
CC molecules. The present sequence is a recombination vector of invention.
XX
SQ Sequence 632 BP; 149 A; 169 C; 143 G; 171 T; 0 other;

Query Match 85.0%; Score 278; DB 24; Length 632;
Best Local Similarity 92.9%; Pred. No. 1.5e-78;
Matches 303; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

```
Qy          2 ACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCA 61
```

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                ||||||||||||||||||||||||||||| |||||||||||||| ||||||||||||||||
Db        242 ACATCCAGATGACCCAGTCTCCATCCTCTCTGTCTGCATCTGTGGGAGACAGAGTCACCA 301

Qy         62 TCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAG 121
               |||||||||| || |||||||||||||||||||| ||||||||||||||||||||||||
Db        302 TCACTTGCCGAGCCAGTCAGGGCATTAGCAATTACTTAGCCTGGTATCAGCAGAAACCAG 361

Qy        122 GGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTC 181
               |||| ||||| |||||||||| |||||||||||||||||||| |||||||||| |
Db        362 GGAAGGTTCCCAAGCTCCTGATTTATGCTGCATCCACTTTGCAATCTGGGGTCCCATCGC 421

Qy        182 GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTG 241
               |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        422 GGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTTACCATCAGCAGCCTGCAGCCTG 481

Qy        242 AAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCC 301
               |||||||||| || |||||||||||||||| ||||||||||||    |   ||||||
Db        482 AAGATGTTGCCACCTATTACTGTCAAAAGTACAACAGTGCCCCTCCACTT---TTCGGCG 538

Qy        302 AAGGGACCAAGGTGGAAATCAAACGT 327
               |||||||||||||| |||||||||
Db        539 GAGGGACCAAGGTGGAGATCAAACGT 564


RESULT 8
ABQ58923
ID   ABQ58923 standard; cDNA; 565 BP.
XX
AC   ABQ58923;
XX
DT   02-AUG-2002  (first entry)
XX
DE   Human colon cancer related nucleotide sequence SEQ ID NO:2618.
XX
KW   Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW   genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200229086-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US30732.
XX
PR   02-OCT-2000; 2000US-237271P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI   Thiaglingam A, Lewis ME;
XX
DR   WPI; 2002-426115/45.
XX
PT   New isolated nucleic acid that is differentially expressed in cancer
PT   tissues useful for determining the presence of colon cancer in a cell
PT   or tissue type, and in antisense therapy -
XX
PS   Claim 1; Fig 1; 796pp; English.
XX
CC   ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC   expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC   encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC   used in antisense therapy. An antibody immunoreactive with a polypeptide
CC   encoded by (I) is useful for detecting cancer in a patient sample, and
CC   for detecting the presence or absence of a polynucleotide encoded by a
CC   nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC   from (I) can be used for determining the presence of a nucleic acid which
CC   hybridises to (I), and for determining the phenotype of cells in a sample
CC   of cells from a patient. (I) is useful for determining the presence of
CC   colon cancer in a cell or tissue type, for determining the presence or
CC   state of other type of cancer, in antisense therapy, to generate
CC   macroarrays on a solid surface, to identify a chromosome on which the
CC   corresponding gene resides, and in tissue profiling, forensics, genetic
CC   analysis, mapping and diagnostic applications. (I) can be used to raise
CC   antibodies, and to screen for peptide analogues and antagonists.
XX
SQ   Sequence 565 BP; 128 A; 155 C; 142 G; 134 T; 6 other;

  Query Match             84.5%;  Score 276.4;  DB 24;  Length 565;
  Best Local Similarity   92.6%;  Pred. No. 4.6e-78;
  Matches  302;  Conservative    0;  Mismatches   21;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||| | ||||||||||||||||||||||||||||||
Db        104 GACATCCAGATGACCCAGTCTCCATCTTTCCTGTCTGCATCTGTAGGAGACAGAGTCACC 163

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        164 ATCACTTGCCGGGCGAGTCAGGGCATTGCCAATTATTTAGCCTGGTATCAGCAGAAACCA 223

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||||||  ||| ||||||||||||||||||| |||||||||| | ||||||||||||
Db        224 GGGAAAGTTCCAAAGGTCCTGATCTATGCTGCATTCACTTTGCAAGCTGGGGTCCCATCT 283

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||  |||  ||||||||||| |||||||||||||||| ||||||||||||
Db        284 CGGTTCAGTGGCGGTGCTTCTGGGACAGAGTTCACTCTCACCATCAGTAGCCTGCAGCCT 343

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||  ||| | ||||||||||||||||||||||||||||||||  |   |||||||||
Db        344 GAAGATGCTGCGATTTATTACTGTCAAAAGTATAACAGTGCCCCTCAG---ACGTTCGGC 400

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              || ||||||||| |||| ||||||||
Db        401 CAGGGGACCAAGTTGGAGATCAAACG 426


RESULT 9
AAD31829
ID   AAD31829 standard; cDNA; 737 BP.
XX
AC   AAD31829;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human pancreatic tumour protein encoding cDNA clone 53796.2.
XX
KW   Human; pancreatic tumour protein; pancreatic cancer; therapy; diagnosis;
KW   cancer; vaccine; cytostatic; ss.
XX
OS   Homo sapiens.
XX
PN   WO200212327-A2.
XX
PD   14-FEB-2002.
XX
PF   30-JUL-2001; 2001WO-US23969.
XX
PR   03-AUG-2000; 2000US-223102P.
PR   21-SEP-2000; 2000US-234451P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Pyle RA, Xu J;
XX
DR   WPI; 2002-241738/29.
XX
PT   New polynucleotides derived from pancreatic tumor cDNA library, useful
PT   as vaccines for preventing and treating pancreatic cancer, as well as
PT   for the diagnosis and monitoring of such cancers -
XX
PS   Claim 1; Page 107; 120pp; English.
XX
CC   The invention relates to polynucleotides derived from pancreatic tumour
CC   cDNA library, encoding pancreatic tumour proteins. The invention also
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CC   relates to therapy and diagnosis of cancer, such as pancreatic cancer.
CC   The polypeptides and polynucleotides of the invention are useful as
CC   vaccines and pharmaceutical compositions for preventing and treating
CC   pancreatic cancer, as well as for the diagnosis and monitoring of such
CC   cancers. The present sequence is human pancreatic tumour protein
CC   encoding cDNA.
XX
SQ   Sequence 737 BP; 188 A; 211 C; 181 G; 153 T; 4 other;

  Query Match             84.0%;  Score 274.8;  DB 24;  Length 737;
  Best Local Similarity   90.2%;  Pred. No. 1.7e-77;
  Matches  294;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 143

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        144 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA 203

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||  |  ||||||||||  || |||||| |||||  ||| ||   ||||||||||
Db        204 GGGAGTGCCCCTAAGCTCCTACTCCATGCTGTATCCAACTTGGAAAGTGGGGTCCCATCC 263

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||
Db        264 AGGTTCAGTGGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGCCT 323

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||  |||||||||||||||||||| |||||  |  |||  |||||||    || ||||||
Db        324 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTAACCCTCCGGTCACTTTCGGC 383

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||| ||||||||
Db        384 GGAGGGACCAAGGTGGAGATCAAACG 409


RESULT 10
ABA94230
ID   ABA94230 standard; DNA; 306 BP.
XX
AC   ABA94230;
XX
DT   13-MAR-2002  (first entry)
XX
DE   CB2iE7 kappa light chain variable region nucleotide sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW   ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..306
FT                   /*tag=  a
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US14902.
XX
PR   10-MAY-2000; 2000US-0568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M,  Miller DJ,  Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   P-PSDB; ABB07183.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody),
PT   promoting neurite outgrowth, regeneration, remyelination and
PT   neuroprotection in central nervous system, useful to treat
PT   post-infectious encephalomyelitis -
XX
PS   Claim 43; Fig 42; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC   CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture.
CC   (I) is also useful for stimulating remyelination of CNS axons. The
CC   antibodies are useful for preventing infection by a bacterium, virus or
CC   like pathogen that causes demyelination or other neurodegenerative
CC   condition in a subject. Methods where (I) is administered to a patient
CC   are useful for treating multiple sclerosis, Parkinson's disease,
CC   Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
CC   demyelinating disease, CNS diseases, and other conditions in the CNS
CC   where nerves are damaged as by trauma. The present sequence represents
CC   the CB2iE7 kappa light chain variable region nucleotide sequence.
XX
SQ   Sequence 306 BP; 77 A; 84 C; 70 G; 75 T; 0 other;

  Query Match             83.9%;  Score 274.4;  DB 24;  Length 306;
  Best Local Similarity   97.9%;  Pred. No. 1.6e-77;
  Matches  278;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        181 CGGTTCAATGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAACCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCC 284
              ||||||||||||||||||||||||||||||||||||    |||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAAGTGCCC 284


RESULT 11
AAA27390
ID   AAA27390 standard; cDNA; 936 BP.
XX
AC   AAA27390;
XX
DT   16-AUG-2000  (first entry)
XX
DE   Human IGFAM-10 immunoglobulin coding sequence.
XX
KW   Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;
KW   infection; inflammation; haematopoiesis; AIDS; allergy; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             19..732
FT                   /*tag=  a
FT                   /product= "IGFAM-10"
FT   sig_peptide     19..84
FT                   /*tag=  b
FT   mat_peptide     85..729
FT                   /*tag=  c
XX
PN   WO200029583-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US27566.
XX
PR   19-NOV-1998;   99US-0113635.
PR   22-DEC-1998;   98US-0113635.
PR   07-APR-1999;   99US-0128194.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Yue H,  Tang YT,  Corley NC,  Guegler KJ,  Gorgone GA,  Baughn MR;
PI   Lu DAM,  Lal P,  Hillman JL,  Yang J;
XX
DR   WPI; 2000-387796/33.
DR   P-PSDB; AAY96298.
XX
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders
PT   -
XX
PS   Claim 9; Page 99-100; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-10 gene, which was isolated from a cDNA library of colon
CC   tissue. It is expressed in reproductive, gastrointestinal and
CC   cardiovascular tissue, where cancer and inflammation are common. The
CC   gene, protein, its antibodies, agonists and antagonists are suitable for
CC   diagnosing and treating many diseases, including cancer, immune system
CC   disorders (such as inflammation, AIDS, allergies, anaemia,
CC   arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC   disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC   multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC   systemic lupus erythematosus and ulcerative colitis), complications of
CC   cancer, haemodialysis and extracorporeal circulation, trauma and
CC   haematopoietic cancer (such as leukaemia) and infections caused by
CC   bacteria, viruses, fungi or parasites.
XX
SQ   Sequence 936 BP; 239 A; 276 C; 214 G; 207 T; 0 other;

  Query Match             83.1%;  Score 271.6;  DB 21;  Length 936;
  Best Local Similarity   89.6%;  Pred. No. 1.9e-76;
  Matches  292;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 144

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        145 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 204

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||| |||||||   ||||||||||||
Db        205 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 264
                                                ^
Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        265 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 324

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||  | |||||  |||||||||   || ||||||
Db        325 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGATCACCTTCGGC 384

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||     |||| || |||||
Db        385 CAAGGGACACGACTGGAGATTAAACG 410


RESULT 12
AAT75423
ID   AAT75423 standard; cDNA; 396 BP.
XX
AC   AAT75423;
XX
DT   12-SEP-1997  (first entry)
XX
DE   Human anti-tumour antigen antibody light chain variable region cDNA.
XX
KW   Human; tumour antigen; cancer; monoclonal; antibody; light chain;
KW   variable region; medicine; pharmacology; biochemistry; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1..66
FT                   /*tag=  a
FT   mat_peptide     67..396
FT                   /*tag=  b
XX
PN   JP09100300-A.
XX
PD   15-APR-1997.
XX
PF   03-OCT-1995;   95JP-0278266.
XX
PR   03-OCT-1995;   95JP-0278266.
XX
PA   (HAGI/) HAGIWARA Y.
XX
DR   WPI; 1997-276726/25.
DR   P-PSDB; AAW22842.
XX
PT   Anticancer human monoclonal antibody variable region sequences - and
PT   related DNA and RNA
XX
PS   Claim 12; Page 11; 14pp; Japanese.
XX
CC   The present sequence encodes a human anti-tumour antigen
CC   monoclonal antibody (MAb) light chain variable region, useful in
CC   medicine, pharmacology and biochemistry. The isotype of a MAb
CC   secreted by the human/human hybridoma HT was determined to be mu
CC   and kappa. Human MAb was purified, and the antigen recognised by
CC   human MAb CLN"-IgM identified by western blotting.
XX
SQ   Sequence 396 BP; 101 A; 107 C; 97 G; 91 T; 0 other;

  Query Match             82.6%;  Score 270;  DB 18;  Length 396;
  Best Local Similarity   91.4%;  Pred. No. 4.5e-76;
  Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        127 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 186

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||| |||||||   ||||||||||||
Db        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
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Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 306

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| |||||||| ||  | ||||| |||||| |   |||||||||
Db        307 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCAG---ACGTTCGGC 363

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        364 CAAGGGACCAAGGTGGAAATCAAACG 389
```

RESULT 13
AAX36070
ID AAX36070 standard; DNA; 720 BP.
XX
AC AAX36070;
XX
DT 15-JUL-1999 (first entry)
XX
DE DNA encoding a single chain antibody (ScFv).
XX
KW Screening; functional polypeptide; ligand; non-functional;
KW enrichment; single chain antibody; ScFv; ss.
XX
OS Unidentified.
XX
PN WO9920749-A1.
XX
PD 29-APR-1999.
XX
PF 20-OCT-1998; 98WO-GB03135.
XX
PR 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PI Tomlinson I, Winter G;
XX
DR WPI; 1999-288302/24.
DR P-PSDB; AAY02472.
XX
PT Screening for functional polypeptides which bind a ligand
XX
PS Disclosure; Fig 2; 67pp; English.
XX
CC The specification describes a method for screening for functional
CC polypeptides which bind a ligand. The method comprises contacting a
CC repertoire of polypeptides with a generic ligand, and then screening
CC selected functional polypeptides with a target ligand. The method
CC permits the removal from a chosen repertoire of polypeptides, those
CC which are non-functional, e.g. as a result of the introduction of
CC frame-shift mutations, stop codons, folding mutants or expression
CC mutants which would be or are incapable of binding to any target
CC ligand. The method also permits the enrichment of a chosen repertoire
CC of polypeptides for those polypeptides which are functional, well folded
CC and highly expressed. The polypeptides obtained can be used in
CC diagnostic, prophylactic and therapeutic procedures. The present
CC sequence encodes the single chain antibody (ScFv) that forms the basis
CC of a library according to the invention.
XX
SQ Sequence 720 BP; 168 A; 181 C; 214 G; 157 T; 0 other;

Query Match 82.6%; Score 270; DB 20; Length 720;
Best Local Similarity 91.4%; Pred. No. 5.6e-76;
Matches 298; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

```
Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||||||| |||||||   ||||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| |||||||| ||  | ||||| |||||   | ||||||||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCT---AATACGTTCGGC 693

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        694 CAAGGGACCAAGGTGGAAATCAAACG 719
```

RESULT 14
AAA11630
ID AAA11630 standard; DNA; 729 BP.
XX
AC AAA11630;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human immunoglobulin light chain kappa region subgroup type I DNA.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
XX
OS Homo sapiens.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
DR WPI; 2000-258930/23.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
PS Example 2; Page 154; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,

```
CC   immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC   antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC   antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC   apoptosis by binding to cell surface Fas or inhibit it by competitive
CC   inhibition of ligand binding. (I) are used to treat and/or prevent
CC   diseases associated with the Fas/Fas ligand system, especially systemic
CC   lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC   versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC   anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC   dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC   cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC   (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC   inhibit apoptosis in normal cells but selectively induce it in abnormal
CC   cells. They bind to both human and murine Fas, so can be evaluated in
CC   murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC   the native ligand, do not induce liver disease, and have reduced risk of
CC   inducing a human anti-murine antibody response. This sequence represents
CC   a human immunoglobulin light chain kappa variable region subgroup type I
CC   which is used in the construction of humanised anti-Fas antibody
CC   constructs described in the method of the invention.
XX
SQ   Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

  Query Match             82.6%;  Score 270;  DB 21;  Length 729;
  Best Local Similarity   91.4%;  Pred. No. 5.6e-76;
  Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 132

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  |||||||  ||||||||||||||||||
Db        133 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 192

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||| |||||||   ||||||||||
Db        193 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 252

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        253 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 312

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||  | ||||| ||||||   | |||||||||
Db        313 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC 369

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        370 CAAGGGACCAAGGTGGAAATCAAACG 395


RESULT 15
ABL46009
ID   ABL46009 standard; DNA; 729 BP.
XX
AC   ABL46009;
XX
DT   26-APR-2002  (first entry)
XX
DE   Humanised anti-Fas antibody related PCR primer SEQ ID NO 76.
XX
KW   Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
KW   light chain subunit; apoptosis; immunosuppressive; antiallergic;
KW   autoimmune disease; allergy; atopic; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   JP2001342148-A.
XX
PD   11-DEC-2001.
XX
PF   28-MAR-2001; 2001JP-0093106.
XX
PR   29-MAR-2000; 2000JP-0090918.
XX
PA   (SANY ) SANKYO CO LTD.
XX
DR   WPI; 2002-145113/19.
XX
PT   Drug containing humanised anti-Fas antibody, used for preventing and
PT   treating autoimmune diseases, allergy, and atopy -
XX
PS   Example 15 (Preparatory); Page 40; 194pp; Japanese.
XX
CC   The invention relates to a preventive or treating agent for diseases
CC   caused by abnormality in Fas/Fas ligand system containing as the active
CC   component an antibody having as the light chain subunit a polypeptide
CC   containing residues 1-218 of one of 3, 239 residue amino acid sequences,
CC   or residues 1-451 of one of 3, 470 residue amino acid sequences, all
CC   fully defined in the specification and having an activity of combining
CC   specifically with mammalian Fas and an activity of inducing apoptosis
CC   in a cell expressing Fas. The agent has immunosuppressive and
CC   antiallergic activity and is used for preventing and treating autoimmune
CC   diseases, allergy, atopy and others. The present sequence is that of a
CC   PCR primer, useful to the invention.
XX
SQ   Sequence 729 BP; 192 A; 200 C; 182 G; 155 T; 0 other;

  Query Match             82.6%;  Score 270;  DB 24;  Length 729;
  Best Local Similarity   91.4%;  Pred. No. 5.6e-76;
  Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 132

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||| |||||| |||||||||  |||||||  ||||||||||||||||||
Db        133 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 192

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||| |||||||   ||||||||||
Db        193 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 252

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        253 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 312

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||  | ||||| ||||||   | |||||||||
Db        313 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC 369

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        370 CAAGGGACCAAGGTGGAAATCAAACG 395


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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	294	89.9	514	15	US-10-066-543-2025	Sequence 2025, Ap
c 2	294	89.9	537	15	US-10-066-543-186	Sequence 186, App
3	279.2	85.4	321	12	US-09-801-185A-36	Sequence 36, Appl
4	278	85.0	490	12	US-09-918-995-37859	Sequence 37859, A
5	274.8	84.0	737	11	US-09-919-344-7	Sequence 7, Appli
6	274.8	84.0	819	15	US-10-158-646-65	Sequence 65, Appl
7	270	82.6	720	10	US-09-192-854-1	Sequence 1, Appli
8	270	82.6	720	11	US-09-968-561A-1	Sequence 1, Appli
9	270	82.6	729	15	US-10-216-484-125	Sequence 125, App
10	264.8	81.0	321	15	US-10-035-637-1	Sequence 1, Appli
11	263.6	80.6	974	11	US-09-859-053-29	Sequence 29, Appl
12	263.4	80.6	324	12	US-09-848-798-101	Sequence 101, App
13	263.4	80.6	324	12	US-09-848-798-112	Sequence 112, App
14	261.8	80.1	324	12	US-09-848-798-110	Sequence 110, App
15	261.8	80.1	324	12	US-09-848-798-210	Sequence 210, App
16	260.4	79.6	326	10	US-09-798-058-3	Sequence 3, Appli
17	260.4	79.6	494	11	US-09-878-178-1811	Sequence 1811, Ap
18	260.4	79.6	494	15	US-10-046-935-1811	Sequence 1811, Ap
19	260.4	79.6	494	15	US-10-146-502-1811	Sequence 1811, Ap
20	260.4	79.6	714	15	US-10-153-382-18	Sequence 18, Appl
21	259.8	79.4	728	11	US-09-844-684-15	Sequence 15, Appl
22	259.8	79.4	728	15	US-10-040-244-15	Sequence 15, Appl
23	258.6	79.1	324	12	US-09-848-798-220	Sequence 220, App
24	258.6	79.1	324	12	US-09-848-798-224	Sequence 224, App
25	258.2	79.0	716	11	US-09-844-684-13	Sequence 13, Appl
26	258.2	79.0	716	15	US-10-040-244-13	Sequence 13, Appl
27	257.2	78.7	324	15	US-10-067-800-65	Sequence 65, Appl
28	257	78.6	321	12	US-09-848-798-102	Sequence 102, App
29	257	78.6	321	12	US-09-848-798-218	Sequence 218, App
30	257	78.6	321	12	US-09-848-798-221	Sequence 221, App
31	257	78.6	321	12	US-09-848-798-222	Sequence 222, App
32	257	78.6	324	12	US-09-848-798-204	Sequence 204, App
33	256.8	78.5	321	15	US-10-073-644C-3	Sequence 3, Appli
34	256.8	78.5	387	12	US-09-019-441-3	Sequence 3, Appli
35	256.8	78.5	387	15	US-10-103-686-3	Sequence 3, Appli
36	256.2	78.3	384	10	US-09-905-243-20	Sequence 20, Appl
37	256	78.3	356	12	US-09-918-995-18784	Sequence 18784, A
38	255.6	78.2	390	10	US-09-905-243-57	Sequence 57, Appl
39	255.4	78.1	324	12	US-09-848-798-100	Sequence 100, App
40	255.4	78.1	324	12	US-09-848-798-206	Sequence 206, App
41	255.2	78.0	321	15	US-10-060-585-9	Sequence 9, Appli
42	255.2	78.0	321	15	US-10-172-317-3	Sequence 3, Appli
43	253.8	77.6	321	12	US-09-848-798-98	Sequence 98, Appl
44	253.8	77.6	321	12	US-09-848-798-107	Sequence 107, App
45	253.6	77.6	321	15	US-10-091-300-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-10-066-543-2025
; Sequence 2025, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2025
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-2025

Query Match 89.9%; Score 294; DB 15; Length 514;
Best Local Similarity 96.0%; Pred. No. 8.2e-92;
Matches 313; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

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Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 137

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        138 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 197

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCTGGGGTCCCATCT 257

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||
Db        258 CGGTTCAGTGGCAGTGGATCTGGGACACATTTCACTCTCACCATCGGCAGCCTGCAGCCT 317

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||| ||||||||| |||||||||||    || | |||||||||
Db        318 GAAGATGTTGCAACTTATTTCTGTCAAAAATATAACAGTGCC---CCCGGGACGTTCGGC 374

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||| ||||||||
Db        375 CAAGGGACCAAGGTGGACATCAAACG 400


RESULT 2
US-10-066-543-186/c
; Sequence 186, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Pyle, Ruth A.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Indirias, Carol Yoseph
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Smith, Carole L.
;  APPLICANT:  Durham, Margarita
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.563
;  CURRENT APPLICATION NUMBER: US/10/066,543
;  CURRENT FILING DATE:  2002-01-31
;  NUMBER OF SEQ ID NOS: 3417
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
;  LENGTH: 537
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: 529
;  OTHER INFORMATION: n = A,T,C or G
US-10-066-543-186

  Query Match             89.9%;  Score 294;  DB 15;  Length 537;
  Best Local Similarity   96.0%;  Pred. No. 8.3e-92;
  Matches  313;  Conservative    0;  Mismatches   10;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 378

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 318

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 GGAAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCTGGGGTCCCATCT 258

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||| |||||||||||||||| ||||||||||||||
Db        257 CGGTTCAGTGGCAGTGGATCTGGGACACATTTCACTCTCACCATCGGCAGCCTGCAGCCT 198

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||| ||||||||| |||||||||||    || | |||||||||
Db        197 GAAGATGTTGCAACTTATTTCTGTCAAAAATATAACAGTGCC---CCCGGGACGTTCGGC 141

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||| ||||||||
Db        140 CAAGGGACCAAGGTGGACATCAAACG 115


RESULT 3
US-09-801-185A-36
; Sequence 36, Application US/09801185A
; Publication No. US20030092059A1
;   GENERAL INFORMATION:
;        APPLICANT: BASF Aktiengesellschaft
;        TITLE OF INVENTION: Human Antibodies that Bind Human TNFalpha
;        NUMBER OF SEQUENCES: 37
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: LAHIVE & COCKFIELD
;             STREET: 28 State Street
;             CITY: Boston
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/801,185A
;             FILING DATE: 07-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/599,226
;             FILING DATE: 09-FEB-1996
;             APPLICATION NUMBER: US 60/031,476
;             FILING DATE: 25-NOV-1996
;             APPLICATION NUMBER: US 09/125,098
;             FILING DATE: 07-AUG-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: DeConti, Giulio A., Jr.
;             REGISTRATION NUMBER: 31,503
;             REFERENCE/DOCKET NUMBER: BBI-043CPUSCN
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)227-7400
;             TELEFAX: (617)227-5941
;   INFORMATION FOR SEQ ID NO: 36:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 321 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-801-185A-36

  Query Match             85.4%;  Score 279.2;  DB 12;  Length 321;
  Best Local Similarity   93.5%;  Pred. No. 9.4e-87;
  Matches  303;  Conservative    0;  Mismatches   18;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||||||| || ||||| ||||||||||||||||| ||||||
Db         61 ATCACTTGTCGGGCAAGTCAGGGCATCAGAAATTACTTAGCCTGGTATCAGCAAAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||| ||||||| |||   | |||  ||| || |||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAGGTATAACCGTG---CACCGTATACTTTTGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              || ||||||||||||||||||||||
Db        298 CAGGGGACCAAGGTGGAAATCAAA 321


RESULT 4
US-09-918-995-37859
; Sequence 37859, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37859
;   LENGTH: 490
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(490)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37859

  Query Match             85.0%;  Score 278;  DB 12;  Length 490;
  Best Local Similarity   92.9%;  Pred. No. 2.9e-86;
  Matches  303;  Conservative    0;  Mismatches   20;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||| |||||||||||||||||||||||||||||||||||||| ||||||| |||||||
Db        120 GACATCCAAATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACACAGTCACC 179

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db        180 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAGTTACTTAGCCTGGTATCAGCAGAAACCA 239

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Db        240 GGAAAAGTTCCTCAGCTCCTGATCTATGCTGCGTCCACTTTGCAATCAGGGGTCCCATCT 299

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        300 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT 359

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||| |||||||||||||| ||||||||||||   |||  || || |||
Db        360 GAAGATGTTGCAACCTATTACTGTCAAAAATATAACAGTGCC---CCGTACACTTTTGGC 416

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              || |||||||||| |||| || |||||
Db        417 CAGGGGACCAAGCTGGAGATTAAACG 442


RESULT 5
US-09-919-344-7
; Sequence 7, Application US/09919344
; Patent No. US20020137911A1
; GENERAL INFORMATION:
;  APPLICANT: Pyle, Ruth A.
;  APPLICANT:  Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF PANCREATIC CANCER
;  FILE REFERENCE: 210121.543
;  CURRENT APPLICATION NUMBER: US/09/919,344
;  CURRENT FILING DATE:  2001-07-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 737
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 669, 685, 718, 722
;   OTHER INFORMATION: n = A,T,C or G
US-09-919-344-7

  Query Match             84.0%;  Score 274.8;  DB 11;  Length 737;
  Best Local Similarity   90.2%;  Pred. No. 4.4e-85;
  Matches  294;  Conservative    0;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 143

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        144 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA 203

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              ||||  |  |||||||||||  || |||||| |||||  ||| ||   ||||||||||||
Db        204 GGGAGTGCCCCTAAGCTCCTACTCCATGCTGTATCCAACTTGGAAAGTGGGGTCCCATCC 263

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||||
Db        264 AGGTTCAGTGGCAGTGGATCTGGGACGGATTACACTCTCACCATCAGCAGCCTGCAGCCT 323

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||||||||||||| ||||| | |||  |||||||   || ||||||
Db        324 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTAACCCTCCGGTCACTTTCGGC 383

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||| ||||||||
Db        384 GGAGGGACCAAGGTGGAGATCAAACG 409


RESULT 6
US-10-158-646-65
; Sequence 65, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy K.W.
;  APPLICANT:  Sornasse, Thierry
;  TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;  FILE REFERENCE: PA-0030-1 US
;  CURRENT APPLICATION NUMBER: US/10/158,646
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: 60/295,239
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PERL Program
; SEQ ID NO 65
;   LENGTH: 819
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030073105A1 1329729.1
US-10-158-646-65

  Query Match             84.0%;  Score 274.8;  DB 15;  Length 819;
  Best Local Similarity   92.3%;  Pred. No. 4.6e-85;
  Matches  301;  Conservative    0;  Mismatches   22;  Indels    3;  Gaps    1;
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```
Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| |||||||
Db         86 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACAAAGTCACC 145

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        146 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAGCCT 205

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||| ||  ||||| |||||||||||| |||||||||||||||||  |||||||||
Db        206 GGGACAGCCCCTAACCTCCTGATCTATGGTGCATCCACTTTGCAATCAGCTGTCCCATCT 265

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 325

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||||||||||||||||||| |   |  || ||||||
Db        326 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCTT---ATCACCTTCGGC 382

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||    |||| || |||||
Db        383 CAAGGGACACGACTGGAGATTAAACG 408
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RESULT 7
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-192-854-1

Query Match 82.6%; Score 270; DB 10; Length 720;
Best Local Similarity 91.4%; Pred. No. 2e-83;
Matches 298; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

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Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||||| |||||||   ||||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||   | ||||| |||||    | ||||||||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCT---AATACGTTCGGC 693

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||||||||||
Db        694 CAAGGGACCAAGGTGGAAATCAAACG 719
```

RESULT 8
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-561A-1

Query Match 82.6%; Score 270; DB 11; Length 720;
Best Local Similarity 91.4%; Pred. No. 2e-83;
Matches 298; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

```
Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||||||||||||||||||||||||||| |||||||   ||||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| ||||||||| ||   | ||||| |||||    | ||||||||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCT---AATACGTTCGGC 693

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||||||||||
Db        694 CAAGGGACCAAGGTGGAAATCAAACG 719
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RESULT 9
US-10-216-484-125
; Sequence 125, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG

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;  CURRENT APPLICATION NUMBER: US/10/216,484
;  CURRENT FILING DATE:  2002-08-09
;  PRIOR APPLICATION NUMBER: US/09/499,662
;  PRIOR FILING DATE: 2000-02-09
;  PRIOR APPLICATION NUMBER: US 09/053,583
;  PRIOR FILING DATE: 1998-04-01
;  NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 125
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-484-125

  Query Match            82.6%;  Score 270;  DB 15;  Length 729;
  Best Local Similarity  91.4%;  Pred. No. 2e-83;
  Matches  298;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 132

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              ||||||||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||
Db        133 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 192

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||| |||||||   ||||||||||
Db        193 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 252

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Db        253 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 312

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||  |||||||||  |||||||||  ||   | |||||  ||||||    | |||||||||
Db        313 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTC---GAACGTTCGGC 369

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        370 CAAGGGACCAAGGTGGAAATCAAACG 395


RESULT 10
US-10-035-637-1
; Sequence 1, Application US/10035637
; Publication No. US20030031667A1
; GENERAL INFORMATION:
;  APPLICANT: Deo, Yashwant M.
;  APPLICANT:  Keler, Tibor
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO DENDRITIC
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: MXI-166CP
;  CURRENT APPLICATION NUMBER: US/10/035,637
;  CURRENT FILING DATE:  2001-11-07
;  PRIOR APPLICATION NUMBER: 09/851,614
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/203,126
;  PRIOR FILING DATE: 2000-05-08
;  PRIOR APPLICATION NUMBER: USSN 60/230,739
;  PRIOR FILING DATE: 2000-09-07
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(321)
US-10-035-637-1

  Query Match            81.0%;  Score 264.8;  DB 15;  Length 321;
  Best Local Similarity  90.7%;  Pred. No. 9.5e-82;
  Matches  294;  Conservative    0;  Mismatches   27;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| |||||||||||||| ||||||| |  ||||||||||||||||||||||||
Db         61 ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGGTGGTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              | |||||  ||||||  ||||||||||||||||||||| |||||||.  ||||||||||
Db        121 GAGAAAGCCCCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||  |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              ||||||  |||||||||||||| ||| |||||||  |||  |||||   | |||||||||
Db        241 GAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTACCCTC---GGACGTTCGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              |||||||||||||||||||||||
Db        298 CAAGGGACCAAGGTGGAAATCAAA 321


RESULT 11
US-09-859-053-29
; Sequence 29, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
;  APPLICANT: Tsuji, Takashi
;  APPLICANT:  Tezuka, Katsunari
;  APPLICANT:  Hori, No. US20020102658A1uaki
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
;  TITLE OF INVENTION:  COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
;  TITLE OF INVENTION:  PHARMACEUTICAL USE THEREOF
;  FILE REFERENCE: 06501-079001
;  CURRENT APPLICATION NUMBER: US/09/859,053
;  CURRENT FILING DATE:  2001-05-16
;  PRIOR APPLICATION NUMBER: JP 2001-99508
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: JP 2000-147116
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 974
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)...(38)
;   NAME/KEY: CDS
;   LOCATION: (39)...(746)
;   NAME/KEY: 3'UTR
;   LOCATION: (750)...(974)
;   NAME/KEY: sig_peptide
;   LOCATION: (39)...(104)
US-09-859-053-29

  Query Match            80.6%;  Score 263.6;  DB 11;  Length 974;
  Best Local Similarity  90.2%;  Pred. No. 3.8e-81;
  Matches  294;  Conservative    0;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||||
Db        105 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 164

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| |||||||||||||| ||||||| |  ||||||||||||||||||||||||
Db        165 ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGGTTGTTAGCCTGGTATCAGCAGAAACCA 224
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Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  |||||  |||||||||||||| ||||||| |||||||   ||||||||||
Db        225 GGGAAAGCCCCTAAACTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 284

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
               ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 344

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||| || |||||| ||  |||||||  |   ||| | |||||||||
Db        345 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTC---CCGTGGACGTTCGGC 401

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||||||
Db        402 CAAGGGACCAAGGTGGAAATCAAACG 427


RESULT 12
US-09-848-798-101
; Sequence 101, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I01
US-09-848-798-101

  Query Match             80.6%;  Score 263.4;  DB 12;  Length 324;
  Best Local Similarity   88.8%;  Pred. No. 2.9e-81;
  Matches  285;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | ||  | ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              |||||||| |||||| |||||||| ||||||   ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | ||||||||||  |||||||| ||   | |||||  |||||||    || ||  ||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||||  ||||  ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 13
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US-09-848-798-112
; Sequence 112, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I12
US-09-848-798-112

  Query Match             80.6%;  Score 263.4;  DB 12;  Length 324;
  Best Local Similarity   88.8%;  Pred. No. 2.9e-81;
  Matches  285;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | ||  | ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              |||||||| |||||| |||||||| ||||||   ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
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Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
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Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 14
US-09-848-798-110
; Sequence 110, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
;   LENGTH: 324
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I10
US-09-848-798-110

  Query Match            80.1%;  Score 261.8;  DB 12;  Length 324;
  Best Local Similarity   88.5%;  Pred. No. 1.1e-80;
  Matches  284;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| ||||||  ||||||||  ||||||   ||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||| |||||||   |||||||  |||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCTATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | ||||||||||| ||||||||| ||  | |||||  |||||||   ||  ||  ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTATAGTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||||  ||||  ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 15
US-09-848-798-210
; Sequence 210, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-848-798-210

  Query Match            80.1%;  Score 261.8;  DB 12;  Length 324;
  Best Local Similarity   88.5%;  Pred. No. 1.1e-80;
  Matches  284;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| |||||||||  ||||||   ||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  ||||||||||||||||||||||||||  |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCTATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | ||||||||||| ||||||||| ||  | |||||  |||||||   ||  ||  ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCCCGTACACTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||||  ||||  ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
5783.490 Million cell updates/sec

Title: US-09-627-896B-25
Perfect score: 327
Sequence: 1 gacatccagatgacccagtc.....ccaaggtggaaatcaaacgt 327

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	279.2	85.4	321	3	US-08-599-226-36	Sequence 36, Appl
2	279.2	85.4	321	4	US-09-125-098-36	Sequence 36, Appl
3	263.4	80.6	324	4	US-09-240-274-101	Sequence 101, App
4	263.4	80.6	324	4	US-09-240-274-112	Sequence 112, App
5	261.8	80.1	324	4	US-09-240-274-110	Sequence 110, App
6	261.8	80.1	324	4	US-09-240-274-210	Sequence 210, App
7	260.4	79.6	324	2	US-08-378-939-31	Sequence 31, Appl
8	260.4	79.6	324	2	US-08-378-939-33	Sequence 33, Appl
9	259.8	79.4	19040	4	US-09-343-485A-3	Sequence 3, Appli
10	258.6	79.1	324	4	US-09-240-274-220	Sequence 220, App
11	258.6	79.1	324	4	US-09-240-274-224	Sequence 224, App
12	257	78.6	321	4	US-09-240-274-102	Sequence 102, App
13	257	78.6	321	4	US-09-240-274-218	Sequence 218, App
14	257	78.6	321	4	US-09-240-274-221	Sequence 221, App
15	257	78.6	321	4	US-09-240-274-222	Sequence 222, App
16	257	78.6	324	4	US-09-240-274-204	Sequence 204, App
17	256.8	78.5	387	3	US-08-803-085-3	Sequence 3, Appli
18	255.4	78.1	324	4	US-09-240-274-100	Sequence 100, App
19	255.4	78.1	324	4	US-09-240-274-206	Sequence 206, App
20	254	77.7	439	4	US-09-042-353-360	Sequence 360, App
21	254	77.7	439	4	US-08-758-417A-208	Sequence 208, App
22	254	77.7	642	1	US-08-157-101A-8	Sequence 8, Appli
23	254	77.7	1066	1	US-08-157-101A-4	Sequence 4, Appli
24	253.8	77.6	321	4	US-09-240-274-98	Sequence 98, Appl
25	253.8	77.6	321	4	US-09-240-274-107	Sequence 107, App
26	252.2	77.1	321	4	US-09-240-274-105	Sequence 105, App
27	252.2	77.1	321	4	US-09-240-274-216	Sequence 216, App
28	251.4	76.9	388	4	US-09-042-353-358	Sequence 358, App
29	251.4	76.9	388	4	US-08-758-417A-206	Sequence 206, App
30	250.6	76.6	321	4	US-09-240-274-201	Sequence 201, App
31	249	76.1	321	4	US-09-240-274-205	Sequence 205, App
32	249	76.1	321	4	US-09-240-274-211	Sequence 211, App
33	249	76.1	321	4	US-09-240-274-215	Sequence 215, App
34	249	76.1	321	4	US-09-240-274-217	Sequence 217, App
35	248.8	76.1	321	2	US-08-378-939-13	Sequence 13, Appl
36	247.6	75.7	324	2	US-08-378-939-23	Sequence 23, Appl
37	247.4	75.7	321	4	US-09-240-274-109	Sequence 109, App
38	247.4	75.7	321	4	US-09-240-274-113	Sequence 113, App
39	246.4	75.4	847	1	US-08-053-131-184	Sequence 184, App
40	246.4	75.4	847	1	US-08-096-762-184	Sequence 184, App
41	246.4	75.4	847	4	US-09-042-353-47	Sequence 47, Appl
42	246.4	75.4	847	4	US-08-758-417A-312	Sequence 312, App
43	246	75.2	324	2	US-08-378-939-17	Sequence 17, Appl
44	246	75.2	384	1	US-08-259-372A-13	Sequence 13, Appl
45	246	75.2	384	1	US-08-468-671-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-599-226-36
; Sequence 36, Application US/08599226
; Patent No. 6090382
; GENERAL INFORMATION:
; APPLICANT: Salfeld, Jochen G.
; APPLICANT: Allen, Deborah J.
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Kaymakcalan, Zehra
; APPLICANT: Labkovsky, Boris
; APPLICANT: Mankovich, John A.
; APPLICANT: McGuinness, Brian T.
; APPLICANT: Roberts, Andrew J.
; APPLICANT: Sakorafas, Paul
; APPLICANT: Schoenhaut, David
; APPLICANT: Vaughan, Tristan J.
; APPLICANT: White, Michael
; APPLICANT: Wilton, Andrew J.
; TITLE OF INVENTION: Human Antibodies that Bind Human TNFa
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,226
; FILING DATE: 08-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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US-08-599-226-36

  Query Match             85.4%;  Score 279.2;  DB 3;  Length 321;
  Best Local Similarity   93.5%;  Pred. No. 1e-81;
  Matches  303;  Conservative    0;  Mismatches   18;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||||||| || ||||| |||||||||||||||||| ||||||
Db         61 ATCACTTGTCGGGCAAGTCAGGGCATCAGAAATTACTTAGCCTGGTATCAGCAAAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||| ||||||| |||   | |||  ||| || |||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAGGTATAACCGTG---CACCGTATACTTTTGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              || ||||||||||||||||||||||
Db        298 CAGGGGACCAAGGTGGAAATCAAA 321


RESULT 2
US-09-125-098-36
; Sequence 36, Application US/09125098
; Patent No. 6258562
;  GENERAL INFORMATION:
;    APPLICANT:  Salfeld, Jochen G.
;    APPLICANT:  Allen, Deborah J.
;    APPLICANT:  Hoogenboom, Hendricus R.J.M.
;    APPLICANT:  Kaymakcalan, Zehra
;    APPLICANT:  Labkovsky, Boris
;    APPLICANT:  Mankovich, John A.
;    APPLICANT:  McGuinness, Brian T.
;    APPLICANT:  Roberts, Andrew J.
;    APPLICANT:  Sakorafas, Paul
;    APPLICANT:  Schoenhaut, David
;    APPLICANT:  Vaughan, Tristan J.
;    APPLICANT:  White, Michael
;    APPLICANT:  Wilton, Andrew J.
;    TITLE OF INVENTION:  Human Antibodies that Bind Human TNFa
;    NUMBER OF SEQUENCES:  37
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 State Street, suite 510
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/125,098
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/599,226
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A., Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-043
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617)227-7400
;      TELEFAX:  (617)227-5941
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-125-098-36

  Query Match             85.4%;  Score 279.2;  DB 4;  Length 321;
  Best Local Similarity   93.5%;  Pred. No. 1e-81;
  Matches  303;  Conservative    0;  Mismatches   18;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||||||| || ||||| |||||||||||||||||| ||||||
Db         61 ATCACTTGTCGGGCAAGTCAGGGCATCAGAAATTACTTAGCCTGGTATCAGCAAAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTACAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||||||||||||||||||||||| ||||||| |||   | |||  ||| || |||
Db        241 GAAGATGTTGCAACTTATTACTGTCAAAGGTATAACCGTG---CACCGTATACTTTTGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAA 324
              || ||||||||||||||||||||||
Db        298 CAGGGGACCAAGGTGGAAATCAAA 321


RESULT 3
US-09-240-274-101
; Sequence 101, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-101

  Query Match             80.6%;  Score 263.4;  DB 4;  Length 324;
  Best Local Similarity   88.8%;  Pred. No. 1.4e-76;
  Matches  285;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||| ||||||||||||||||||||||||||||||
```

```
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| |||||||||  ||||||  ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| ||||||||| ||  | ||||| ||||||||   || || ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              ||||||| |||| ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 4
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112

  Query Match             80.6%;  Score 263.4;  DB 4;  Length 324;
  Best Local Similarity   88.8%;  Pred. No. 1.4e-76;
  Matches  285;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| |||||||||  ||||||  ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| ||||||||| ||  | ||||| ||||||||   || || ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              ||||||| |||| ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 5
US-09-240-274-110
; Sequence 110, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I10
US-09-240-274-110

  Query Match             80.1%;  Score 261.8;  DB 4;  Length 324;
  Best Local Similarity   88.5%;  Pred. No. 4.7e-76;
  Matches  284;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| |||||||||  ||||||  ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||||| |||||||   ||||||| |||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCTATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| ||||||||| ||  | ||||| ||||||||   || || ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTATAGTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              ||||||| |||| ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 6
US-09-240-274-210
; Sequence 210, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
```

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;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
;    LENGTH: 324
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-240-274-210

  Query Match             80.1%;  Score 261.8;  DB 4;  Length 324;
  Best Local Similarity   88.5%;  Pred. No. 4.7e-76;
  Matches  284;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| |||||||||   ||||||   ||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||   |||||||   ||||||||||   ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCGGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | ||||||||||| |||||||| ||   | ||||| |||| |||   || || |||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCCCGTACACTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              ||||||| |||| ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 7
US-08-378-939-31
; Sequence 31, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  324 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..324
US-08-378-939-31

  Query Match             79.6%;  Score 260.4;  DB 2;  Length 324;
  Best Local Similarity   89.6%;  Pred. No. 1.3e-75;
  Matches  292;  Conservative    0;  Mismatches   31;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||| ||| ||||||||||||||||||||||||||||||||||| ||||||| |||||||
Db          1 GACATTCAGCTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACACAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||||||||||| ||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGGCAAGTCAGGGCATTAGCAATAATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||| |||||||| |||||||||||||||||||| |||| ||    ||||||||||
Db        121 GGAAAAGCTCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGGAAAGTGGGGTCCCATCA 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||||||||||||| || |||||||||     |||    || ||||||
Db        241 GAAGATTTTGCAACTTATTACTGTCAACAGGATAACAGT---TATCCTTTCACTTTCGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||| ||||||||
Db        298 GGAGGGACCAAGGTGGAGATCAAACG 323


RESULT 8
US-08-378-939-33
; Sequence 33, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
```

```
;       NAME:  ERNST, BARBARA G
;       REGISTRATION NUMBER:  30,377
;       REFERENCE/DOCKET NUMBER:  1808-118
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 783-6040
;       TELEFAX:  (202) 783-6031
;   INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  324 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..324
US-08-378-939-33

  Query Match           79.6%;  Score 260.4;  DB 2;  Length 324;
  Best Local Similarity   89.6%;  Pred. No. 1.3e-75;
  Matches  292;  Conservative    0;  Mismatches   31;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||| ||| |||||||||||||||||||||||||||||||| ||||||| |||||||
Db          1 GACATTCAGCTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACACAGTCACC 60

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||||||||||||| |||||||||||||||||||||||||
Db         61 ATCACTTGTCGGGCAAGTCAGGGCATTAGCAATAATTTAGCCTGGTATCAGCAGAAACCA 120

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||| |||||||| |||||||||||||||||||| |||| ||    ||||||||||
Db        121 GGAAAAGCTCCTAAGCGCCTGATCTATGCTGCATCCAGTTTGGAAAGTGGGGTCCCATCA 180

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||||||||||||||||||| || ||||||||     |||    || ||||||
Db        241 GAAGATTTTGCAACTTATTACTGTCAACAGGATAACAGT---TATCCTTTCACTTTCGGC 297

Qy        301 CAAGGGACCAAGGTGGAAATCAAACG 326
              |||||||||||||| ||||||||
Db        298 GGAGGGACCAAGGTGGAGATCAAACG 323


RESULT 9
US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
;  APPLICANT: REFF, MITCHELL R.
;  APPLICANT:  BARNETT, RICHARD S.
;  APPLICANT:  MCLACHLAN, KAREN R.
;  TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
;  TITLE OF INVENTION:  MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
;  TITLE OF INVENTION:  VECTORS FOR ACCOMPLISHING THE SAME
;  FILE REFERENCE: 037003-0275807
;  CURRENT APPLICATION NUMBER: US/09/343,485A
;  CURRENT FILING DATE:  1999-06-30
;  PRIOR APPLICATION NUMBER: 09/023,715
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: 08/819,866
;  PRIOR FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 19040
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

  Query Match           79.4%;  Score 259.8;  DB 4;  Length 19040;
  Best Local Similarity   89.3%;  Pred. No. 9.6e-75;
  Matches  292;  Conservative    0;  Mismatches   32;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||| |||||||||||||||||| ||||||||||
Db       7611 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 7670

Qy         61 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCA 120
              |||||||| |||| ||||||| ||||||  ||||||||   ||||||||||||||||||
Db       7671 ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA 7730

Qy        121 GGGAAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCT 180
              || |||| |||||||||||||||||||| |||||||| |||||||   ||||||||||
Db       7731 GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 7790

Qy        181 CGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||| |||||||||||||||||||| |||||||||| |||||||||||||||||
Db       7791 AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 7850

Qy        241 GAAGATGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGC 300
              |||||| |||| |||||||||||| | ||  | | ||| ||||||   | |||||||||
Db       7851 GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTC---GGACGTTCGGC 7907

Qy        301 CAAGGGACCAAGGTGGAAATCAAACGT 327
              ||||||||||||||||||||||||||||
Db       7908 CAAGGGACCAAGGTGGAAATCAAACGT 7934


RESULT 10
US-09-240-274-220
; Sequence 220, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH51
US-09-240-274-220

  Query Match           79.1%;  Score 258.6;  DB 4;  Length 324;
  Best Local Similarity   87.9%;  Pred. No. 5.1e-75;
  Matches  282;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | || |||||||||||| ||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACACAGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||||||| || | ||||||||||||||||||||| ||||||||||
Db         63 TTGCCGGGCCAGTCAGGGCATAAGGAGTTATTTAGCCTGGTATCAGCAAAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||| |||||||||||||||||||||||||   |||||||||| ||||
```

```
Db        123 AGCCCCTAAGCTCCTAATCTATGCTGCATCCACTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| |||||||||||||||||||||| |||||||||| |||||||||||||||||||||
Db        183 CAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACAATCAGCAGCCTGCAGCCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||||||||||| ||  ||| | |  ||| ||    || ||||||| ||
Db        243 TTTTGCAACTTATTACTGTCAACAGCTTAATAATTACCCCCCTTTCACTTTCGGCCCTGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||| ||||| ||||||||
Db        303 GACCAAAGTGGATATCAAACG 323


RESULT 11
US-09-240-274-224
; Sequence 224, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-224

  Query Match           79.1%;  Score 258.6;  DB 4;  Length 324;
  Best Local Similarity  87.9%;  Pred. No. 5.1e-75;
  Matches  282;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              |||||||| |||||| |||||||||  ||||||   ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  || |||||||||||||||||||||||||||| |||||||  ||||||||||  ||||
Db        123 AGCCCCCAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||| |||||||||||||| ||||  |||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCGCTCTCACCATCAGCAGTCTGCTACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| |||||||| ||  | ||||| ||||||||  | ||  ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGGGTTACAGTACCCCTCCGTACAGTTTTGGCCAGGG 302

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||| |||| ||||||||
Db        303 GACCAAGCTGGAGATCAAACG 323


RESULT 12
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

  Query Match           78.6%;  Score 257;  DB 4;  Length 321;
  Best Local Similarity  89.7%;  Pred. No. 1.7e-74;
  Matches  288;  Conservative    0;  Mismatches   30;  Indels    3;  Gaps    1;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              |||||||| |||||| |||||||||  ||||||   ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||| |||||||  ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 245
              |||||||||||||||||||||||| |||||||||||||| ||||  |||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| |||||||| ||  | ||||| ||||||||  | ||  ||||| ||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CTGTGGACGTTCGGCCAAGG 299

Qy        306 GACCAAGGTGGAAATCAAACG 326
              ||||||||||||||||||||
Db        300 GACCAAGGTGGAAATCAAACG 320


RESULT 13
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49
```

US-09-240-274-218

Query Match 78.6%; Score 257; DB 4; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.7e-74;
Matches 288; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

```
Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| ||||||||  ||||||   ||||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| |||||||| ||  | ||||| ||   ||| | ||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CCGTGGACGTTCGGCCAAGG 299

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||
Db        300 GACCAAGGTGGAAATCAAACG 320
```

RESULT 14
US-09-240-274-221
; Sequence 221, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 221
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH52
US-09-240-274-221

Query Match 78.6%; Score 257; DB 4; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.7e-74;
Matches 288; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

```
Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| ||||| ||| |||||||   |||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
              | |||||||||| |||||||| ||  | ||||| ||   ||| | ||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACC---CCGTGGACGTTCGGCCAAGG 299

Qy        306 GACCAAGGTGGAAATCAAACG 326
              |||||||||||||||||||||
Db        300 GACCAAGGTGGAAATCAAACG 320
```

RESULT 15
US-09-240-274-222
; Sequence 222, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 222
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-222

Query Match 78.6%; Score 257; DB 4; Length 321;
Best Local Similarity 89.7%; Pred. No. 1.7e-74;
Matches 288; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

```
Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCATGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTATCAGCAGAAACCAGGGAA 125
              ||||||||| |||||| ||||| ||| |||||||   |||||||||||||||||||||||
Db         63 TTGCCGGGCAAGTCAGAGCATTGGCACTTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 AGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTT 185
              ||  |||||||||||||||||||||||||||| |||||||   ||||||||||  ||||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TGTTGCAACTTATTACTGTCAAAAGTATAACAGTGCCCCTCCGAGTACGTTCGGCCAAGG 305
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Qy        306 GACCAAGGTGGAAATCAAACG 326
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Db        300 GACCAAGGTGGAAATCAAACG 320
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Search completed: July 18, 2003, 19:59:06
Job time : 18.3396 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:46:48 ; Search time 948.849 Seconds
(without alignments)
10397.705 Million cell updates/sec

Title: US-09-627-896B-26
Perfect score: 339
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	339	100.0	339	9	HSVK4H2FG	X70465 H.sapiens D
2	327.8	96.7	400	6	E01736	E01736 Genomic DNA
3	327.8	96.7	619	6	E01735	E01735 Genomic DNA
4	326.2	96.2	341	6	E01737	E01737 Genomic DNA
5	326.2	96.2	355	9	HSU86791	U86791 Human Ig li
6	326.2	96.2	372	9	HUMIGLCDR	L11700 Human immun
7	321.4	94.8	339	9	HSIGKVBD	Z18328 H.sapiens m
8	321.4	94.8	342	6	AR058974	AR058974 Sequence
9	321.4	94.8	342	6	AR088798	AR088798 Sequence
10	321.4	94.8	342	6	AR088878	AR088878 Sequence
11	321.4	94.8	342	6	E05868	E05868 DNA sequenc
12	321.4	94.8	405	9	HUMIGKAW	M29467 Human Ig re
13	321.4	94.8	460	9	S50732	S50732 immunoglobu
14	321.4	94.8	979	9	BC017870	BC017870 Homo sapi
15	319.8	94.3	342	9	AF455557	AF455557 Homo sapi
16	319.8	94.3	360	9	HSVKAP4	X83714 H.sapiens m
17	319.8	94.3	835	9	AB064111	AB064111 Homo sapi
18	319	94.1	360	6	I12039	I12039 Sequence 3
19	318.2	93.9	357	6	AX300034	AX300034 Sequence
20	315	92.9	339	9	AF099194	AF099194 Homo sapi
21	315	92.9	342	9	AB063957	AB063957 Homo sapi
22	315	92.9	813	9	AB064080	AB064080 Homo sapi
23	315	92.9	816	9	AB064075	AB064075 Homo sapi
24	314	92.6	1028	6	A29532	A29532 FLAG sequen
25	314	92.6	1330	6	A29530	A29530 Hum4 VL-CC4
26	314	92.6	1330	6	AR096955	AR096955 Sequence
27	314	92.6	1359	6	A29534	A29534 pSC49FLAG s
28	313.4	92.4	340	9	AY043136	AY043136 Homo sapi
29	313.4	92.4	342	6	A62121	A62121 Sequence 15
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31	313.4	92.4	402	9	HSBUD114L	Z46347 H.sapiens m
32	312.4	92.2	1027	6	AR096963	AR096963 Sequence
33	311.8	92.0	427	9	HSVKIVR	X02990 Human mRNA
34	311.8	92.0	944	9	BC018761	BC018761 Homo sapi
35	311.6	91.9	423	6	E37603	E37603 Monoclonal
36	310.4	91.6	388	9	HSIGKLV36	X72457 H.sapiens m
37	310.2	91.5	339	9	HSIGKVBE	Z18329 H.sapiens m
38	310.2	91.5	342	6	AX355947	AX355947 Sequence
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40	310.2	91.5	407	6	E05213	E05213 cDNA sequen
41	309.8	91.4	347	9	AF103492	AF103492 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS HSVK4H2FG 339 bp DNA linear PRI 17-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody light chain variable region,subgroup V(k)4 (H2F IgG line).
ACCESSION X70465
VERSION X70465.1 GI:38442
KEYWORDS anti-DNA antibody; complementarity determining region; Ig kappa light chain; Ig light chain; Ig variable region; IgG; immunoglobulin; systemic lupus erythematosus.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 339)

```
  AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
            and Diamond,B.
  TITLE     Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype
  JOURNAL   J. Exp. Med. 174 (6), 1639-1652 (1991)
  MEDLINE   92078875
   PUBMED   1660528
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                     /isolate="patient HER(SLE)"
                     /db_xref="taxon:9606"
                     /cell_line="EBV-transformed 3I(+) B cell line, H2F IgG"
                     /tissue_type="spleen"
     misc_feature    <1. .>339
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     misc_feature    70. .120
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     misc_feature    166. .186
                     /note="complementarity determining region, CDR 2"
     misc_feature    284. .303
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  Matches  339;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 2
E01736
LOCUS       E01736                   400 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Genomic DNA encoding V region of L-chain of monoclonal antibody
            against pseudomonas aeruginosa exotoxin.
ACCESSION   E01736
VERSION     E01736.1  GI:2169989
KEYWORDS    JP 1988267295-A/5.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
  TITLE     HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
  JOURNAL   Patent: JP 1988267295-A 5 04-NOV-1988;
            SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
COMMENT     OS   Human
            PN   JP 1988267295-A/5
            PD   04-NOV-1988
            PF   26-NOV-1987 JP 1987298513
            PR   03-DEC-1986 JP 86P   288340
            PI   NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO, PI
            NOGUCHI HIROSHI
            PC   C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00,(C12P21/02,
            PC   C12R1:19),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: No;
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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db         61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db        121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db        181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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RESULT 3
E01735
LOCUS       E01735                   619 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Genomic DNA encoding V region of L chain of monoclonal antibody
            against pseudomonas aeruginosa exotoxin.
ACCESSION   E01735
VERSION     E01735.1  GI:2169988
KEYWORDS    JP 1988267295-A/4.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
  TITLE     HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
  JOURNAL   Patent: JP 1988267295-A 4 04-NOV-1988;
            SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
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COMMENT     OS   Human
            PN   JP 1988267295-A/4
            PD   04-NOV-1988
            PF   26-NOV-1987 JP 1987298513
            PR   03-DEC-1986 JP 86P   288340
            PI   NAKATANI TOMOSUKE, NOMURA NORIKO, HORIGOME KAZUHIKO, PI
            NOGUCHI HIROSHI
            PC   C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00,(C12P21/02,
            PC   C12R1:19),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            CC   hypothetical: No;
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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 4
E01737
LOCUS       E01737                   341 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Genomic DNA encoding V region of L-chain of monoclonal antibody
            against pseudomonas aeruginosa exotoxin.
ACCESSION   E01737
VERSION     E01737.1  GI:2169990
KEYWORDS    JP 1988267295-A/6.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 341)
  AUTHORS   Nakatani,T., Nomura,N., Horigome,K. and Noguchi,H.
  TITLE     HUMAN ANTIBODY, ANTIBODY GENE AND CORRESPONDING RECOMBINANT
  JOURNAL   Patent: JP 1988267295-A 6 04-NOV-1988;
            SUMITOMO CHEM CO LTD, SUMITOMO PHARMACEUT CO LTD
COMMENT     OS   Human
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            PD   04-NOV-1988
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            PC   C12P21/02,C07H21/04,C07K13/00,C07K15/12,C12N15/00,(C12P21/02,
            PC   C12R1:19),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
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Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120
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Db        301 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 5
HSU86791
LOCUS       HSU86791                 355 bp    mRNA    linear   PRI 04-MAR-1997
DEFINITION  Human Ig light chain gene variable domain (CLL-L1B) mRNA, partial
            cds.
ACCESSION   U86791
VERSION     U86791.1  GI:1864112
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 355)
  AUTHORS   Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magnac,C.,
            Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.
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  TITLE     Restricted VH clan usage by siblings affected with Chronic
            Lymphocytic Leukemia
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 355)
  AUTHORS   Pritsch,O., Troussard,X., Davi,F., Macro,M., Dumas,G., Magnac,C.,
            Clerget,F., Schroeder,H.W., Leporrier,M. and Dighiero,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JAN-1997) Unite d'Immunohematologie et
            d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris
            75724
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BASE COUNT       89 a     97 c     91 g     78 t
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Query Match 96.2%; Score 326.2; DB 9; Length 355;
Best Local Similarity 97.6%; Pred. No. 5.4e-96;
Matches 331; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | |||||||||||||||||||||||| ||||||
Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAGATCAAA 339
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RESULT 6
HUMIGLCDR
LOCUS       HUMIGLCDR               372 bp    mRNA    linear   PRI 08-MAR-1994
DEFINITION  Human immunoglobulin light chain variable region complementarity
            determining region (CDR3) mRNA.
ACCESSION   L11700
VERSION     L11700.1  GI:436562
KEYWORDS    V-region; complementarity determining region; immunoglobulin light
            chain; monoclonal antibody.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Hoon,D.S., Wang,Y., Sze,L., Kanda,H., Watanabe,T., Morrison,S.L.,
            Morton,D.L. and Irie,R.F.
  TITLE     Molecular cloning of a human monoclonal antibody reactive to
            ganglioside GM3 antigen on human cancers
  JOURNAL   Cancer Res. 53 (21), 5244-5250 (1993)
  MEDLINE   94036806
   PUBMED   7916649
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="L612 EBV transformed B-cell"
                     /cell_type="B-lymphocyte"
                     /tissue_type="blood"
     misc_feature    283. .309
                     /standard_name="complementarity determining region 3
                     (CDR3)"
                     /note="putative"
BASE COUNT       91 a     105 c     90 g     86 t
ORIGIN
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Query Match 96.2%; Score 326.2; DB 9; Length 372;
Best Local Similarity 97.6%; Pred. No. 5.4e-96;
Matches 331; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  |||||||||||||||||||||||||||||||
Db        301 CCTCCGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 7
HSIGKVBD
LOCUS       HSIGKVBD                339 bp    mRNA    linear   PRI 02-FEB-1995
DEFINITION  H.sapiens mRNA for immunoglobulin V-region of kappa chain.
ACCESSION   Z18328
VERSION     Z18328.1  GI:33300
KEYWORDS    anti-lamine antibody; cardiolipin/B2glycoprotein antibody;
            immunoglobulin light chain; kappa chain; monoclonal antibody;
            myelin-associated glycoprotein antibody; V-region.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Mariette,X., Tsapis,A. and Brouet,J.C.
  TITLE     Nucleotidic Sequence Analysis Of The Variable Domains Of Four Human
            Monoclonal IgM With An Antibody Activity To Myelin-Associated
            Glycoprotein
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 339)
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  AUTHORS   Mariette,X.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-OCT-1992) Xavier Mariette, Laboratoire d'
            Immunopathologie, Hopital, Saint-Louis, 1, avenue Claude Vellefaux,
            Paris, 75010, France
FEATURES             Location/Qualifiers
     source          1. .339
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="Epstein-Barr transformed lymphoblastoid cell
                     line"
                     /tissue_type="blood"
     V_region        1. .339
                     /product="kappa chain"
                     /note="VK IV family"
     V_segment       1. .314
     J_segment       315. .339
BASE COUNT       85 a     93 c     86 g     75 t
ORIGIN

  Query Match            94.8%;  Score 321.4;  DB 9;  Length 339;
  Best Local Similarity  96.8%;  Pred. No. 2e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||| ||||||||| | | |
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCACCAATATTATGGGATT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| ||||||||||||||||||||||||||||||||
Db        301 CCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 8
AR058974
LOCUS       AR058974                342 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5837845.
ACCESSION   AR058974
VERSION     AR058974.1  GI:5984551
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
  TITLE     Human monoclonal antibody specifically binding to surface antigen
            of cancer cell membrane
  JOURNAL   Patent: US 5837845-A 4 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="unknown"
BASE COUNT       88 a     92 c     87 g     75 t
ORIGIN

  Query Match            94.8%;  Score 321.4;  DB 6;  Length 342;
  Best Local Similarity  96.8%;  Pred. No. 2e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||||||||||||||||||||||||
Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 9
AR088798
LOCUS       AR088798                342 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from patent US 5990287.
ACCESSION   AR088798
VERSION     AR088798.1  GI:10015561
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
  TITLE     Human monoclonal antibody specifically binding to surface antigen
            of cancer cell membrane
  JOURNAL   Patent: US 5990287-A 4 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="unknown"
BASE COUNT       88 a     92 c     87 g     75 t
ORIGIN

  Query Match            94.8%;  Score 321.4;  DB 6;  Length 342;
  Best Local Similarity  96.8%;  Pred. No. 2e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||||||||||||||||||||||||
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Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 10
AR088878
LOCUS       AR088878                342 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 4 from patent US 5990297.
ACCESSION   AR088878
VERSION     AR088878.1  GI:10015639
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
  TITLE     Human monoclonal antibody specifically binding to surface antigen
            of cancer cell membrane
  JOURNAL   Patent: US 5990297-A 4 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="unknown"
BASE COUNT       88 a     92 c     87 g     75 t
ORIGIN

  Query Match             94.8%;  Score 321.4;  DB 6;  Length 342;
  Best Local Similarity   96.8%;  Pred. No. 2e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||| ||||||||| ||||| ||||||  ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||||||||||||||||||||||||||
Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 11
E05868
LOCUS       E05868                  342 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence coding monoclonal antibody.
ACCESSION   E05868
VERSION     E05868.1  GI:2174055
KEYWORDS    JP 1993304987-A/4.
SOURCE      Unidentified.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Hosokawa,S., Tagawa,T., Hirakawa,Y., Ito,N. and Nagaike,K.
  TITLE     HUMAN TYPE MONOCLONAL ANTIBODY AND GENE CODING THE SAME, HYBRIDOMA
            AND ANTITUMOR AGENT
  JOURNAL   Patent: JP 1993304987-A 4 19-NOV-1993;
            MITSUBISHI KASEI CORP
COMMENT     PN   JP 1993304987-A/4
            PD   19-NOV-1993
            PF   22-JUN-1992 JP 1992162849
            PR   28-JUN-1991 JP 91P   158859, 28-JUN-1991 JP 91P   158860, PR
            28-JUN-1991 JP 91P   158861
            PI   HOSOKAWA SEIKO, TAGAWA TOSHIAKI, HIRAKAWA YOKO, ITO NORIHIKO,
            PI   NAGAIKE KAZUHIRO
            PC   C12P21/08,A61K39/395,C12N5/28,C12N15/13//A61B10/00,C12N15/08,
            PC   G01N33/577,
            PC   (C12P21/08,C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   *source: tissue_type=human antibody GAH hybridoma.
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
BASE COUNT       88 a     92 c     87 g     75 t
ORIGIN

  Query Match             94.8%;  Score 321.4;  DB 6;  Length 342;
  Best Local Similarity   96.8%;  Pred. No. 2e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||| ||||||||| ||||| ||||||  ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||||||||||||||||||||||||||
Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 12
HUMIGKAW
LOCUS       HUMIGKAW                405 bp    mRNA    linear   PRI 04-JAN-1995
DEFINITION  Human Ig rearranged kappa-chain mRNA V-J1-region, hybridoma AE6-5,
            5' end.
ACCESSION   M29467
VERSION     M29467.1  GI:185920
KEYWORDS    J-region; V-region; immunoglobulin-kappa; processed gene; variable
            region subgroup VK-IV.
SOURCE      Human (patient POP) hybridoma AE6-5 DNA, clone pHuUCVK, derived
            from B-CLL cell line UC729-6.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 405)
  AUTHORS   Spatz,L.A., Wong,K.K., Williams,M., Desai,R., Golier,J.,
            Berman,J.E., Alt,F.W. and Latov,N.
  TITLE     Cloning and sequence analysis of the VH and VL regions of an
            anti-myelin/DNA antibody from a patient with peripheral neuropathy
            and chronic lymphocytic leukemia
  JOURNAL   J. Immunol. 144 (7), 2821-2828 (1990)
  MEDLINE   90203623
   PUBMED   2156935
COMMENT     Draft entry and printed sequence for [1] kindly submitted by
            L.A.Spatz, 26-OCT-1989, for release after publication. Columbia
            University, Department of Neurology BB-322, 630 W. 168th street,
            New York, NY 10032.
FEATURES             Location/Qualifiers
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                     /map="2p12"
     gene            1. .405
                     /gene="IGKV"
     CDS             1. .>405
                     /gene="IGKV"
                     /note="Ig kappa-chain V-J1-region precursor"
                     /codon_start=1
                     /protein_id="AAA58916.1"
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                     /db_xref="GDB:G00-119-341"
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     sig_peptide     1. .60
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                     /note="Ig kappa-chain signal peptide"
     mat_peptide     61. .>405
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BASE COUNT       95 a    110 c    101 g     99 t
ORIGIN

  Query Match             94.8%;  Score 321.4;  DB 9;  Length 405;
  Best Local Similarity   96.8%;  Pred. No. 2.1e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||| |||||||||||||||||| ||||| |||||| ||
Db        121 ATCAACTGCAAGTCCAGCCAGAGTCTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGG 240

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 300

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 360

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        361 CCTCCGATGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 399


RESULT 13
S50732
LOCUS       S50732                  460 bp    mRNA    linear   PRI 08-MAY-1993
DEFINITION  immunoglobulin M light chain V region=anti-lipid A antibody [human,
            hybridoma cell line HR78, mRNA Partial, 460 nt].
ACCESSION   S50732
VERSION     S50732.1  GI:261239
KEYWORDS    .
SOURCE      Homo sapiens hybridoma cell line HR78.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 460)
  AUTHORS   Dorai,H., Bubbers,J.E. and Gillies,S.D.
  TITLE     Cloning and reexpression of a functional human IgM anti-lipid A
            antibody
  JOURNAL   Hybridoma 11 (5), 667-675 (1992)
  MEDLINE   93093632
   PUBMED   1459589
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 120606] from the original journal article.
            This sequence comes from Fig. 3A.
FEATURES             Location/Qualifiers
     source          1. .460
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1. .460
                     /partial
                     /gene="immunoglobulin M light chain V region"
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                     /gene="immunoglobulin M light chain V region"
                     /note="anti-lipid A antibody; This sequence comes from
                     Fig. 3A"
                     /codon_start=1
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                     /protein_id="AAB24404.1"
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BASE COUNT      107 a    124 c    120 g    109 t
ORIGIN

  Query Match             94.8%;  Score 321.4;  DB 9;  Length 460;
  Best Local Similarity   96.8%;  Pred. No. 2.1e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 157

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||| |||||||||||||||||| ||||| |||||| ||
Db        158 ATCAACTGCAAGTCCAGCCAGAGTCTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 217

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        218 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGTTGCTCATTTACTGGGCATCTACCCGG 277

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 337

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 397

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        398 CCTCCGATGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 436


RESULT 14
BC017870
LOCUS       BC017870                979 bp    mRNA    linear   PRI 06-DEC-2001
DEFINITION  Homo sapiens, Similar to immunoglobulin kappa constant, clone
            MGC:22669 IMAGE:4274551, mRNA, complete cds.
ACCESSION   BC017870
VERSION     BC017870.1  GI:17389701
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2001) National Institutes of Health, Mammalian
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            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 35 Row: i Column: 15
            This clone was selected for full length sequencing because it
            passed the following selection criteria: GenomeScan gene
            prediction, Similarity but not identity to protein.
FEATURES             Location/Qualifiers
     source          1. .979
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_83"
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                     /note="Vector: pDNR-LIB"
     CDS             31. .753
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                     /protein_id="AAH17870.1"
                     /db_xref="GI:17389702"
                     /translation="MVLQTQVFISLLLWISGAYGDIVMTQSPDSLAVSLGERATINCK
                     SSQSVLYSSNNKNYFSWYQQKPGRPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTIS
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                     LLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
                     ACEVTHQGLSSPVTKSFNRGEC"
BASE COUNT      261 a    275 c    230 g    213 t
ORIGIN

  Query Match             94.8%;  Score 321.4;  DB 9;  Length 979;
  Best Local Similarity   96.8%;  Pred. No. 2.3e-94;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         91 GACATCGTGATGACCCAGTCTCCAGATTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 150

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||  ||
Db        151 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTTTCT 210

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        211 TGGTACCAGCAGAAACCAGGACGGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 270

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 330

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 390

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  ||||||||||||||||||||||||||||||||
Db        391 CCTCAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 429
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RESULT 15
AF455557
LOCUS       AF455557                342 bp    mRNA    linear   PRI 09-JAN-2002
DEFINITION  Homo sapiens clone RIZMVL6 anti-cardiolipin immunoglobulin light
            chain mRNA, partial cds.
ACCESSION   AF455557
VERSION     AF455557.1  GI:18092613
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Lieby,P., Soley,A., Cerutti,M., Freyssinet,J.M., Pasquali,J.L. and
            Martin,T.
  TITLE     Anticardiolipin antibodies in normal individuals
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 342)
  AUTHORS   Lieby,P., Soley,A., Cerutti,M., Freyssinet,J.M., Pasquali,J.L. and
            Martin,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-DEC-2001) Laboratoire d'immunopathologie, Institut
            d'Immunologie et d'Hematologie, 1 place de l'Hopital, Strasbourg
            67091, France
FEATURES             Location/Qualifiers
     source          1. .342
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                     /db_xref="taxon:9606"
                     /chromosome="2"
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                     /clone="RIZMVL6"
     CDS             <1. .>342
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                     /protein_id="AAL59376.1"
                     /db_xref="GI:18092614"
                     /translation="DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQ
                     KPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLRAEDVAVYYCQQYYNTPR
                     TFGQGTKVEIKR"
BASE COUNT       86 a     93 c     88 g     75 t
ORIGIN

  Query Match             94.3%;  Score 319.8;  DB 9;  Length 342;
  Best Local Similarity   96.5%;  Pred. No. 6.9e-94;
  Matches  327;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||  ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||
Db        241 ATCAGCAGCCTGCGGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAATACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| ||||||||  || ||||||||||||||||||||
Db        301 CCTCGGACGTTCGGACAGGGGACCAAGGTGGAAATCAAA 339


Search completed: July 18, 2003, 13:47:35
Job time : 949.849 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:16:54 ; Search time 587.455 Seconds
(without alignments)
9345.860 Million cell updates/sec

Title: US-09-627-896B-26
Perfect score: 339
Sequence: 1 gacatccagttgacccagtc.....ggaccaaggtggaaatcaaa 339

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	321.4	94.8	886	12	BF674779	BF674779 602137932
	3	319.8	94.3	641	10	AW405821	AW405821 UI-HF-BL0
	4	318.2	93.9	533	10	AW802126	AW802126 IL5-UM007
	5	311.8	92.0	935	12	BG398034	BG398034 602439564
	6	310.2	91.5	643	10	AW390292	AW390292 CM2-ST018
	7	310.2	91.5	691	12	BF128999	BF128999 601811318
	8	305.4	90.1	508	10	AW406572	AW406572 UI-HF-BL0
	9	305.4	90.1	550	10	AW404610	AW404610 UI-HF-BL0
	10	305.4	90.1	904	14	BQ711273	BQ711273 AGENCOURT
	11	303.8	89.6	630	10	AW406512	AW406512 UI-HF-BL0
	12	303.8	89.6	798	12	BG426036	BG426036 602492715
	13	302.4	89.2	921	12	BG569993	BG569993 602590249
c	14	302.2	89.1	553	12	BF870122	BF870122 IL3-ET011
	15	299.4	88.3	757	12	BG484518	BG484518 602505173
	16	299	88.2	625	13	BI820438	BI820438 603034746
	17	297.6	87.8	903	14	BQ708644	BQ708644 AGENCOURT
	18	297	87.6	388	10	AW951579	AW951579 EST363649
	19	296.4	87.4	573	12	BF128829	BF128829 601811013
	20	296.4	87.4	819	12	BG686522	BG686522 602637474
	21	296.4	87.4	842	12	BG757770	BG757770 602714882
	22	296.4	87.4	887	12	BF663188	BF663188 602144432
	23	295.8	87.3	761	12	BG536372	BG536372 602564763
	24	295.6	87.2	957	12	BG756233	BG756233 602713544
	25	294.2	86.8	473	14	BQ083970	BQ083970 K-EST0147
	26	294.2	86.8	661	14	BM831430	BM831430 K-EST0105
	27	294.2	86.8	1057	12	BG539525	BG539525 602568157
	28	292.6	86.3	495	14	BQ082810	BQ082810 K-EST0144
	29	292.6	86.3	665	14	BM768906	BM768906 K-EST0051
	30	292.6	86.3	876	12	BG397563	BG397563 602438602
	31	292.6	86.3	984	14	BQ707260	BQ707260 AGENCOURT
	32	292.4	86.3	769	12	BG534966	BG534966 602554155
	33	291.8	86.1	473	12	BG685769	BG685769 602637868
	34	291.8	86.1	826	12	BG758298	BG758298 602712482
	35	291	85.8	700	14	BM783842	BM783842 K-EST0061
	36	291	85.8	710	12	BG537677	BG537677 602566021
	37	291	85.8	767	12	BG541967	BG541967 602569470
	38	290	85.5	328	10	AW406484	AW406484 UI-HF-BL0
	39	289.6	85.4	503	12	BF830413	BF830413 RC1-HT025
	40	289.4	85.4	492	14	BQ082708	BQ082708 K-EST0144
	41	289.4	85.4	527	14	BM821681	BM821681 K-EST0090
	42	289.4	85.4	541	12	BG547312	BG547312 602574731
	43	289.4	85.4	649	14	BM769427	BM769427 K-EST0052
	44	289.4	85.4	887	12	BF128587	BF128587 601810838
c	45	289.2	85.3	349	10	AW947280	AW947280 CM3-ET003

ALIGNMENTS

RESULT 1
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LOCUS BG757678 964 bp mRNA linear EST 15-MAY-2001
DEFINITION 602711268F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851521 5', mRNA sequence.
ACCESSION BG757678
VERSION BG757678.1 GI:14068331
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1694 row: h column: 18
High quality sequence stop: 784.
FEATURES Location/Qualifiers
source 1. .964

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4851521"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 236 a 280 c 238 g 210 t
ORIGIN

Query Match 95.3%; Score 323; DB 12; Length 964;
Best Local Similarity 97.1%; Pred. No. 7.2e-88;
Matches 329; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db         59 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 118

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db        119 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 178

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 238

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        239 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 298

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 358

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||    ||||||||||||||||||||||||||||||||
Db        359 CCAAAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 397
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RESULT 2
BF674779
LOCUS BF674779 886 bp mRNA linear EST 21-DEC-2000
DEFINITION 602137932F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274551 5', mRNA sequence.
ACCESSION BF674779
VERSION BF674779.1 GI:11948674
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1091 row: p column: 08
High quality sequence stop: 576.

FEATURES Location/Qualifiers
source 1. .886
/organism="Homo sapiens"
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/clone="IMAGE:4274551"
/clone_lib="NIH_MGC_83"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 218 a 214 c 245 g 209 t
ORIGIN

Query Match 94.8%; Score 321.4; DB 12; Length 886;
Best Local Similarity 96.8%; Pred. No. 2.1e-87;
Matches 328; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | |||||||||||||||| ||||||||||||||||||||||||||||||||
Db         91 GACATCGTGATGACCCAGTCTCCAGATTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 150

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||  ||
Db        151 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTTTCT 210

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        211 TGGTACCAGCAGAAACCAGGACGGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 270

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 330

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 390

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  ||||||||||||||||||||||||||||||||
Db        391 CCTCAGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 429
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RESULT 3
AW405821
LOCUS AW405821 641 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BL0-abp-h-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057636 5', mRNA sequence.
ACCESSION AW405821
VERSION AW405821.1 GI:6924878
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 641)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

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FEATURES             Location/Qualifiers
     source          1. .641
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3057636"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      159 a    178 c    163 g    141 t
ORIGIN
```

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  Query Match             94.3%;  Score 319.8;  DB 10;  Length 641;
  Best Local Similarity   96.5%;  Pred. No. 5.9e-87;
  Matches  327;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         53 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 112

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||| |||||||||||||||||||| ||||| |||||| ||
Db        113 ATCAACTGCAAGTCCAGCCAGAGTCTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 172

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        173 TGGTATCAGCAGAAACCAGGGCAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 232

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 292

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        293 ATCAGCAGCCTGCAGGCTGAGGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 352

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| |||||||||||| ||||||||||||||||||||
Db        353 CCTCGGACGTTCGGCCAGGGGACCAAGGTGGAAATCAAA 391
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RESULT 4
AW802126
LOCUS       AW802126                 533 bp    mRNA    linear   EST 16-MAY-2000
DEFINITION  IL5-UM0071-120400-065-d06 UM0071 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW802126
VERSION     AW802126.1  GI:7853996
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 533)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
```

```
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL5-UM0071-120
            400-065-d06&t3=2000-04-12&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 419.
FEATURES             Location/Qualifiers
     source          1. .533
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="UM0071"
                     /dev_stage="Adult"
                     /note="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      131 a    145 c    137 g    120 t
ORIGIN
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  Query Match             93.9%;  Score 318.2;  DB 10;  Length 533;
  Best Local Similarity   96.2%;  Pred. No. 1.7e-86;
  Matches  326;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 74

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         75 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 134

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 194

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 254

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 314

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              || |  || ||||||  |||||||||||||||| ||||||
Db        315 CCCCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA 353
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RESULT 5
BG398034
LOCUS       BG398034                 935 bp    mRNA    linear   EST 12-MAR-2001
DEFINITION  602439564F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565991 5',
            mRNA sequence.
ACCESSION   BG398034
VERSION     BG398034.1  GI:13291482
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 935)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
```

```
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1283  row: o  column: 16
            High quality sequence stop: 764.
FEATURES              Location/Qualifiers
     source           1. .935
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4565991"
                      /clone_lib="NIH_MGC_48"
                      /tissue_type="primary B-cells from tonsils (cell line)"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                      for average insert size 1.8kb. Library constructed by Ling
                      Hong in the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies).
                      Note: this is a NIH_MGC Library."
BASE COUNT       231 a    249 c    234 g    221 t
ORIGIN

  Query Match             92.0%;  Score 311.8;  DB 12;  Length 935;
  Best Local Similarity   95.0%;  Pred. No. 1.9e-84;
  Matches  322;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 125

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||| |||||||||||||||||||| ||||| |||||| ||
Db        126 ATCAACTGCAAGTCCAGCCAGACTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 185

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 245

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 305

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        306 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATACTACT 365

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||   || |||||||  ||||||  | |||||  ||||||
Db        366 CCTATCACTTTCGGCCCTGGGACCCAAGTGGATATCAAA 404


RESULT 6
AW390292
LOCUS       AW390292                 643 bp    mRNA    linear   EST 04-FEB-2000
DEFINITION  CM2-ST0182-221099-023-f04 ST0182 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW390292
VERSION     AW390292.1  GI:6894951
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
  TITLE     The FAPESP/LICR Human Cancer Genome Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM2&t2=CM2-ST0182-
            221099-023-f04&t3=1999-10-22&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 7
            High quality sequence stop: 641.
FEATURES              Location/Qualifiers
     source           1. .643
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone_lib="ST0182"
                      /dev_stage="Adult"
                      /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                      Site_2: SmaI; A mini-library was made by cloning products
                      derived from  ORESTES PCR (U.S. Letters Patent application
                      No. 196,716 -  Ludwig Institute for Cancer Research)
                      profiles into  the pUC 18 vector. Reverse transcription of
                      tissue mRNA and cDNA amplification were performed under
                      low stringency conditions."
BASE COUNT       162 a    173 c    162 g    146 t
ORIGIN

  Query Match             91.5%;  Score 310.2;  DB 10;  Length 643;
  Best Local Similarity   94.7%;  Pred. No. 5.1e-84;
  Matches  321;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 128

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||| ||||||||| |||||| || ||||| |||||| ||
Db        129 ATCAACTGCAAGTCCAGCCAGAGTATTTTATACAACTCCAAAAATAAGAACTACTTAGCT 188

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||
Db        189 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCTTTTACTGGGCATCTACGCGG 248

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 AAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGCGACAGATTTCACTCTCACC 308

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db        309 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTTTAGTCAT 368

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||| ||||||||||||||||||||||||||||||||||
Db        369 CCTCAAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 407


RESULT 7
BF128999
LOCUS       BF128999                 691 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601811318F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054205 5',
            mRNA sequence.
ACCESSION   BF128999
VERSION     BF128999.1  GI:10968039
KEYWORDS    EST.
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 691)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM894  row: c  column: 06
            High quality sequence stop: 682.
FEATURES             Location/Qualifiers
     source          1. .691
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4054205"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      160 a    175 c    178 g    176 t      2 others
ORIGIN

  Query Match             91.5%;  Score 310.2;  DB 12;  Length 691;
  Best Local Similarity   96.8%;  Pred. No. 5.2e-84;
  Matches  328;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 289

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| ||||||  ||
Db        290 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 349

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 409

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 469

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTA-- 527

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              || | ||||||||||||||||||||||||||||||||
Db        528 -CTGGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 565


RESULT 8
AW406572
LOCUS       AW406572                508 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-acu-g-10-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3060307 5', mRNA sequence.
ACCESSION   AW406572
VERSION     AW406572.1  GI:6925629
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .508
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3060307"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      115 a    139 c    126 g    128 t
ORIGIN

  Query Match             90.1%;  Score 305.4;  DB 10;  Length 508;
  Best Local Similarity   93.8%;  Pred. No. 1.4e-82;
  Matches  318;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| | |||||||
Db        121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTCCTTAACT 180

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||| |||||||||||||||||| || ||||||||||||||||||||||||||
Db        181 TGGTACCAGCTGAAACCAGGACAGCCTCCTAAGATGATCATTTACTGGGCATCTACCCGG 240

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 300

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||| |||||||||||||||||||||||||||||||||||||||||| |||||| |
Db        301 ATCAGCGGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATCATAGTATT 360

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||    || || ||||| |||||||| |||| ||||||
Db        361 CCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 399


RESULT 9
AW404610
LOCUS       AW404610                550 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-acc-a-06-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3058451 5', mRNA sequence.
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ACCESSION   AW404610
VERSION     AW404610.1  GI:6923667
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M.B. Soares Lab
            cDNA Library Arrayed by: M.B. Soares Lab
            DNA Sequencing by: M.B. Soares Lab
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .550
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3058451"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      140 a    150 c    139 g    121 t
ORIGIN

  Query Match             90.1%;  Score 305.4;  DB 10;  Length 550;
  Best Local Similarity   93.8%;  Pred. No. 1.4e-82;
  Matches  318;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 81

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              ||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||  ||
Db         82 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 141

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||
Db        142 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAACTGCTCATTTACGGGGCATCTACCCGG 201

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 261

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        262 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTATTGTCAGCAATATTATAGTACT 321

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||   || ||||||||||||||    |||| || |||
Db        322 CCCATCACCTTCGGCCAAGGGACACGACTGGAGATTAAA 360

RESULT 10
BQ711273
LOCUS       BQ711273                 904 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353747 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278306
            5', mRNA sequence.
ACCESSION   BQ711273
VERSION     BQ711273.1  GI:21850172
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2466  row: b  column: 03
            High quality sequence stop: 679.
FEATURES             Location/Qualifiers
     source          1. .904
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6278306"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      208 a    264 c    219 g    212 t      1 others
ORIGIN

  Query Match             90.1%;  Score 305.4;  DB 14;  Length 904;
  Best Local Similarity   93.8%;  Pred. No. 1.7e-82;
  Matches  318;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 122

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              ||||||||||||||||||||||||||||||||||||||||||| ||||| | |||| ||
Db        123 TTCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTCCTTAGCT 182

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||
Db        183 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTTCTGGGCATCTACCCGG 242

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              |||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        243 GAATCTGGGGTCCCTGACCGCTTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 302

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        303 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTAGT 362

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||   || || |||||  |||||||| |||| |||| |
Db        363 CCTCCGACTTTTGGCCAGGGGACCAAGCTGGAGATCAGA 401

RESULT 11
AW406512
LOCUS       AW406512                 630 bp    mRNA    linear   EST 16-FEB-2000
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DEFINITION  UI-HF-BL0-acu-a-09-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3060017 5', mRNA sequence.
ACCESSION   AW406512
VERSION     AW406512.1  GI:6925569
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 630)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .630
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      162 a    178 c    156 g    134 t
ORIGIN

  Query Match            89.6%;  Score 303.8;  DB 10;  Length 630;
  Best Local Similarity  93.5%;  Pred. No. 4.6e-82;
  Matches  317;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 79

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||| |||||||||||||||||| ||||||| ||||  |
Db         80 ATCAACTGCAAGTCCAGCCAGAGTCTTTTATACAGCTCCAACAATAAGAATTTCTTAGTT 139

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        140 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTCCTGGGCATCTACCCGG 199

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 259

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        260 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTATT 319

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||    || ||||||||||||||     |||| || |||
Db        320 CCCTTCACCTTCGGCCAAGGGACACGACTGGAGATTAAA 358


RESULT 12
BG426036
```

```
LOCUS       BG426036                798 bp    mRNA    linear   EST 14-MAR-2001
DEFINITION  602492715F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4606658 5',
            mRNA sequence.
ACCESSION   BG426036
VERSION     BG426036.1  GI:13332542
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1345  row: n  column: 03
            High quality sequence stop: 542.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4606658"
                     /clone_lib="NIH_MGC_75"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.65
                     kb (range 0.5-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      192 a    213 c    212 g    181 t
ORIGIN

  Query Match            89.6%;  Score 303.8;  DB 12;  Length 798;
  Best Local Similarity  93.5%;  Pred. No. 5e-82;
  Matches  317;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 150

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||| | |||||||||||| ||||| ||||||  |
Db        151 ATCAACTGCAAGTCCAGCCAGAGTGTTTTGTCCAGCTCCAACAATAAGAACTACTTAGTT 210

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||| |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        211 TGGTACCAGCACAAACCAGGACAGCCTCCTAAACTGCTCATTTCCTGGGCATCTACCCGG 270

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 330

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||| ||||||||||||||||||||||||||||||| ||||||| ||||||| ||
Db        331 ATCAGCAGTCTGCAGGCTGAAGATGTGGCAGTTTATTACTGCCAGCAATGTTATAGTGCT 390

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  || ||||||  ||||||||||||||| ||||||
Db        391 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA 429
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RESULT 13
BG569993
LOCUS       BG569993                 921 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602590249F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4716948 5',
            mRNA sequence.
ACCESSION   BG569993
VERSION     BG569993.1  GI:13577646
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1566  row: a  column: 13
            High quality sequence stop: 596.
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4716948"
                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      269 a    251 c    238 g    163 t
ORIGIN

  Query Match             89.2%;  Score 302.4;  DB 12;  Length 921;
  Best Local Similarity   95.0%;  Pred. No. 1.4e-81;
  Matches  323;  Conservative    0;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 149

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||| || ||||| |||||||||||
Db        150 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAATAATAAGAACTACTTAACT 209

Qy        121 TGGTACCAGCAGAAACCAGGACAGC-CTCCTAAGCTGCTCATTTACTGGGCATCTACCCG 179
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        210 TGGTACCAGCAGAAACCAGGACAGCACTCCTAAGCTGCTCATTTACTGGGCATCTACCCG 269

Qy        180 GGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 GGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 329

Qy        240 CATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTAC 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        330 CATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATACTAC 389

Qy        300 TGCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||    || || |||||| ||||||||| |||| ||||||
Db        390 TCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 429

RESULT 14
BF870122/c
LOCUS       BF870122                 553 bp    mRNA    linear   EST 17-JAN-2001
DEFINITION  IL3-ET0116-281000-308-H01 ET0116 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF870122
VERSION     BF870122.1  GI:12260252
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 553)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL3&t2=IL3-ET0116-
            281000-308-H01&t3=2000-10-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 46
            High quality sequence stop: 99.
FEATURES             Location/Qualifiers
     source          1. .553
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="ET0116"
                     /dev_stage="Adult"
                     /note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT      125 a    140 c    150 g    138 t
ORIGIN

  Query Match             89.1%;  Score 302.2;  DB 12;  Length 553;
  Best Local Similarity   93.2%;  Pred. No. 1.3e-81;
  Matches  316;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 492

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||| |||||  ||| ||| || ||
Db        491 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTTAAACAATTTGAACTACATAGCT 432

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||| | |||||||||||||| ||||||||||||||||||||||||
Db        431 TGGTACCAGCAGAAAGCCGGACAGCCTCCTAAGTTACTCATTTACTGGGCATCTACCCGG 372
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Db        371 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTATGGGACAGATTTCACTCTCACC 312

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||| |||||||||||||||||||||||||||| |||||   |||
Db        311 ATCAGCAGCCTGCAGGCAGAAGATGTGGCAGTTTATTACTGTCAGCAACATTATGCAACT 252

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| ||||||||||||||| ||||||||||||||||||
Db        251 CCTCGGACGTTCGGCCAAGGGGCCAAGGTGGAAATCAAA 213


RESULT 15
BG484518
LOCUS       BG484518                757 bp    mRNA    linear   EST 21-MAR-2001
DEFINITION  602505173F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4618290 5',
            mRNA sequence.
ACCESSION   BG484518
VERSION     BG484518.1  GI:13416797
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 757)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1376  row: b  column: 19
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
     source          1. .757
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4618290"
                     /clone_lib="NIH_MGC_77"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
BASE COUNT      195 a    202 c    203 g    157 t
ORIGIN

  Query Match             88.3%;  Score 299.4;  DB 12;  Length 757;
  Best Local Similarity   95.0%;  Pred. No. 1.1e-80;
  Matches  322;  Conservative    0;  Mismatches   11;  Indels    6;  Gaps    1;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||| | ||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         92 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGGGAGGGCCACC 151

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||      || |||||||||| ||
Db        152 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTC------CACGAATTACTTAGCT 205

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||||
Db        206 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAACTGCTCATTTATTGGGCATCTACCCGG 265

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 325

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        326 ATCAGTAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTCCT 385

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||| |||||||||||||||||||||||||||||||||
Db        386 CCTCCAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 424


Search completed: July 18, 2003, 09:26:08
Job time : 591.455 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:14:58 ; Search time 87.8822 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-09-627-896B-26
Perfect score: 339
Sequence: 1 gacatccagttgacccagtc.....ggaccaaggtggaaatcaaa 339

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	327.8	96.7	400	9	AAN80499	Encodes V region o
2	327.8	96.7	1373	9	AAN80941	Encodes Vchi regio
3	326.2	96.2	619	9	AAN80498	Encodes V region o
4	321.4	94.8	342	14	AAQ33032	MAb GAH variable r
5	319	94.1	360	15	AAQ71718	Monoclonal antibod
6	318.2	93.9	357	24	ABA94219	ebvHigM MSI19D10 l
7	315.2	93.0	463	21	AAC98443	Human colon cancer
8	315	92.9	360	22	AAH47729	Nucleotide sequenc
9	314	92.6	1028	14	AAQ45606	Sequence of pATDFL
10	314	92.6	1028	20	AAZ39437	DNA sequence of Hu
11	314	92.6	1028	20	AAZ23975	Plasmid pATDFLAG F
12	314	92.6	1330	14	AAQ45605	Sequence of Hum4 V
13	314	92.6	1330	20	AAZ39436	DNA sequence of Hu
14	314	92.6	1330	20	AAZ23974	Human Hum4L-CC49 V
15	314	92.6	1359	14	AAQ45607	Sequence of pSC49F
16	314	92.6	1359	20	AAZ39438	DNA sequence of pS
17	314	92.6	1359	20	AAZ23976	Plasmid pSC49FLAG
18	313.4	92.4	1048	20	AAZ23970	Human Hum4 VL ClaI
19	313.4	92.4	1088	20	AAZ39432	Nucleotide sequenc
20	311.8	92.0	792	24	ABQ56219	Human ovarian anti
21	311.8	92.0	1033	22	AAS00145	Human cDNA clone H
22	311.8	92.0	1088	15	AAQ56735	Sequence of Hum4VL
23	311.6	91.9	339	21	AAA96146	Nucleotide sequenc
24	311.6	91.9	423	20	AAX90025	Human monoclonal a
25	310.8	91.7	1361	15	AAQ56740	Sequence of plasmi
26	310.2	91.5	342	18	AAT60383	Anti-TGF beta-1 sc
27	310.2	91.5	342	24	ABK24413	Light chain DNA fr
28	310.2	91.5	407	13	AAQ26047	V-region of L-chai
29	310.2	91.5	804	24	ABQ56211	Human ovarian anti
30	310	91.4	339	21	AAA96134	Nucleotide sequenc
31	310	91.4	339	21	AAA96150	Nucleotide sequenc
32	309	91.2	339	21	AAA96158	Nucleotide sequenc
33	306.8	90.5	339	21	AAA96138	Nucleotide sequenc
34	306.8	90.5	339	21	AAA96140	Nucleotide sequenc
35	305.4	90.1	342	22	AAF29082	Human HIV-1 monocl
36	305.4	90.1	660	20	AAX77410	JP11127855 Seq ID
37	305.4	90.1	1097	14	AAQ45602	Sequence of the Hu
38	301.6	89.0	836	14	AAQ45604	Sequence of single
39	301.6	89.0	836	20	AAZ39435	Nucleotide sequenc
40	301.6	89.0	836	20	AAZ23973	Human SCFV1 DNA.
41	300.8	88.7	447	20	AAZ20412	IgM antibody CEM 1
42	300.4	88.6	9511	24	AAD28297	LNBOTDC vector #2.
43	300.4	88.6	9511	24	AAD28332	LNBOTDC vector #2.
44	298.8	88.1	339	21	AAA96132	Nucleotide sequenc
45	298.8	88.1	339	21	AAA96148	Nucleotide sequenc

ALIGNMENTS

RESULT 1
AAN80499
ID AAN80499 standard; DNA; 400 BP.
XX
AC AAN80499;
XX
DT 03-DEC-1990 (first entry)
XX
DE Encodes V region of L chain of anti-P.aeruginosa exotoxin Ab #2.
XX
KW Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..20
FT /*tag= a
XX
PN EP270077-A.
XX
PD 08-JUN-1988.
XX
PF 01-DEC-1987; 87EP-0117760.
XX
PR 03-DEC-1986; 86JP-0288340.
PR 26-NOV-1987; 87JP-0298513.
XX
PA (SUMO) SUMITOMO CHEM IND KK.
XX
PI Nakatani T, Nomura N, Horigome K, Noguchi H;
XX

```
DR   WPI; 1988-156310/23.
DR   P-PSDB; AAP80894.
XX
PT   New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT   plus recombinant vectors and host cells, useful for treating
PT   infections.
XX
PS   Claim 5; page 27; 39pp; English.
XX
CC   Sequence encodes variable region of light chain of anti-exotoxin
CC   antibody. It encodes the same protein sequence as AAN80498 except
CC   that the signal sequence of AAN80498 contains an intron.
CC   See also AAN80495-N80496, AAN80498 and AAN80941-2.
XX
SQ   Sequence 400 BP; 93 A; 109 C; 101 G; 97 T; 0 other;

  Query Match             96.7%;  Score 327.8;  DB 9;  Length 400;
  Best Local Similarity   97.9%;  Pred. No. 2.4e-95;
  Matches  332;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 120

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        121 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 180

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 240

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 300

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 360

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| |||||||||||||||||||||||||||||||||
Db        361 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 399


RESULT 2
AAN80941
ID   AAN80941 standard; DNA; 1373 BP.
XX
AC   AAN80941;
XX
DT   03-DEC-1990  (first entry)
XX
DE   Encodes Vchi region of FK-001 from lambda gFK1.
XX
KW   Pseudomonas aeruginosa; anti-exotoxin antibody; FK-001;
KW   lambda gFK1; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             532..882
FT                   /*tag=  a
FT                   /product=V region
XX
PN   EP270077-A.
XX
PD   08-JUN-1988.
XX
PF   01-DEC-1987;   87EP-0117760.
XX
PR   03-DEC-1986;   86JP-0288340.
PR   26-NOV-1987;   87JP-0298513.
XX
PA   (SUMO ) SUMITOMO CHEM IND KK.
XX
PI   Nakatani T,  Nomura N,  Horigome K,  Noguchi H;
XX
DR   WPI; 1988-156310/23.
XX
PT   New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT   plus recombinant vectors and host cells, useful for treating
PT   infections.
XX
PS   Disclosure; ; p; English.
XX
CC   Genomic DNA was isolated from the Epstein Barr virus-transformed
CC   human cell line FK001, fragmented and a gene library constructed.
CC   The library was screened with H or L chain probes and positive
CC   clones were identified including lambda gFK1. This clone contained
CC   an 11.5kb insert encoding the V and C regions of kappa chain.
CC   EcoRI digested vector pSV2neo was end-filled and then blunt-end
CC   ligated to a SalI linker to form pSV2neoSalI. This plasmid and
CC   gFK1 were both digested with SalI and ligated together to form
CC   pSV2neogFK1 which was itself digested with PvuI. The plasmid
CC   pSV2dhfr was likewise digested with PvuI and a mixture of the two
CC   was used to transform mouse myeloma cells which then expressed
CC   the antibody.
CC   See also AAN80495-N80496, AAN80498-N80499 and AAN80942.
XX
SQ   Sequence 1373 BP; 396 A; 264 C; 306 G; 407 T; 0 other;

  Query Match             96.7%;  Score 327.8;  DB 9;  Length 1373;
  Best Local Similarity   97.9%;  Pred. No. 4e-95;
  Matches  332;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 602

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        603 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 662

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 722

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 782

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 842

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| |||||||||||||||||||||||||||||||||
Db        843 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 881


RESULT 3
AAN80498
ID   AAN80498 standard; DNA; 619 BP.
XX
AC   AAN80498;
XX
DT   03-DEC-1990  (first entry)
XX
DE   Encodes V region of L chain of anti-P.aeruginosa exotoxin Ab #1.
XX
KW   Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;
KW   ds.
XX
OS   Homo sapiens.
XX
```

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FH   Key             Location/Qualifiers
FT   sig_peptide     1..49
FT                   /*tag=  a
FT   sig_peptide     269..279
FT                   /*tag=  b
FT   intron          50..268
FT                   /*tag=  c
XX
PN   EP270077-A.
XX
PD   08-JUN-1988.
XX
PF   01-DEC-1987;   87EP-0117760.
XX
PR   03-DEC-1986;   86JP-0288340.
PR   26-NOV-1987;   87JP-0298513.
XX
PA   (SUMO ) SUMITOMO CHEM IND KK.
XX
PI   Nakatani T,  Nomura N,  Horigome K,  Noguchi H;
XX
DR   WPI; 1988-156310/23.
DR   P-PSDB; AAP80894.
XX
PT   New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -
PT   plus recombinant vectors and host cells, useful for treating
PT   infections.
XX
PS   Claim 5; page 26; 39pp; English.
XX
CC   Sequence encodes variable region of light chain of anti-exotoxin
CC   antibody. The signal sequence contains an intron which is spliced
CC   out prior to translation.
CC   See also AAN80495-N80496, AAN80499 and AAN80941-2.
XX
SQ   Sequence 619 BP; 177 A; 139 C; 134 G; 169 T; 0 other;

  Query Match             96.2%;  Score 326.2;  DB 9;  Length 619;
  Best Local Similarity   97.6%;  Pred. No. 9.3e-95;
  Matches  331;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 339

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||| |||||||||||||||||||||||| ||||| |||||| ||
Db        340 ATCAACTGCAAGTCCACCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 399

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 459

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 519

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 579

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||| ||||||||||||||||||||||||||||||||
Db        580 CCTCGTACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 618


RESULT 4
AAQ33032
ID   AAQ33032 standard; cDNA; 342 BP.
XX
AC   AAQ33032;
XX
DT   06-MAY-1993  (first entry)
XX
DE   MAb GAH variable region of light chain.
XX
KW   Monoclonal antibody; hybridoma; PCR; variable region;
KW   constant region; heavy chain; light chain; ss.
XX
OS   Synthetic.
XX
PN   EP520499-A.
XX
PD   30-DEC-1992.
XX
PF   26-JUN-1992;   92EP-0110841.
XX
PR   28-JUN-1991;   91JP-0158859.
PR   28-JUN-1991;   91JP-0158860.
PR   28-JUN-1991;   91JP-0158861.
XX
PA   (MITU ) MITSUBISHI KASEI CORP.
XX
PI   Hirakawa Y,  Hosokawa S,  Ito N,  Nagaike K,  Tagawa T;
XX
DR   WPI; 1993-001328/01.
DR   P-PSDB; AAR30144.
XX
PT   Human monoclonal antibody specific for a cancer cell membrane
PT   surface antigen - prepd. from a hybridoma obtd. by cell fusion
PT   between human lymphocytes derived from cancer patients and mouse
PT   myeloma cells
XX
PS   Claim 13; Page 31 + 15; 37pp; English.
XX
CC   A human MAb specifically binding to a surface antigen of cancer
CC   cell membrane comprises variable regions of the heavy and light
CC   chains having the amino acid sequences of AAR30143-44 respectively,
CC   encoded by DNA sequences AAQ38670 and AAQ33032 respectively.
XX
SQ   Sequence 342 BP; 88 A; 92 C; 87 G; 75 T; 0 other;

  Query Match             94.8%;  Score 321.4;  DB 14;  Length 342;
  Best Local Similarity   96.8%;  Pred. No. 2.5e-93;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||| ||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||||||||||||||||||||||||
Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 5
AAQ71718
ID   AAQ71718 standard; cDNA; 360 BP.
XX
AC   AAQ71718;
```

```
XX
DT   13-APR-1995  (first entry)
XX
DE   Monoclonal antibody L612 light chain variable region.
XX
KW   Immunoglobulin; L612; light chain; variable region;
KW   monoclonal antibody; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..360
FT                   /*tag=  a
FT   misc_feature    58..108
FT                   /*tag=  b
FT                   /label= CDR 1
FT   misc_feature    154..174
FT                   /*tag=  c
FT                   /label= CDR 2
FT   misc_feature    271..297
FT                   /*tag=  d
FT                   /label= CDR 3
XX
PN   WO9419457-A.
XX
PD   01-SEP-1994.
XX
PF   09-FEB-1994;   94WO-US01469.
XX
PR   26-FEB-1993;   93US-0026320.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Irie RF;
XX
DR   WPI; 1994-294324/36.
DR   P-PSDB; AAR61240.
XX
PT   New transformed human B lymphoblastoid cell line - producing
PT   monoclonal antibody reactive with GM3 and GM4 ganglioside(s), for
PT   treating tumours, esp. melanoma
XX
PS   Disclosure; Page 31-32; 39pp; English.
XX
CC   Lymphocytes were sepd. from regional lymph nodes of a patient who had
CC   undergone mastectomy for breast cancer. The B lymphocyte fraction
CC   was incubated for 20 hrs with Epstein-Barr virus, then cloned by
CC   limiting dilution and tested for immunoadherence. Clones producing
CC   antibodies reactive with the UCLA-SO-M12 melanoma cell line were
CC   recloned 7 times in serum-free medium contg. growth factors. The
CC   resulting L612 is a B-lymphoblastoid cell line transformed by the
CC   Epstein-Barr virus. It is deposited at the ATCC under CRL 10724.
CC   HuMab L612 binds to renal cell carcinomas. The DNA sequence of the
CC   variable regions for both the light and heavy chains of the L612
CC   antibody were determined by PCR and are given in AAQ71718 and AAQ71717
CC   respectively.
XX
SQ   Sequence 360 BP; 88 A; 104 C; 85 G; 83 T; 0 other;

  Query Match             94.1%;  Score 319;  DB 15;  Length 360;
  Best Local Similarity   98.5%;  Pred. No. 1.5e-92;
  Matches  322;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         13 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 60

Qy         73 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG 132
              |||||||||||||||||||||||||||||| ||||| |||||| ||||||||||||||
Db         61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTACCTTGGTACCAGCAG 120

Qy        133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 180

Qy        193 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 240

Qy        253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTC 312
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        241 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCCGACGTTC 300

Qy        313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||||||||||||||||||||||||
Db        301 GGCCAAGGGACCAAGGTGGAAATCAAA 327


RESULT 6
ABA94219
ID   ABA94219 standard; DNA; 357 BP.
XX
AC   ABA94219;
XX
DT   13-MAR-2002  (first entry)
XX
DE   ebvHigM MSI19D10 light chain variable region nucleotide sequence.
XX
KW   Neuromodulatory; central nervous system; CNS; sHIgM22; LYM 22; AKJR4;
KW   ebvHigM MsI19D10; ebv HIgM CB2bG8; CB2iE12; CB2iE7; MSI19E5; virucide;
KW   antiparkinsonian; neuroprotective; nootropic; vulnerary; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..357
FT                   /*tag=  a
XX
PN   WO200185797-A1.
XX
PD   15-NOV-2001.
XX
PF   30-MAY-2000; 2000WO-US14902.
XX
PR   10-MAY-2000; 2000US-0568351.
XX
PA   (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI   Rodriguez M,  Miller DJ,  Pease LR;
XX
DR   WPI; 2002-066596/09.
DR   P-PSDB; ABB07172.
XX
PT   Novel neuromodulatory agent (a human IgM monoclonal antibody),
PT   promoting neurite outgrowth, regeneration, remyelination and
PT   neuroprotection in central nervous system, useful to treat
PT   post-infectious encephalomyelitis -
XX
PS   Claim 43; Fig 20; 219pp; English.
XX
CC   The invention provides a neuromodulatory agent (I) capable of promoting
CC   neurite outgrowth, regeneration, remyelination and neuroprotection in
CC   central nervous system (CNS). (I) is capable of inducing remyelination,
CC   promoting cellular proliferation of glial cells, and promoting Ca2+
CC   signaling with oligodendrocytes. An humanised antibody to (I) can be
CC   selected from antibody sHIgM22 (LYM 22), ebvHigM MsI19D10, ebv HIgM
CC   CB2bG8, AKJR4, CB2iE12, CB2iE7 or MSI19E5. (I) is useful for stimulating
CC   remyelination of CNS axons, stimulating proliferation of glial cells in
CC   CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC   of such therapy. (I) is capable of binding to structures and cells within
CC   CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC   of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC   (TMEV) or for treating a human being having multiple sclerosis, or a
CC   human or domestic animal with a viral demyelinating disease, or a post-
CC   neural disease of CNS. (I) is also useful for an in vitro method of
CC   stimulating the proliferation of glial cells from mixed cell culture.
```

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CC   (I) is also useful for stimulating remyelination of CNS axons. The
CC   antibodies are useful for preventing infection by a bacterium, virus or
CC   like pathogen that causes demyelination or other neurodegenerative
CC   condition in a subject. Methods where (I) is administered to a patient
CC   are useful for treating multiple sclerosis, Parkinson's disease,
CC   Alzheimer's disease, amyotrophic lateral sclerosis (ALS), a viral
CC   demyelinating disease, CNS diseases, and other conditions in the CNS
CC   where nerves are damaged as by trauma. The present sequence represents
CC   the ebvHigM MSI19D10 light chain variable region nucleotide sequence.
XX
SQ   Sequence 357 BP; 88 A; 101 C; 86 G; 82 T; 0 other;

  Query Match             93.9%;  Score 318.2;  DB 24;  Length 357;
  Best Local Similarity   96.2%;  Pred. No. 2.8e-92;
  Matches  326;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  || ||||||||  ||||||||  ||||| ||||||
Db        301 CCTCTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA 339


RESULT 7
AAC98443
ID   AAC98443 standard; cDNA; 463 BP.
XX
AC   AAC98443;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human colon cancer antigen nucleotide sequence SEQ ID NO:453.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW   immunomodulatory; muscular; gynaecological; gastrointestinal;
KW   nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW   neural disorder; immune system disorder; muscular disorder;
KW   reproductive disorder; gastrointestinal disorder; renal disorder;
KW   infectious disease; cardiovascular disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055351-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05883.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587534/55.
DR   P-PSDB; AAB53686.
XX
PT   Colon cancer associated gene sequences, referred to as colon cancer
PT   antigens, useful for the treatment, prevention, and diagnosis of colon
PT   disorders such as colon cancer -
XX
PS   Claim 1; Page 935; 2104pp; English.
XX
CC   AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC   called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC   human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC   neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC   vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC   can be used in gene therapy. The colon cancer antigen polynucleotides,
CC   proteins and antibodies to the proteins are useful for the prevention,
CC   treatment and diagnosis of colon disorders, such as colon cancer. The
CC   polynucleotides may be used in diagnostics and research, such as for
CC   chromosome identification, and as hybridisation probes. The proteins
CC   may also be used to prevent diseases such as neural disorders, immune
CC   system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, wounds, renal disorders, infectious
CC   diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC   AAB54007 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 463 BP; 106 A; 126 C; 113 G; 112 T; 6 other;

  Query Match             93.0%;  Score 315.2;  DB 21;  Length 463;
  Best Local Similarity   95.3%;  Pred. No. 2.8e-91;
  Matches  323;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 126

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db        127 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAACT 186

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        187 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCCTTTACTGGGCATCTACCCGG 246

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 306

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||| |||||||||||||||||||| |||||||||||||||||||||||| ||||
Db        307 ATCAGCAGNCTGCAGGCTGAAGATGTGGCAGATTATTACTGTCAGCAATATTATACTACT 366

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||  ||||||| ||||||||||  |
Db        367 CCCTGGACGTTCGGCCACTGGACCAANGTGGAAATCANA 405


RESULT 8
AAH47729
ID   AAH47729 standard; DNA; 360 BP.
XX
AC   AAH47729;
XX
DT   30-NOV-2001  (first entry)
XX
DE   Nucleotide sequence of seq Id No. 72.
XX
KW   Gene library; immunoglobulin; antibody library; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200162907-A1.
XX
```

```
PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-JP01298.
XX
PR   22-FEB-2000; 2000JP-0050543.
XX
PA   (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI   Kurosawa Y,  Akahori Y,  Iba Y,  Morino K,  Shinohara M,  Takahashi M;
PI   Okuno Y,  Shiraki K;
XX
DR   WPI; 2001-565420/63.
DR   P-PSDB; AAG65565.
XX
PT   Producing gene libraries and antibody libraries, involves selecting a
PT   light chain that binds to a heavy chain product to produce a functional
PT   formation, and producing a gene library of the light chain variable
PT   regions -
XX
PS   Examples; p 147-148; 181pp; Japanese.
XX
CC   The invention relates to producing gene libraries, comprising
CC   immunoglobulin light and heavy variable region. The method involves
CC   selecting light chain that binds with the heavy chain product to produce
CC   a functional conformation, producing a gene library comprising a
CC   collection of these light chain variable genes, and combining with gene
CC   library of heavy chain variable genes. The method is used for production
CC   of gene and antibody libraries.
XX
SQ   Sequence 360 BP; 89 A; 100 C; 89 G; 82 T; 0 other;

  Query Match             92.9%;  Score 315;  DB 22;  Length 360;
  Best Local Similarity   95.6%;  Pred. No. 3e-91;
  Matches  324;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||    || || ||||| ||||||||| |||| ||||||
Db        301 CCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 339


RESULT 9
AAQ45606
ID   AAQ45606 standard; DNA; 1028 BP.
XX
AC   AAQ45606;
XX
DT   04-DEC-1993  (first entry)
XX
DE   Sequence of pATDFLAG encoding signal peptide, H4VL, linker and
DE   FLAG adapter.
XX
KW   Single chain antibody; SCFV1; human subgroup 4 germline antibody;
KW   variable light; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             293..775
FT                   /*tag=  a
FT                   /note= "ENCODES SIGNAL,H4VL,LINKER
FT                         see AAR38320 FT"
FT   CDS             784..816
FT                   /*tag=  c
FT                   /product= flag peptide
XX
PN   WO9312231-A.
XX
PD   24-JUN-1993.
XX
PF   13-DEC-1991;   91WO-AU00583.
XX
PR   13-DEC-1991;   91WO-AU00583.
XX
PA   (DOWC ) DOW CHEM AUSTRALIA LTD.
XX
PI   Johnson KS,  Mezes PS,  Richard RA;
XX
DR   WPI; 1993-214173/26.
DR   P-PSDB; AAR38320, AAR40753.
XX
PT   New composite antibody binding to tumour associated TAG-72
PT   antigen - includes light chain variable region from human
PT   subgroup 4 germline gene, useful, opt. as conjugate, for
PT   diagnosis or treatment of cancer
XX
PS   Example; Figure 28; 150pp; English.
XX
CC   The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605)
CC   to incorporate a flag-coating sequence 3' to any human VH gene
CC   to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG,
CC   when digested with XhoI and Nhe I and purified becomes the human
CC   CH discovery plasmid contg. Hum4 VL in this SCFV format. pSC49FLAG
CC   contains murine antibody CC49VH inserted into sites of XhoI - NheI
CC   of pATDFLAG. It was evaluated for biological activity with the
CC   purpose of serving as a positive control for the FLAG assay
CC   system to detect binding to TAG-72.
XX
SQ   Sequence 1028 BP; 289 A; 226 C; 244 G; 269 T; 0 other;

  Query Match             92.6%;  Score 314;  DB 14;  Length 1028;
  Best Local Similarity   95.6%;  Pred. No. 9.7e-91;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  |||||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696
```

```
RESULT 10
AAZ39437
ID   AAZ39437 standard; DNA; 1028 BP.
XX
AC   AAZ39437;
XX
DT   29-FEB-2000  (first entry)
XX
DE   DNA sequence of Hum4 VL-UNIHOPE linker-FLAG peptide of pATDFLAG.
XX
KW   Tumor associated sialylated glycoprotein; TAG-72; cancer antigen;
KW   carcinoma lesion; diagnostic; cancer; antibody;
KW   anti-mouse antibody hypersensitivity reaction; ss.
XX
OS   Synthetic.
XX
PN   US5976845-A.
XX
PD   02-NOV-1999.
XX
PF   07-JUN-1995;   95US-0487743.
XX
PR   16-JUN-1994;   94US-0261354.
PR   19-APR-1990;   90US-0510697.
PR   20-OCT-1992;   92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS,  Richard RA,  Mezes PS;
XX
DR   WPI; 1999-619651/53.
DR   P-PSDB; AAY57184.
XX
PT   Production of humanized anti-TAG-72 antibodies, used for the detection,
PT   in vivo imaging and treatment of cancers  -
XX
PS   Example 5; Fig 28A-C; 85pp; English.
XX
CC   The invention relates to producing humanized anti-tumor associated
CC   sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies
CC   have binding specificity for the cancer antigen TAG-72. These antibodies
CC   have variable regions with VL segments derived from human subgroup IV
CC   germline gene and a VH segment (encoded by the VHalphaTAG germline gene)
CC   which is capapble of combining with the VL to form a threee dimensional
CC   structure having the ability to bind TAG-72. They can be used for the in
CC   vivo detection of carcinoma lesions. They can also be used for in vitro
CC   diagnostics. They can also be modified with therapeutic agents e.g. a
CC   radionuclide, drug, biological response modifier, toxin or another
CC   antibody for the treatment of cancers. The humanized anti-TAG-72
CC   antibodies can reduce harmful anti-mouse antibody hypersensitivity
CC   reactions.
XX
SQ   Sequence 1028 BP; 289 A; 227 C; 243 G; 269 T; 0 other;

  Query Match             92.6%;  Score 314;  DB 20;  Length 1028;
  Best Local Similarity   95.6%;  Pred. No. 9.7e-91;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| ||||||  ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  ||||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 11
AAZ23975
ID   AAZ23975 standard; DNA; 1028 BP.
XX
AC   AAZ23975;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Plasmid pATDFLAG FLAG DNA adapter.
XX
KW   Human; antibody; humanized; anti-tumor; sialylated glycoprotein antibody;
KW   TAG-72; cytostatic; cancer antigen; detection; carcinoma lesion;
KW   diagnostic; treatment; ss.
XX
OS   Synthetic.
XX
PN   US5976531-A.
XX
PD   02-NOV-1999.
XX
PF   16-JUN-1994;   94US-0261354.
XX
PR   19-APR-1990;   90US-0510697.
PR   20-OCT-1992;   92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS,  Mezes PS,  Richard RA;
XX
DR   WPI; 1999-632731/54.
DR   P-PSDB; AAY50693.
XX
PT   New humanized anti-TAG-72 antibodies, used for the detection, in vivo
PT   imaging and treatment of cancers  -
XX
PS   Example 5; Figure 28A-C; 83pp; English.
XX
CC   This invention describes novel humanized anti-tumor associated
CC   sialylated glycoprotein antibodies (TAG-72) which have cytostatic
CC   activity. The antibodies have binding specificity for the cancer antigen
CC   TAG-72.  They can be used for the in vivo detection of carcinoma lesions.
CC   They can also be used for in vitro diagnostics. They can also be modified
CC   with therapeutic agents e.g. a radionuclide, drug, biological response
CC   modifier, toxin or another antibody for the treatment of cancers. The
CC   humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
CC   hypersensitivity reactions.
XX
SQ   Sequence 1028 BP; 289 A; 227 C; 243 G; 269 T; 0 other;

  Query Match             92.6%;  Score 314;  DB 20;  Length 1028;
  Best Local Similarity   95.6%;  Pred. No. 9.7e-91;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| ||||||  ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478
```

```
Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  ||||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 12
AAQ45605
ID   AAQ45605 standard; DNA; 1330 BP.
XX
AC   AAQ45605;
XX
DT   04-DEC-1993  (first entry)
XX
DE   Sequence of Hum4 VL-CC49VH SCFV present in pSCFVUHH.
XX
KW   Single chain antibody; SCFV1; human subgroup 4 germline antibody;
KW   variable heavy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             293..1117
FT                   /*tag=  a
FT                   /note= "ENCODES SIGNAL,H4VL,LINKER,CC49VH (SEE
FT                          AAR38319 FT)"
XX
PN   WO9312231-A.
XX
PD   24-JUN-1993.
XX
PF   13-DEC-1991;   91WO-AU00583.
XX
PR   13-DEC-1991;   91WO-AU00583.
XX
PA   (DOWC ) DOW CHEM AUSTRALIA LTD.
XX
PI   Johnson KS,  Mezes PS,  Richard RA;
XX
DR   WPI; 1993-214173/26.
DR   P-PSDB; AAR38319.
XX
PT   New composite antibody binding to tumour associated TAG-72
PT   antigen - includes light chain variable region from human
PT   subgroup 4 germline gene, useful, opt. as conjugate, for
PT   diagnosis or treatment of cancer
XX
PS   Example; Figure 26; 150pp; English.
XX
CC   Plasmid pSCFV UHH expresses a biologically active, TAG-72 binding
CC   SCFV consisting of the Hum4 VL and CC49 VH. The expression plasmid
CC   utilises the beta-lactamase penP promoter, pectate lyase pelB
CC   signal sequence and the penP terminator region. Different Ig light
CC   chain variable regions can be inserted in the NcoI-HindIII sites,
CC   different SCFV linkers can be inserted in the HindIII-XhoI sites
CC   and different Ig heavy chain variable regions can be inserted in
CC   the XhoI-Nhe I sites.
XX
SQ   Sequence 1330 BP; 362 A; 300 C; 319 G; 349 T; 0 other;

  Query Match             92.6%;  Score 314;  DB 14;  Length 1330;
  Best Local Similarity   95.6%;  Pred. No. 1.1e-90;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||| ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  ||||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 13
AAZ39436
ID   AAZ39436 standard; DNA; 1330 BP.
XX
AC   AAZ39436;
XX
DT   29-FEB-2000  (first entry)
XX
DE   DNA sequence of Hum4 VL-CC49VH SCFV present in pSCFVUIIII.
XX
KW   Tumor associated sialylated glycoprotein; TAG-72; cancer antigen;
KW   carcinoma lesion; diagnostic; cancer; antibody; SCFV;
KW   anti-mouse antibody hypersensitivity reaction; ss.
XX
OS   Synthetic.
XX
PN   US5976845-A.
XX
PD   02-NOV-1999.
XX
PF   07-JUN-1995;   95US-0487743.
XX
PR   16-JUN-1994;   94US-0261354.
PR   19-APR-1990;   90US-0510697.
PR   20-OCT-1992;   92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS,  Richard RA,  Mezes PS;
XX
DR   WPI; 1999-619651/53.
DR   P-PSDB; AAY57183.
XX
PT   Production of humanized anti-TAG-72 antibodies, used for the detection,
PT   in vivo imaging and treatment of cancers  -
XX
PS   Example 4; Fig 26A-D; 85pp; English.
XX
CC   The invention relates to producing humanized anti-tumor associated
CC   sialylated glycoprotein (TAG-72) antibodies (anti-TAG). The antibodies
CC   have binding specificity for the cancer antigen TAG-72. These antibodies
CC   have variable regions with VL segments derived from human subgroup IV
CC   germline gene and a VH segment (encoded by the VHalphaTAG germline gene)
CC   which is capapble of combining with the VL to form a threee dimensional
CC   structure having the ability to bind TAG-72. They can be used for the in
CC   vivo detection of carcinoma lesions. They can also be used for in vitro
```

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CC   diagnostics. They can also be modified with therapeutic agents e.g. a
CC   radionuclide, drug, biological response modifier, toxin or another
CC   antibody for the treatment of cancers. The humanized anti-TAG-72
CC   antibodies can reduce harmful anti-mouse antibody hypersensitivity
CC   reactions.
XX
SQ   Sequence 1330 BP; 362 A; 302 C; 317 G; 349 T; 0 other;

  Query Match             92.6%;  Score 314;  DB 20;  Length 1330;
  Best Local Similarity   95.6%;  Pred. No. 1.1e-90;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  |||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 14
AAZ23974
ID   AAZ23974 standard; DNA; 1330 BP.
XX
AC   AAZ23974;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Human Hum4L-CC49 VH SCVF DNA.
XX
KW   Human; antibody; humanized; anti-tumor; sialylated glycoprotein antibody;
KW   TAG-72; cytostatic; cancer antigen; detection; carcinoma lesion;
KW   diagnostic; treatment; ss.
XX
OS   Homo sapiens.
XX
PN   US5976531-A.
XX
PD   02-NOV-1999.
XX
PF   16-JUN-1994;   94US-0261354.
XX
PR   19-APR-1990;   90US-0510697.
PR   20-OCT-1992;   92US-0964536.
XX
PA   (DOWC ) DOW CHEM CO.
XX
PI   Johnson KS,  Mezes PS,  Richard RA;
XX
DR   WPI; 1999-632731/54.
DR   P-PSDB; AAY50692.
XX
PT   New humanized anti-TAG-72 antibodies, used for the detection, in vivo
PT   imaging and treatment of cancers  -
XX
PS   Example 4; Figure 26A-D; 83pp; English.
XX
CC   This invention describes novel humanized anti-tumor associated
CC   sialylated glycoprotein antibodies (TAG-72) which have cytostatic
CC   activity. The antibodies have binding specificity for the cancer antigen
CC   TAG-72.  They can be used for the in vivo detection of carcinoma lesions.
CC   They can also be used for in vitro diagnostics. They can also be modified
CC   with therapeutic agents e.g. a radionuclide, drug, biological response
CC   modifier, toxin or another antibody for the treatment of cancers. The
CC   humanized anti-TAG-72 antibodies can reduce harmful anti-mouse antibody
CC   hypersensitivity reactions.
XX
SQ   Sequence 1330 BP; 362 A; 302 C; 317 G; 349 T; 0 other;

  Query Match             92.6%;  Score 314;  DB 20;  Length 1330;
  Best Local Similarity   95.6%;  Pred. No. 1.1e-90;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  |||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 15
AAQ45607
ID   AAQ45607 standard; DNA; 1359 BP.
XX
AC   AAQ45607;
XX
DT   04-DEC-1993  (first entry)
XX
DE   Sequence of pSC49FLAG.
XX
KW   Single chain antibody; SCFV1; human subgroup 4 germline antibody;
KW   variable heavy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             293..1147
FT                   /*tag=  a
FT                   /note= "ENCODES SIGNAL,HV4L,LINKER,CC49VH,FLAG
FT                           - SEE AAR38321 FT"
XX
PN   WO9312231-A.
XX
PD   24-JUN-1993.
XX
PF   13-DEC-1991;   91WO-AU00583.
XX
PR   13-DEC-1991;   91WO-AU00583.
XX
PA   (DOWC ) DOW CHEM AUSTRALIA LTD.
XX
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PI   Johnson KS,  Mezes PS,  Richard RA;
XX
DR   WPI; 1993-214173/26.
DR   N-PSDB; AAQ44607.
XX
PT   New composite antibody binding to tumour associated TAG-72
PT   antigen - includes light chain variable region from human
PT   subgroup 4 germline gene, useful, opt. as conjugate, for
PT   diagnosis or treatment of cancer
XX
PS   Example; Figure 30; 150pp; English.
XX
CC   The plasmid pATGFLAG was generated from pSCFVUHH (see AAQ45605)
CC   to incorporate a flag-coating sequence 3' to any human VH gene
CC   to be expressed contiguously with Hum4 VL. The plasmid pATGFLAG,
CC   when digested with XhoI and Nhe I and purified becomes the human
CC   CH discovery plasmid contg. Hum4 VL in this SCFV format. pSC49FLAG
CC   contains murine antibody CC49VH inserted into sites of XhoI - NheI
CC   of pATDFLAG. It was evaluated for biological activity with the
CC   purpose of serving as a positive control for the FLAG assay
CC   system to detect binding to TAG-72.
XX
SQ   Sequence 1359 BP; 374 A; 308 C; 325 G; 352 T; 0 other;

  Query Match          92.6%;  Score 314;  DB 14;  Length 1359;
  Best Local Similarity   95.6%;  Pred. No. 1.1e-90;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  |||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


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Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq3:*
13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	315.2	93.0	463	10	US-09-925-299-453	Sequence 453, App
	2	315.2	93.0	463	12	US-09-925-299-453	Sequence 453, App
	3	311.8	92.0	1033	10	US-09-799-514-2	Sequence 2, Appli
	4	305.2	90.0	788	15	US-10-158-646-58	Sequence 58, Appl
	5	303	89.4	463	11	US-09-187-693-26	Sequence 26, Appl
	6	300.4	88.6	9511	11	US-09-897-006-34	Sequence 34, Appl
	7	300.4	88.6	9511	12	US-09-897-511A-34	Sequence 34, Appl
	8	294.4	86.8	305	12	US-09-995-529-5	Sequence 5, Appli
	9	292.6	86.3	342	11	US-09-274-163E-1	Sequence 1, Appli
	10	291	85.8	343	11	US-09-274-163E-3	Sequence 3, Appli
	11	291	85.8	343	11	US-09-274-163E-5	Sequence 5, Appli
	12	288	85.0	1230	15	US-10-158-646-59	Sequence 59, Appl
	13	280.2	82.7	460	11	US-09-187-693-22	Sequence 22, Appl
	14	279	82.3	456	11	US-09-187-693-24	Sequence 24, Appl
	15	276.4	81.5	476	11	US-09-187-693-30	Sequence 30, Appl
	16	273.4	80.6	384	10	US-09-905-243-54	Sequence 54, Appl
	17	272.6	80.4	453	11	US-09-187-693-28	Sequence 28, Appl
	18	268.4	79.2	327	11	US-09-828-708-112	Sequence 112, App
	19	268.4	79.2	327	11	US-09-828-708-115	Sequence 115, App
c	20	251.6	74.2	266	10	US-09-604-287A-409	Sequence 409, App
c	21	251.6	74.2	266	12	US-09-551-621-409	Sequence 409, App
c	22	251.6	74.2	266	15	US-10-007-805-409	Sequence 409, App
c	23	251.6	74.2	266	15	US-10-076-622-409	Sequence 409, App
	24	246.2	72.6	339	15	US-10-121-464-5	Sequence 5, Appli
	25	244.6	72.2	339	15	US-10-121-464-1	Sequence 1, Appli
	26	241.4	71.2	339	15	US-10-121-464-3	Sequence 3, Appli
	27	233.8	69.0	1045	15	US-10-198-846-13629	Sequence 13629, A
	28	228	67.3	962	15	US-10-198-846-10845	Sequence 10845, A
	29	225.8	66.6	393	11	US-09-879-461-13	Sequence 13, Appl
	30	225.8	66.6	393	11	US-09-879-461-57	Sequence 57, Appl
	31	225.4	66.5	347	11	US-09-998-831-8	Sequence 8, Appli
	32	225.4	66.5	396	11	US-09-249-011A-7	Sequence 7, Appli
	33	223.8	66.0	390	15	US-10-146-305-5	Sequence 5, Appli
	34	223.8	66.0	1960	11	US-09-249-011A-21	Sequence 21, Appl
	35	223.8	66.0	3344	15	US-10-176-380-17	Sequence 17, Appl
	36	222.2	65.5	4661	11	US-09-897-006-10	Sequence 10, Appl
	37	222.2	65.5	4661	12	US-09-897-511A-10	Sequence 10, Appl
	38	220.6	65.1	660	11	US-09-995-693-3	Sequence 3, Appli
	39	220.6	65.1	660	15	US-10-232-408-3	Sequence 3, Appli
	40	220.6	65.1	723	10	US-09-791-578-5	Sequence 5, Appli
	41	220.6	65.1	723	10	US-09-791-540-5	Sequence 5, Appli
	42	220.6	65.1	758	11	US-09-956-086-1	Sequence 1, Appli
	43	220.6	65.1	758	11	US-09-956-087-1	Sequence 1, Appli
	44	220.6	65.1	782	10	US-09-791-578-3	Sequence 3, Appli
	45	220.6	65.1	782	10	US-09-791-540-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-925-299-453
; Sequence 453, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (315)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (393)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (404)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (426)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (453)
; OTHER INFORMATION: n equals a,t,g, or c

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US-09-925-299-453

  Query Match             93.0%;  Score 315.2;  DB 10;  Length 463;
  Best Local Similarity   95.3%;  Pred. No. 2.8e-98;
  Matches  323;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Db         67 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 126

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db        127 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAACT 186

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        187 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCCTTTACTGGGCATCTACCCGG 246

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 306

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||| |||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db        307 ATCAGCAGNCTGCAGGCTGAAGATGTGGCAGATTATTACTGTCAGCAATATTATACTACT 366

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        367 CCCTGGACGTTCGGCCACTGGACCAANGTGGAAATCANA 405


RESULT 2
US-09-925-299-453
; Sequence 453, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
;   LENGTH: 463
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (315)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (393)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (404)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (426)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (435)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (453)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-453

  Query Match             93.0%;  Score 315.2;  DB 12;  Length 463;
  Best Local Similarity   95.3%;  Pred. No. 2.8e-98;
  Matches  323;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 126

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db        127 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAACT 186

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        187 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCCTTTACTGGGCATCTACCCGG 246

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 306

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||| |||||||||||||||||||| |||||||||||||||||||||||||| ||||
Db        307 ATCAGCAGNCTGCAGGCTGAAGATGTGGCAGATTATTACTGTCAGCAATATTATACTACT 366

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        367 CCCTGGACGTTCGGCCACTGGACCAANGTGGAAATCANA 405


RESULT 3
US-09-799-514-2
; Sequence 2, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
;  APPLICANT:  Young et al.
;  TITLE OF INVENTION:  Immunoglobulin Superfamily Polynucleotides, Polypeptides, and An
;  FILE REFERENCE:  PT015P1
;  CURRENT APPLICATION NUMBER: US/09/799,514
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER:  PCT/US00/23662
;  PRIOR FILING DATE:  2000-08-29
;  PRIOR APPLICATION NUMBER:  60/152,248
;  PRIOR FILING DATE:  1999-09-03
;  NUMBER OF SEQ ID NOS:  19
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 1033
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-799-514-2

  Query Match             92.0%;  Score 311.8;  DB 10;  Length 1033;
  Best Local Similarity   95.0%;  Pred. No. 5.9e-97;
  Matches  322;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 129

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||| |||||||||||||||| |||| ||||| |||||| ||
Db        130 ATCAACTGCAAGTCCAGCCAGACTGTTTTATACAGCTCCGACAATAAGAACTACTTAGCT 189

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 249

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 309

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 369
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Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        370 CCGTACAGTTTTGGCCAGGGGACCAAGCTGGAAATCAAA 408
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RESULT 4
US-10-158-646-58
; Sequence 58, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 788
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.8
US-10-158-646-58

Query Match 90.0%; Score 305.2; DB 15; Length 788;
Best Local Similarity 95.3%; Pred. No. 9.8e-95;
Matches 326; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

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Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 141

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db        142 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGTTCCAACAATAAGAATTACTTAGCT 201

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 261

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 321

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 381

Qy        301 C---CTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |   | |  || ||||||  |||||||||||||| ||||||
Db        382 CTCGCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA 423
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RESULT 5
US-09-187-693-26
; Sequence 26, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 463
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(463)
; OTHER INFORMATION: n = A,T,C or G
US-09-187-693-26

Query Match 89.4%; Score 303; DB 11; Length 463;
Best Local Similarity 95.4%; Pred. No. 4.4e-94;
Matches 312; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Qy         13 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 72
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACTCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 60

Qy         73 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG 132
              |||||||||||||||||||| ||||||| ||  |||| ||||||  ||||||||||||||
Db         61 TCCAGCCAGAGTGTTTTATACGGCTCCAAGAATCAGAACTACTTAGCTTGGTACCAGCAG 120

Qy        133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 180

Qy        193 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 252
              |||||||||||||| |||||||||||| ||||||||||||||||||||||||||||||||
Db        181 CCTGACCGATTCAGGGGCAGCGGGTCTAGGACAGATTTCACTCTCACCATCAGCAGCCTG 240

Qy        253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTC 312
              |||||||||||||||||||||| | |||||| ||||||||||||||||  | ||||||
Db        241 CAGGCTGAAGATGTGGCAGTTTACTTCTGTCACCAATATTATAGTACTCCGTGGACGTTC 300

Qy        313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||||||||||||||||||||||||
Db        301 GGCCAAGGGACCAAGGTGGAAATCAAA 327
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RESULT 6
US-09-897-006-34
; Sequence 34, Application US/09897006
; Patent No. US20020106729A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory
; TITLE OF INVENTION: Expression Vectors
; FILE REFERENCE: GALA-06415
; CURRENT APPLICATION NUMBER: US/09/897,006
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,851
; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 9511
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-34

Query Match 88.6%; Score 300.4; DB 11; Length 9511;
Best Local Similarity 95.8%; Pred. No. 1.4e-92;
Matches 320; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

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Qy          6 CCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAA 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5703 CGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAA 5762

Qy         66 CTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTA 125
              |||||||||||||||||||||||| ||||||||||||| ||||| || ||| |||||||
Db       5763 CTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACAATAAGAACTATTTAGCTTGGTA 5822

Qy        126 CCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5823 TCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 5882

Qy        186 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5883 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 5942

Qy        246 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCG 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db       5943 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTA---CTCA 5999

Qy        306 AACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 7
US-09-897-511A-34
; Sequence 34, Application US/09897511A
; Publication No. US20030092882A1
; GENERAL INFORMATION:
;  APPLICANT: Bremel, Robert
;  APPLICANT:  Miller, Linda
;  APPLICANT:  Bleck, Gregory
;  TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
;  FILE REFERENCE: GALA-06416
;  CURRENT APPLICATION NUMBER: US/09/897,511A
;  CURRENT FILING DATE:  2001-06-29
;  PRIOR APPLICATION NUMBER: 60/215,925
;  PRIOR FILING DATE: 2000-07-03
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
;   LENGTH: 9511
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-897-511A-34

  Query Match           88.6%;  Score 300.4;  DB 12;  Length 9511;
  Best Local Similarity  95.8%;  Pred. No. 1.4e-92;
  Matches  320;  Conservative    0;  Mismatches   11;  Indels    3;  Gaps    1;

Qy          6 CCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAA 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5703 CGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAA 5762

Qy         66 CTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTA 125
              |||||||||||||||||||||||| ||||||||||||| ||||| || ||| |||||||
Db       5763 CTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACAATAAGAACTATTTAGCTTGGTA 5822

Qy        126 CCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5823 TCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATC 5882

Qy        186 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5883 CGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAG 5942

Qy        246 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCG 305
              |||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db       5943 CAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTA---CTCA 5999

Qy        306 AACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||||||||||||||||||||||||||||||||
Db       6000 GACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 6033


RESULT 8
US-09-995-529-5
; Sequence 5, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Huse, William D.
;  APPLICANT:  Tang, Ying
;  TITLE OF INVENTION: Humanized Collagen Antibodies and
;  TITLE OF INVENTION:  Related Methods
;  FILE REFERENCE: P-IX 4976
;  CURRENT APPLICATION NUMBER: US/09/995,529
;  CURRENT FILING DATE:  2001-11-26
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 305
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-995-529-5

  Query Match           86.8%;  Score 294.4;  DB 12;  Length 305;
  Best Local Similarity  98.0%;  Pred. No. 3.4e-91;
  Matches  298;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        *121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300

Qy        301 CCTC 304
              ||||
Db        301 CCTC 304


RESULT 9
US-09-274-163E-1
; Sequence 1, Application US/09274163E
; Patent No. US20020137897A1
; GENERAL INFORMATION:
;  APPLICANT: STEVENS, Fred J.
;  APPLICANT:  WILKINS STEVENS, Priscilla
;  APPLICANT:  RAFFEN, Rosemarie
;  APPLICANT:  SCHIFFER, Marianne
;  TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
;  FILE REFERENCE: 051583/0224
;  CURRENT APPLICATION NUMBER: US/09/274,163E
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER: US 08/373,380
;  PRIOR FILING DATE: 1995-01-17
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 342
;   TYPE: DNA
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;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(342)
;   OTHER INFORMATION:
US-09-274-163E-1

  Query Match             86.3%;  Score 292.6;  DB 11;  Length 342;
  Best Local Similarity   91.4%;  Pred. No. 1.5e-90;
  Matches  310;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              ||||||||||||||||||||||||||||||||||||||||    ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTATCAGAAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||| ||||| || ||    ||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGCCAGCAGTACTACTCCACC 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||     | ||||| || || |||||  ||||||||||
Db        301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339


RESULT 10
US-09-274-163E-3
; Sequence 3, Application US/09274163E
; Patent No. US20020137897A1
; GENERAL INFORMATION:
;  APPLICANT: STEVENS, Fred J.
;  APPLICANT:  WILKINS STEVENS, Priscilla
;  APPLICANT:  RAFFEN, Rosemarie
;  APPLICANT:  SCHIFFER, Marianne
;  TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
;  FILE REFERENCE: 051583/0224
;  CURRENT APPLICATION NUMBER: US/09/274,163E
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER: US 08/373,380
;  PRIOR FILING DATE: 1995-01-17
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 343
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(342)
;   OTHER INFORMATION:
US-09-274-163E-3

  Query Match             85.8%;  Score 291;  DB 11;  Length 343;
  Best Local Similarity   91.2%;  Pred. No. 5.3e-90;
  Matches  309;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              ||||||||||||||||||||||||||||||||||||||||    ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTATCAGGACAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||| ||||| || ||    ||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGCCAGCAGTACTACTCCACC 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||     | ||||| || || |||||  ||||||||||
Db        301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339
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Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||| ||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTATCAGGACAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||| ||||| || ||    ||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGCCAGCAGTACTACTCCACC 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||     | ||||| || || |||||  ||||||||||
Db        301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339


RESULT 11
US-09-274-163E-5
; Sequence 5, Application US/09274163E
; Patent No. US20020137897A1
; GENERAL INFORMATION:
;  APPLICANT: STEVENS, Fred J.
;  APPLICANT:  WILKINS STEVENS, Priscilla
;  APPLICANT:  RAFFEN, Rosemarie
;  APPLICANT:  SCHIFFER, Marianne
;  TITLE OF INVENTION: OPTIMUM RECOMBINANT ANTIBODY PRODUCTION
;  FILE REFERENCE: 051583/0224
;  CURRENT APPLICATION NUMBER: US/09/274,163E
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER: US 08/373,380
;  PRIOR FILING DATE: 1995-01-17
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
;   LENGTH: 343
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(342)
;   OTHER INFORMATION:
US-09-274-163E-5

  Query Match             85.8%;  Score 291;  DB 11;  Length 343;
  Best Local Similarity   91.2%;  Pred. No. 5.3e-90;
  Matches  309;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              ||||||||||||||||||||||||||||||||||||||||    ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACTCTAAGAACTACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||| ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTATCAGCGTAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||| ||||| || ||    ||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGCCAGCAGTACTACTCCACC 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||     | ||||| || || |||||  ||||||||||
Db        301 CCGTACTCCTTCGGTCAGGGTACCAAACTGGAAATCAAA 339
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```
RESULT 12
US-10-158-646-59
; Sequence 59, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
;  APPLICANT: Lasek, Amy K.W.
;  APPLICANT:  Sornasse, Thierry
;  TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
;  FILE REFERENCE: PA-0030-1 US
;  CURRENT APPLICATION NUMBER: US/10/158,646
;  CURRENT FILING DATE:  2002-05-29
;  PRIOR APPLICATION NUMBER: 60/295,239
;  PRIOR FILING DATE: 2001-05-31
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PERL Program
; SEQ ID NO 59
;   LENGTH: 1230
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030073105A1 1101440.15
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 1143-1160
;   OTHER INFORMATION: a, t, c, g, or other
US-10-158-646-59

  Query Match           85.0%;  Score 288;  DB 15;  Length 1230;
  Best Local Similarity   92.4%;  Pred. No. 1e-88;
  Matches  314;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCT-GGCTGTGTCTCTGGGCGAGAGGGCCAC 59
              || ||    | ||||||||||||||  |||||| |||||||||||||||||||||||||
Db        263 GAAATTGTGATGACCCAGTCTCCATCCTCCCTGGGCTGTGTCTCTGGGCGAGAGGGCCAC 322

Qy         60 CATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAAC 119
              |||||||||||| | ||||||||||||||||||||||||||||||| ||||| |||||| |
Db        323 CATCAACTGCAGGGCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGC 382

Qy        120 TTGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCG 179
              |||||||||||| |||||||||||||||||||| |||||||||||||||||||||||||
Db        383 TTGGTACCAGCATAAACCAGGACAGCCTCCTAAGGTGCTCATTTACTGGGCATCTACCCG 442

Qy        180 GGAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 239
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        443 GGAATCCGGGGTCCCAGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCAC 502

Qy        240 CATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTAC 299
              ||||||||| |||||| ||||||||||||||||||||||||||||||||||||||||||
Db        503 CATCAGCAGTCTGCAGTCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTAC 562

Qy        300 TCCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              |||    || || ||||| |||||||||||||| ||||||
Db        563 TCCGTACACTTTTGGCCAGGGGACCAAGGTGGAGATCAAA 602


RESULT 13
US-09-187-693-22
; Sequence 22, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/09/187,693
;  CURRENT FILING DATE:  1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 460
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(460)
;   OTHER INFORMATION: n = A,T,C or G
US-09-187-693-22

  Query Match           82.7%;  Score 280.2;  DB 11;  Length 460;
  Best Local Similarity   93.3%;  Pred. No. 3.2e-86;
  Matches  291;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         27 CTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGT 86
              || | |||| |||||||| |||| ||||||||||||||||||||||||||||||| ||||
Db          9 CTTCNTGGCCGTGTCTCTNGGCGCGAGGGCCACCATCAACTGCAAGTCCAGCCAGCGTGT 68

Qy         87 TTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAGAAACCAGGACAGCC 146
              |||||||| ||||||||| ||||| | |||| ||||||||||||||||||||||||||||
Db         69 TTTATACANCTCCAACAATAAGAACTGCTTAGCTTGGTACCAGCAGAAACCAGGACAGCC 128

Qy        147 TCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAG 206
              |||||||||||||||||||||| |||||||||||||||||||||||| |||||||||||
Db        129 TCCTAAGCTGCTCATTTACTGGACATCTACCCGGGAATCCGGGGTCCCTGCCCGATTCAG 188

Qy        207 TGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGT 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGT 248

Qy        267 GGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTCGGCCAAGGGACCAA 326
              |||||||||||||||||||||||||||||||||| |  || ||||||  ||||||||
Db        249 GGCAGTTTATTACTGTCAGCAATATTATAGTACTCCACTCACTTTCGGCGGAGGGACCAT 308

Qy        327 GGTGGAAATCAA 338
              |||||| |||||
Db        309 GGTGGAGATCAA 320


RESULT 14
US-09-187-693-24
; Sequence 24, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/09/187,693
;  CURRENT FILING DATE:  1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 456
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(456)
;   OTHER INFORMATION: n = A,T,C or G
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US-09-187-693-24

Query Match 82.3%; Score 279; DB 11; Length 456;
Best Local Similarity 93.2%; Pred. No. 8.3e-86;
Matches 302; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

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Qy         17 AGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCA 76
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 AGTCTCCAGACTCCCTGGTTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCA 60

Qy         77 GCCAGAGTGTTTTATACAGCTCCAACAA-CAAGAATTACTTAACTTGGTACCAGCAGAAA 135
              | |||||| ||||||||||||||||||| ||| || | |||| ||||||||||||||||
Db         61 GNCAGAGTATTTTATACAGCTCCAACAATCAAAAACTTCTTAGCTTGGTACCAGCAGAAA 120

Qy        136 CCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCT 195
              ||||||||||||||| ||| |||||||||||||||||||  ||||||||||||||||||
Db        121 CCAGGACAGCCTCCGAAGTTGCTCATTTACTGGGCATCTATTCGGGAATCCGGGGTCCCT 180

Qy        196 GACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAG 240

Qy        256 GCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTCGGC 315
              |||||||||||||||||||||||||||||| ||||||||| |||  | || || |||
Db        241 GCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTATTCCGTGCACTTTTGGC 300

Qy        316 CAAGGGACCAAGGTGGAAATCAAA 339
              || ||||||||| |||| ||||||
Db        301 CAGGGGACCAAGCTGGAGATCAAA 324
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RESULT 15
US-09-187-693-30
; Sequence 30, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 476
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-187-693-30

Query Match 81.5%; Score 276.4; DB 11; Length 476;
Best Local Similarity 92.6%; Pred. No. 6.6e-85;
Matches 289; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Qy        148 CCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATTCAGT 207
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Qy        208 GGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGGCTGAAGATGTG 267
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Qy        268 GCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTCGGCCAAGGGACCAAG 327
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Qy        328 GTGGAAATCAAA 339
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Db        301 GTGGAAATCAAA 312
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Job time : 83.9507 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 09:26:19 ; Search time 17.9759 Seconds
(without alignments)
5783.490 Million cell updates/sec

Title: US-09-627-896B-26
Perfect score: 339
Sequence: 1 gacatccagttgacccagtc.....ggaccaaggtggaaatcaaa 339

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	321.4	94.8	342	1	US-08-360-125-4	Sequence 4, Appli
2	321.4	94.8	342	2	US-08-450-578-4	Sequence 4, Appli
3	321.4	94.8	342	2	US-09-017-628-4	Sequence 4, Appli
4	321.4	94.8	342	2	US-09-014-880-4	Sequence 4, Appli
5	321.4	94.8	342	4	US-08-450-363-4	Sequence 4, Appli
6	319	94.1	360	1	US-08-026-320A-3	Sequence 3, Appli
7	314	92.6	1330	3	US-08-463-903-5	Sequence 5, Appli
8	314	92.6	1330	4	US-07-935-695-5	Sequence 5, Appli
9	312.4	92.2	1027	3	US-08-463-903-19	Sequence 19, Appl
10	312.4	92.2	1027	4	US-07-935-695-19	Sequence 19, Appl
11	309.2	91.2	1361	3	US-08-463-903-21	Sequence 21, Appl
12	309.2	91.2	1361	4	US-07-935-695-21	Sequence 21, Appl
13	308.6	91.0	1088	3	US-08-463-903-3	Sequence 3, Appli
14	308.6	91.0	1088	4	US-07-935-695-3	Sequence 3, Appli
15	301.6	89.0	836	3	US-08-463-903-1	Sequence 1, Appli
16	301.6	89.0	836	4	US-07-935-695-1	Sequence 1, Appli
17	292.4	86.3	302	3	US-08-724-752-6	Sequence 6, Appli
18	284	83.8	470	3	US-08-724-752-13	Sequence 13, Appl
19	281.4	83.0	470	3	US-08-828-741B-10	Sequence 10, Appl
20	281.4	83.0	470	4	US-09-160-567-10	Sequence 10, Appl
21	281.4	83.0	1031	3	US-08-828-741B-5	Sequence 5, Appli
22	281.4	83.0	1031	4	US-09-160-567-5	Sequence 5, Appli
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25	268.6	79.2	339	5	PCT-US93-08435-7	Sequence 7, Appli
26	267	78.8	339	5	PCT-US93-08435-5	Sequence 5, Appli
27	254.2	75.0	339	1	US-08-467-420A-20	Sequence 20, Appl
28	254.2	75.0	339	1	US-08-470-110A-20	Sequence 20, Appl
29	254.2	75.0	339	1	US-08-667-769A-20	Sequence 20, Appl
30	254.2	75.0	339	2	US-08-940-371-20	Sequence 20, Appl
31	254.2	75.0	339	3	US-08-637-647-20	Sequence 20, Appl
32	254.2	75.0	339	5	PCT-US95-17082A-20	Sequence 20, Appl
33	254.2	75.0	5703	1	US-08-467-420A-50	Sequence 50, Appl
34	254.2	75.0	5703	1	US-08-470-110A-50	Sequence 50, Appl
35	254.2	75.0	5703	1	US-08-667-769A-50	Sequence 50, Appl
36	254.2	75.0	5703	2	US-08-940-371-50	Sequence 50, Appl
37	254.2	75.0	5703	3	US-08-637-647-50	Sequence 50, Appl
38	254.2	75.0	5703	5	PCT-US95-17082A-50	Sequence 50, Appl
39	246.2	72.6	339	4	US-09-301-593-5	Sequence 5, Appli
40	246.2	72.6	339	4	US-09-301-593-103	Sequence 103, App
41	246.2	72.6	339	5	PCT-US93-08435-3	Sequence 3, Appli
42	244.6	72.2	339	4	US-09-301-593-1	Sequence 1, Appli
43	244.6	72.2	339	4	US-09-301-593-31	Sequence 31, Appl
44	244.6	72.2	8068	4	US-09-301-593-35	Sequence 35, Appl
45	243.6	71.9	442	3	US-08-724-752-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-360-125-4
; Sequence 4, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246ihiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:  Hybridoma producing human
;      CELL TYPE:  antibody GAH
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-4

  Query Match             94.8%;  Score 321.4;  DB 1;  Length 342;
  Best Local Similarity   96.8%;  Pred. No. 2.9e-97;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

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Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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RESULT 2
US-08-450-578-4
; Sequence 4, Application US/08450578
; Patent No. 5837845
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 5837845ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,578
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  342 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:  Hybridoma producing human
;      CELL TYPE:  antibody GAH
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
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;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-4

  Query Match            94.8%;  Score 321.4;  DB 2;  Length 342;
  Best Local Similarity  96.8%;  Pred. No. 2.9e-97;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 3
US-09-017-628-4
; Sequence 4, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
;  APPLICANT: HOSOKAWA, Saiko
;  APPLICANT: TAGAWA, Toshiaki
;  APPLICANT: HIRAKAWA, Yoko
;  APPLICANT: ITO, No. 5990287ihiko
;  APPLICANT: NAGAIKE, Kazuhiro
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
;  TITLE OF INVENTION: SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;  FILE REFERENCE: 177/527361KH
;  CURRENT APPLICATION NUMBER: US/09/017,628
;  CURRENT FILING DATE: 1998-02-02
;  EARLIER APPLICATION NUMBER: 08/360,125
;  EARLIER FILING DATE: 1994-12-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 342
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Hybridoma producing human antibody GAH
US-09-017-628-4

  Query Match            94.8%;  Score 321.4;  DB 2;  Length 342;
  Best Local Similarity  96.8%;  Pred. No. 2.9e-97;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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RESULT 4
US-09-014-880-4
; Sequence 4, Application US/09014880
; Patent No. 5990297
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA et al.
;    TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODY SPECIFICALLY
;    TITLE OF INVENTION:  BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack, L.L.P.
;      STREET:  2033 K Street, N.W., #800
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20006
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/014,880
;      FILING DATE:  January 28, 1998
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/450,578
;      FILING DATE:  May 25, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-721-8200
;      TELEFAX:  202-721-8250
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  342 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      CELL TYPE:  Hybridoma producing human
;      CELL TYPE:  antibody GAH
US-09-014-880-4

  Query Match             94.8%;  Score 321.4;  DB 2;  Length 342;
  Best Local Similarity   96.8%;  Pred. No. 2.9e-97;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||  | ||||||||||||||||||||||||||||||||
Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 5
US-08-450-363-4
; Sequence 4, Application US/08450363
; Patent No. 6436434
;  GENERAL INFORMATION:
;    APPLICANT:  Saiko HOSOKAWA
;    APPLICANT:  Toshiaki TAGAWA
;    APPLICANT:  Yoko HIRAKAWA
;    APPLICANT:  No. 6436434ihiko ITO
;    APPLICANT:  Kazuhiro NAGAIKE
;    TITLE OF INVENTION:  Human Monoclonal Antibody
;    TITLE OF INVENTION:  Specifically Binding to Surface Antigen of Cancer
;    TITLE OF INVENTION:  Cell Membrane
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 5.25 inch, 500 kb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,363
;      FILING DATE:  May 25, 1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/360,125
;      FILING DATE:  December 20, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/905,534
;      FILING DATE:  June 29, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  342 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:  Hybridoma producing human
;      CELL TYPE:  antibody GAH
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-363-4

  Query Match             94.8%;  Score 321.4;  DB 4;  Length 342;
  Best Local Similarity   96.8%;  Pred. No. 2.9e-97;
  Matches  328;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||| ||||||||| ||||| |||||| ||
Db         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAACTCCAACAATAAGAAATACTTAGCT 120

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAGTATTATAGTACT 300

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
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Db        301 CCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339


RESULT 6
US-08-026-320A-3
; Sequence 3, Application US/08026320A
; Patent No. 5419904
;  GENERAL INFORMATION:
;    APPLICANT:  Irie, Reiko F
;    TITLE OF INVENTION:  HUMAN B-LYMPHOBLASTOID CELL LINE
;    TITLE OF INVENTION:  SECRETING ANTI-GANGLIOSIDE ANTIBODY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Poms, Smith, Lande & Rose
;      STREET:  2029 Century Park East, Suite 3800
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/026,320A
;      FILING DATE:  26-FEB-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/609803
;      FILING DATE:  05-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oldenkamp, David J
;      REGISTRATION NUMBER:  29421
;      REFERENCE/DOCKET NUMBER:  94268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  3107885046
;      TELEFAX:  3102771297
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  360 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      INDIVIDUAL ISOLATE:  Epstein Barr Virus transformed B
;      INDIVIDUAL ISOLATE:  cell
;      CELL TYPE:  B-cell
;      CELL LINE:  L612
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..360
;      OTHER INFORMATION:  /function= "Immunoglobulin light
;      OTHER INFORMATION:  chain"
;      OTHER INFORMATION:  /product= "HuMab L612 Light Chain Variable Region"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  58..108
;      OTHER INFORMATION:  /function= "Complementary
;      OTHER INFORMATION:  determining region 1 (CDR1)"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  154..174
;      OTHER INFORMATION:  /function= "Complementary
;      OTHER INFORMATION:  determining region 2 (CDR2)"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  271..297
;      OTHER INFORMATION:  /function= "Complementary
;      OTHER INFORMATION:  determining region 3 (CDR3)"
US-08-026-320A-3

  Query Match             94.1%;  Score 319;  DB 1;  Length 360;
  Best Local Similarity   98.5%;  Pred. No. 1.9e-96;
  Matches  322;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         13 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAG 60

Qy         73 TCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACTTGGTACCAGCAG 132
              ||||||||||||||||||||||||||||||| ||||| |||||| ||||||||||||||
Db         61 TCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTACCAGCAG 120

Qy        133 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTC 180

Qy        193 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTG 240

Qy        253 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCGAACGTTC 312
              |||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        241 CAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCCTCCGACGTTC 300

Qy        313 GGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||||||||||||||||||||||||
Db        301 GGCCAAGGGACCAAGGTGGAAATCAAA 327


RESULT 7
US-08-463-903-5
; Sequence 5, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
;  APPLICANT: Mezes, Peter S.
;  APPLICANT: Richard, Ruth A.
;  APPLICANT: Affholter, Joseph A.
;  APPLICANT: Kotite, Nicolas J.
;  TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE: 40224A US
;  CURRENT APPLICATION NUMBER: US/08/463,903
;  CURRENT FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: US 07/935,695
;  EARLIER FILING DATE: 1992-08-21
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 5
;   LENGTH: 1330
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4VL-VH scFv from pSCFV UHH
;   LOCATION: 1..1330
US-08-463-903-5

  Query Match             92.6%;  Score 314;  DB 3;  Length 1330;
  Best Local Similarity   95.6%;  Pred. No. 1.6e-94;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||||  | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418
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Qy          61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
               |||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy         181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy         241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy         301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
               ||||  || ||||||  |||||||||||||||  |||||
Db         659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 8
US-07-935-695-5
; Sequence 5, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Richard, Ruth A.
;  APPLICANT:  Affholter, Joseph A.
;  APPLICANT:  Kotite, Nicolas J.
;  TITLE OF INVENTION:  Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE:  40224A US
;  CURRENT APPLICATION NUMBER: US/07/935,695
;  CURRENT FILING DATE:  1992-08-21
;  PRIOR APPLICATION NUMBER:  US 08/463,903
;  PRIOR FILING DATE:  1995-06-05
;  NUMBER OF SEQ ID NOS:  102
;  SOFTWARE:  MS-Word for Windows, Ver. 7.0
; SEQ ID NO 5
;   LENGTH: 1330
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4VL-VH scFv from pSCFV UHH
;   LOCATION: 1..1330
;   OTHER INFORMATION: :
US-07-935-695-5

  Query Match             92.6%;  Score 314;  DB 4;  Length 1330;
  Best Local Similarity   95.6%;  Pred. No. 1.6e-94;
  Matches  323;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy           1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
               |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy          61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
               |||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db         419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy         181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db         539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy         241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         599 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy         301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
               ||||  || ||||||  |||||||||||||||  |||||
Db         659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 9
US-08-463-903-19
; Sequence 19, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
;  APPLICANT: Mezes, Peter S.
;  APPLICANT: Richard, Ruth A.
;  APPLICANT: Affholter, Joseph A.
;  APPLICANT: Kotite, Nicolas J.
;  TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE: 40224A US
;  CURRENT APPLICATION NUMBER: US/08/463,903
;  CURRENT FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: US 07/935,695
;  EARLIER FILING DATE: 1992-08-21
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 19
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
;   LOCATION: 1..1027
US-08-463-903-19

  Query Match             92.2%;  Score 312.4;  DB 3;  Length 1027;
  Best Local Similarity   95.3%;  Pred. No. 4.7e-94;
  Matches  322;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy           1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db         359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy          61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
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Db         419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy         121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db         479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy         181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy         241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         599 ATCAGCAGCCTGCAGGCTGAAGATGCGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy         301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
               ||||  || ||||||  |||||||||||||||  |||||
Db         659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 10
US-07-935-695-19
; Sequence 19, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Richard, Ruth A.
;  APPLICANT:  Affholter, Joseph A.
;  APPLICANT:  Kotite, Nicolas J.
;  TITLE OF INVENTION:  Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE:  40224A US
;  CURRENT APPLICATION NUMBER: US/07/935,695
;  CURRENT FILING DATE:  1992-08-21
;  PRIOR APPLICATION NUMBER:  US 08/463,903
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;  PRIOR FILING DATE:  1995-06-05
;  NUMBER OF SEQ ID NOS:  102
;  SOFTWARE:  MS-Word for Windows, Ver. 7.0
; SEQ ID NO 19
;   LENGTH: 1027
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pATDFLAG
;   LOCATION: 1..1027
;   OTHER INFORMATION: :
US-07-935-695-19

  Query Match           92.2%;  Score 312.4;  DB 4;  Length 1027;
  Best Local Similarity  95.3%;  Pred. No. 4.7e-94;
  Matches  322;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        599 ATCAGCAGCCTGCAGGCTGAAGATGCGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
              ||||  || ||||||  ||||||||||||||  |||||
Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 11
US-08-463-903-21
; Sequence 21, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
;  APPLICANT: Mezes, Peter S.
;  APPLICANT: Richard, Ruth A.
;  APPLICANT: Affholter, Joseph A.
;  APPLICANT: Kotite, Nicolas J.
;  TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE: 40224A US
;  CURRENT APPLICATION NUMBER: US/08/463,903
;  CURRENT FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: US 07/935,695
;  EARLIER FILING DATE: 1992-08-21
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 21
;   LENGTH: 1361
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pSC49FLAG
;   LOCATION: 1..1361
US-08-463-903-21

  Query Match           91.2%;  Score 309.2;  DB 3;  Length 1361;
  Best Local Similarity  94.7%;  Pred. No. 6.2e-93;
  Matches  320;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              |||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCCAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||| |||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGCCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        599 ATCAGCAGCCTGCAGGCTGAAGATGCGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
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Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 12
US-07-935-695-21
; Sequence 21, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Richard, Ruth A.
;  APPLICANT:  Affholter, Joseph A.
;  APPLICANT:  Kotite, Nicolas J.
;  TITLE OF INVENTION:  Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE:  40224A US
;  CURRENT APPLICATION NUMBER: US/07/935,695
;  CURRENT FILING DATE:  1992-08-21
;  PRIOR APPLICATION NUMBER:  US 08/463,903
;  PRIOR FILING DATE:  1995-06-05
;  NUMBER OF SEQ ID NOS:  102
;  SOFTWARE:  MS-Word for Windows, Ver. 7.0
; SEQ ID NO 21
;   LENGTH: 1361
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: Hum4 VL-UNIHOPE linker-FLAG peptide construct in pSC49FLAG
;   LOCATION: 1..1361
;   OTHER INFORMATION: :
US-07-935-695-21

  Query Match           91.2%;  Score 309.2;  DB 4;  Length 1361;
  Best Local Similarity  94.7%;  Pred. No. 6.2e-93;
  Matches  320;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db        359 GACATCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCCAGAGGGCCACC 418

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||| |||||||||||||||||||||||||||||| ||||| |||||| ||
Db        419 ATCAACTGCAAGCCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 478

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db        479 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 538

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 598

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        599 ATCAGCAGCCTGCAGGCTGAAGATGCGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 658

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAA 338
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Db        659 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAA 696


RESULT 13
US-08-463-903-3
; Sequence 3, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
;  APPLICANT: Mezes, Peter S.
;  APPLICANT: Richard, Ruth A.
;  APPLICANT: Affholter, Joseph A.
;  APPLICANT: Kotite, Nicolas J.
;  TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE: 40224A US
;  CURRENT APPLICATION NUMBER: US/08/463,903
;  CURRENT FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: US 07/935,695
;  EARLIER FILING DATE: 1992-08-21
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 3
;   LENGTH: 1088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
;   LOCATION: 1..1088
US-08-463-903-3

  Query Match             91.0%;  Score 308.6;  DB 3;  Length 1088;
  Best Local Similarity   94.4%;  Pred. No. 8.9e-93;
  Matches  320;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
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Db        727 GACACTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 786

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        787 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 846

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db        847 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 906

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
              |||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 GAATCCGGGTGCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 966

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        967 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 1026

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  || ||||||  ||||||||||||||  ||||||
Db       1027 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAAA 1065


RESULT 14
US-07-935-695-3
; Sequence 3, Application US/07935695
; Patent No. 6329507
; GENERAL INFORMATION:
;  APPLICANT:  Mezes, Peter S.
;  APPLICANT:  Richard, Ruth A.
;  APPLICANT:  Affholter, Joseph A.
;  APPLICANT:  Kotite, Nicolas J.
;  TITLE OF INVENTION:  Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE:  40224A US
;  CURRENT APPLICATION NUMBER: US/07/935,695
;  CURRENT FILING DATE:  1992-08-21
;  PRIOR APPLICATION NUMBER:  US 08/463,903
;  PRIOR FILING DATE:  1995-06-05
;  NUMBER OF SEQ ID NOS:  102
;  SOFTWARE:  MS-Word for Windows, Ver. 7.0
; SEQ ID NO 3
;   LENGTH: 1088
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
;   LOCATION: 1..1088
US-07-935-695-3

  Query Match             91.0%;  Score 308.6;  DB 4;  Length 1088;
  Best Local Similarity   94.4%;  Pred. No. 8.9e-93;
  Matches  320;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 GACATCCAGTTGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 60
              ||||    | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GACACTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACC 786

Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||| ||
Db        787 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 846

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 906

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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Db        907 GAATCCGGGTGCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 966

Qy        241 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACT 300
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Db        967 ATCAGCAGCCTGCAGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTTAT 1026

Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA 339
              ||||  || ||||||  ||||||||||||||  ||||||
Db       1027 CCTCTCACTTTCGGCGGAGGGACCAAGGTGGTGATCAAA 1065


RESULT 15
US-08-463-903-1
; Sequence 1, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
;  APPLICANT: Mezes, Peter S.
;  APPLICANT: Richard, Ruth A.
;  APPLICANT: Affholter, Joseph A.
;  APPLICANT: Kotite, Nicolas J.
;  TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
;  FILE REFERENCE: 40224A US
;  CURRENT APPLICATION NUMBER: US/08/463,903
;  CURRENT FILING DATE: 1995-06-05
;  EARLIER APPLICATION NUMBER: US 07/935,695
;  EARLIER FILING DATE: 1992-08-21
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: MS-Word for Windows, Ver. 7.0
; SEQ ID NO 1
;   LENGTH: 836
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: SCFV1 from pCGS515
;   LOCATION: 1..836
US-08-463-903-1

  Query Match             89.0%;  Score 301.6;  DB 3;  Length 836;
  Best Local Similarity   94.3%;  Pred. No. 1.6e-90;
  Matches  313;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;
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Qy         61 ATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAACAAGAATTACTTAACT 120
              ||||||||||||||||||    |  |||||||||||||||||||| ||||| ||||||  ||
Db        137 ATCAACTGCAAGTCCAGCTGCAAGGTTTTATACAGCTCCAACAATAAGAACTACTTAGCT 196

Qy        121 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 180
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Db        197 TGGTACCAGCAGAAACCAGGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGG 256

Qy        181 GAATCCGGGGTCCCTGACCGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACC 240
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
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Qy        301 CCTCGAACGTTCGGCCAAGGGACCAAGGTGGA 332
              ||||  || ||||||  |||||||||||| |
Db        377 CCTCTCACTTTCGGCGGAGGGACCAAGGTGAA 408
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
10397.705 Million cell updates/sec

Title: US-09-627-896B-29
Perfect score: 368
Sequence: 1 aggtgcagctggtgcagtct.....ccctgctcatcgtctcctca 368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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34: em_htg_pln:*
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39: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	368	100.0	368	9	HSVH1I2RM	X70487 H.sapiens D
2	315.2	85.7	370	9	AF021950	AF021950 Homo sapi
3	311.2	84.6	428	9	AF062105	AF062105 Homo sapi
4	308.6	83.9	525	9	HUMIGHDNN	M65093 Human Ig re
5	307.2	83.5	426	9	HSVHIB8	Z47233 H.sapiens m
6	307.2	83.5	512	9	HSU84173	U84173 Homo sapien
7	307.2	83.5	515	9	HSU79581	U79581 Human clone
8	305.8	83.1	521	9	HSU84180	U84180 Homo sapien
9	305.6	83.0	528	9	HUMIGHDYN	M65104 Human Ig re
10	304.6	82.8	387	9	AF062189	AF062189 Homo sapi
11	303.8	82.6	515	9	HSU84178	U84178 Homo sapien
12	303	82.3	372	9	AB067158	AB067158 Homo sapi
13	302.8	82.3	363	9	U00583	U00583 Human immun
14	300.8	81.7	518	9	HSU84161	U84161 Homo sapien
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17	299.2	81.3	512	9	HSU84187	U84187 Homo sapien
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19	297.4	80.8	429	9	HSZ80853	Z80853 H.sapiens r
20	296.8	80.7	369	9	AB063921	AB063921 Homo sapi
21	296.8	80.7	369	12	AF527046	AF527046 Synthetic
22	296.4	80.5	483	9	HS203M5	Z47272 H.sapiens m
23	296.4	80.5	510	9	HS203E2	Z47264 H.sapiens m
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25	296.4	80.5	510	9	HS203E7	Z47266 H.sapiens m
26	296.4	80.5	510	9	HS203E9	Z47267 H.sapiens m
27	296.4	80.5	525	9	HS203G4	Z47271 H.sapiens m
28	296.2	80.5	381	9	AF062216	AF062216 Homo sapi
29	295.8	80.4	432	9	AF062193	AF062193 Homo sapi
30	294.8	80.1	483	9	HS203M7	Z47273 H.sapiens m
31	294.8	80.1	510	9	HS203E1	Z47263 H.sapiens m
32	294.8	80.1	525	9	HS203G1	Z47268 H.sapiens m
33	294.8	80.1	525	9	HS203G2	Z47269 H.sapiens m
34	294.8	80.1	525	9	HS203G3	Z47270 H.sapiens m
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36	294.2	79.9	525	9	HUMIGHDPN	M65095 Human Ig re
37	293.4	79.7	441	9	HSU84158	U84158 Homo sapien
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39	293.2	79.7	2287	6	AR037308	AR037308 Sequence
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41	293.2	79.7	2287	6	I90051	I90051 Sequence 1
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ALIGNMENTS

RESULT 1
HSVH1I2RM
LOCUS HSVH1I2RM 368 bp DNA linear PRI 23-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody heavy chain variable region,subgroup V(H)1 (III-2R IgM line).
ACCESSION X70487 X63851
VERSION X70487.1 GI:38449
KEYWORDS anti-DNA antibody; complementarity determining region; Ig heavy chain; Ig kappa light chain; Ig variable region; IgM; immunoglobulin; systemic lupus erythematosus.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 368)

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  AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
            and Diamond,B.
  TITLE     Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype
  JOURNAL   J. Exp. Med. 174 (6), 1639-1652 (1991)
  MEDLINE   92078875
   PUBMED   1660528
FEATURES             Location/Qualifiers
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                     /sub_clone="pBluescript"
                     /cell_line="EBV-transformed 3I(+) B cell line,III-2R IgM"
                     /tissue_type="spleen"
                     /clone_lib="genomic DNA in Charon 40"
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     misc_feature    90. .104
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     misc_feature    138. .197
                     /note="complementarity determining region, CDR 2"
BASE COUNT       84 a     92 c    116 g     76 t
ORIGIN

  Query Match             100.0%;  Score 368;  DB 9;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-102;
  Matches  368;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Qy        361 TCTCCTCA 368
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Db        361 TCTCCTCA 368


RESULT 2
AF021950
LOCUS       AF021950                370 bp    mRNA    linear   PRI 02-APR-1998
DEFINITION  Homo sapiens ID:CLL008 IgM heavy chain variable region mRNA,
            partial cds.
ACCESSION   AF021950
VERSION     AF021950.1  GI:3004689
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 370)
  AUTHORS   Chiorazzi,N.
  TITLE     Differences in Ig variable region gene use and mutation in IgM vs
            IgG CLL suggest selection for distinct surface membrane Ig
            receptors
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 370)
  AUTHORS   Chiorazzi,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-SEP-1997) Medicine, North Shore University Hospital,
            350 Community Drive, Manhasset, NY 11030, USA
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BASE COUNT       77 a     92 c    123 g     78 t
ORIGIN

  Query Match             85.7%;  Score 315.2;  DB 9;  Length 370;
  Best Local Similarity   91.0%;  Pred. No. 1.4e-85;
  Matches  335;  Conservative    0;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |    |
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTTTGGG 301

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              |  |    || |    | | ||||||||||||||||||||||||||||| ||| ||
Db        302 GTGGTTCGGGGAGTTATTATATCTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 361

Qy        361 TCTCCTCA 368
              ||||||||
Db        362 TCTCCTCA 369


RESULT 3
AF062105
LOCUS       AF062105                428 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 21u-19 immunoglobulin heavy chain variable
            region (IGH) mRNA, partial cds.
ACCESSION   AF062105
VERSION     AF062105.1  GI:3170672
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   Wang,X. and Stollar,B.D.
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  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
  MEDLINE   99459182
   PUBMED   10527689
REFERENCE   2  (bases 1 to 428)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1. .428
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.33"
                     /clone="21u-19"
                     /cell_type="peripheral B lymphocyte"
                     /tissue_type="blood"
                     /note="from elderly repertoire 21u"
     gene            1. .>428
                     /gene="IGH"
     CDS             1. .>428
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC18141.1"
                     /db_xref="GI:3170673"
                     /translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                     GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
                     SSLRSEDTAVYYCARDRVSGGSGYNWFDPGAREPWSPSPQG"
     sig_peptide     1. .57
                     /gene="IGH"
     V_region        58. .>428
                     /gene="IGH"
BASE COUNT       89 a    107 c    144 g     88 t
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  Query Match             84.6%;  Score 311.2;  DB 9;  Length 428;
  Best Local Similarity   92.1%;  Pred. No. 2.3e-84;
  Matches  339;  Conservative    0;  Mismatches   28;  Indels    1;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         59 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 118

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        119 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 178

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||| |||| |||||| ||||
Db        179 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 238

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        239 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 298

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        299 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCGGG 358

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                || | |  | |  |||||||||||||| ||||||||||||||||||||| ||| ||
Db        359 TCAGTGGTGGTAGTGGATACAACTGGTTCGA-CCCTGGGGCCAGGGAACCCTGGTCACCG 417

Qy        361 TCTCCTCA 368
              ||||||||
Db        418 TCTCCTCA 425


RESULT 4
HUMIGHDNN
LOCUS       HUMIGHDNN               525 bp    DNA     linear   PRI 23-MAY-1996
DEFINITION  Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L22,
            subgroup VH-I.
ACCESSION   M65093
VERSION     M65093.1  GI:185322
KEYWORDS    V-region; immunoglobulin heavy chain subgroup VH-I; rearranged DNA.
SOURCE      Homo sapiens tonsil DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Kipps,T.J. and Duffy,S.F.
  TITLE     Relationship of the CD5 B cell to human tonsillar lymphocytes that
            express autoantibody-associated cross-reactive idiotypes
  JOURNAL   J. Clin. Invest. 87 (6), 2087-2096 (1991)
  MEDLINE   91250563
   PUBMED   1710233
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="14q32.33"
                     /cell_type="B lymphocytes"
                     /tissue_type="tonsil"
     gene            11. .525
                     /gene="IGH@"
     CDS             join(11. .56,143. .525)
                     /partial
                     /gene="IGH@"
                     /codon_start=1
                     /product="Ig heavy chain"
                     /protein_id="AAB00781.1"
                     /db_xref="GI:185323"
                     /db_xref="GDB:G00-118-731"
                     /translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                     GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
                     SSLRSEDTAVYYCAREGYCSSTSCSNWFDPWGQGTLVTVSS"
     sig_peptide     join(11. .56,143. .153)
                     /gene="IGH@"
                     /note="G00-118-731"
     exon            <11. .56
                     /gene="IGH@"
                     /product="Ig heavy chain"
                     /note="G00-118-731"
     intron          57. .142
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     exon            143. .525
                     /gene="IGH@"
                     /product="Ig heavy chain"
                     /note="G00-118-731"
BASE COUNT      111 a    134 c    163 g    117 t
ORIGIN

  Query Match             83.9%;  Score 308.6;  DB 9;  Length 525;
  Best Local Similarity   91.4%;  Pred. No. 1.5e-83;
  Matches  339;  Conservative    0;  Mismatches   29;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        155 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 214

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        215 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 274

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||| |||| |||||| ||||
Db        275 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 334

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        335 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 394
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Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGAGGGAT 454

Qy        301 ATTATGTTTGGGGGAGCGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              ||| | | |  |||  |   ||||||||||||||||||||||||||||||| |||
Db        455 ATTGTAGTAGTACCAGCTGCTCGAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA 514

Qy        358 TCGTCTCCTCA 368
              ||||||||||
Db        515 CCGTCTCCTCA 525


RESULT 5
HSVHIB8
LOCUS       HSVHIB8                   426 bp    mRNA    linear   PRI 15-FEB-1996
DEFINITION  H.sapiens mRNA for immunoglobulin heavy chain V-region (clone
            CDN3IB8).
ACCESSION   Z47233
VERSION     Z47233.1  GI:1197314
KEYWORDS    immunoglobulin; immunoglobulin heavy chain; variable region.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 113)
  AUTHORS   Demaison,C., David,D., Letourneur,F., Zouali,M., Saragosti,S. and
            Theze,J.
  TITLE     A cDNA/anchor-PCR approach to analyse the human VH gene repertoire
            expressed by peripheral CD19+ B cells reveals a strong bias usage
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 426)
  AUTHORS   Demaison,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-DEC-1994) Christophe Demaison, Immunologie, Unite
            d'Immunogenetique Cellulaire-institut Pasteur, 25, rue du Docteur
            Roux, Paris, 75015, FRANCE
REFERENCE   3  (bases 1 to 426)
  AUTHORS   Demaison,C., David,D., Letourneur,F., Theze,J., Saragosti,S. and
            Zouali,M.
  TITLE     Analysis of human VH gene repertoire expression in peripheral CD19+
            B cells
  JOURNAL   Immunogenetics 42 (5), 342-352 (1995)
  MEDLINE   96006568
   PUBMED   7590967
FEATURES             Location/Qualifiers
     source          1. .426
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CDN3IB8"
                     /cell_type="B-lymphocyte"
                     /tissue_type="peripheral blood lymphocyte"
                     /dev_stage="adult"
     sig_peptide     1. .57
     V_region        58. .426
                     /product="immunoglobulin variable region"
BASE COUNT       89 a    111 c    142 g     84 t
ORIGIN

  Query Match             83.5%;  Score 307.2;  DB 9;  Length 426;
  Best Local Similarity   89.7%;  Pred. No. 3.9e-83;
  Matches  330;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         59 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 118

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        119 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 178

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||| |||||| ||||   |||||| ||||
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Db        179 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCTTTGGTACAGCAAACTACG 238

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        239 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 298

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |    ||
Db        299 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGTGGGGCCC 358

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              |||  |  ||   | ||    ||   |||  ||||||||||||||||||| ||| ||
Db        359 CCAATGACTACGGTGACTACGGGGGGGCGGACTACTGGGGCCAGGGAACCCTGGTCACCG 418

Qy        361 TCTCCTCA 368
              ||||||||
Db        419 TCTCCTCA 426


RESULT 6
HSU84173
LOCUS       HSU84173                  512 bp    DNA     linear   PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate HOW IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84173
VERSION     U84173.1  GI:2344939
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
   PUBMED   8977195
REFERENCE   2  (bases 1 to 512)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Homo sapiens"
                     /isolate="patient HOW"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /note="CLL: chronic lymphocytic leukemia"
     gene            1. .512
                     /gene="VH1-69"
     CDS             join(1. .46,133. .>512)
                     /gene="VH1-69"
                     /note="Allele: variants 2,11"
                     /codon_start=1
                     /product="IgM heavy chain VH1 region precursor"
                     /protein_id="AAC51700.1"
                     /db_xref="GI:2344940"
                     /translation="MDWTWRFLFVVAASTGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                     GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
                     SSLRSEDTAVYYCARDRSGSYYVKNWFDPWGQGTLVTVSS"
     sig_peptide     join(1. .46,133. .143)
                     /gene="VH1-69"
     mat_peptide     144. .512
                     /gene="VH1-69"
                     /product="IgM heavy chain VH1 region"
                     /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
BASE COUNT      113 a    128 c    159 g    112 t
ORIGIN

  Query Match             83.5%;  Score 307.2;  DB 9;  Length 512;
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  Best Local Similarity   89.7%;  Pred. No. 3.9e-83;
  Matches  330;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        145 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 264

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||  ||||   |||||| ||||
Db        265 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATTTTTGGTACAGCAAACTACG 324

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 384

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACAGAA 444

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              |      |          | |||||||||||||||||||||||||||||||||| ||| ||
Db        445 GTGGGAGCTACTACGTGAAAAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 504

Qy        361 TCTCCTCA 368
              ||||||||
Db        505 TCTCCTCA 512


RESULT 7
HSU79581
LOCUS       HSU79581                 515 bp    DNA     linear   PRI 01-FEB-1997
DEFINITION  Human clone OR immunoglobulin heavy chain gene, partial cds.
ACCESSION   U79581
VERSION     U79581.1  GI:1813665
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Bahler,D.W., Miklos,J.A. and Swerdlow,S.H.
  TITLE     Ongoing Ig Gene Hypermutation by Salivary Gland Mucosa-Associated
            Lymphoid Tissue-Type Lymphomas
  JOURNAL   Blood (1997) In press
REFERENCE   2  (bases 1 to 515)
  AUTHORS   Bahler,D.W., Miklos,J.A. and Swerdlow,S.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-NOV-1996) Pathology, Montefiore University Hospital,
            200 Lothrop Street, Pittsburgh, PA 15213-2582, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /clone="OR"
     CDS             join(1. .46,133. .>515)
                     /codon_start=1
                     /product="immunoglobulin heavy chain"
                     /protein_id="AAB41736.1"
                     /db_xref="GI:1813666"
                     /translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
                     GGTFSTYAISWVRQAPGQGLEWMGGIIPIFGTANHAQKFQGRVTITADESTSTAYMEL
                     SSLRSEDTAVYYCAREGYDSSGSPKPFDYWGQGTLVTVSSG"
BASE COUNT      112 a    130 c    160 g    113 t
ORIGIN

  Query Match           83.5%;  Score 307.2;  DB 9;  Length 515;
  Best Local Similarity   89.7%;  Pred. No. 3.9e-83;
  Matches  330;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| | ||| ||||||||||||||||||||||||||
Db        205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCACCTATGCTATCAGCTGGGTGCGACAGGCCC 264

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||  ||||||  |||
Db        265 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGAACAGCAAACCACG 324

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 384

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATATTACTGTGCGAGAGAGGGCT 444

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              || ||  | | ||   |   ||    || ||| ||||||||||||||||||| ||| ||
Db        445 ATGATAGTAGTGGTTCCCCGAAACCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCG 504

Qy        361 TCTCCTCA 368
              ||||||||
Db        505 TCTCCTCA 512


RESULT 8
HSU84180
LOCUS       HSU84180                 521 bp    DNA     linear   PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate LID IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84180
VERSION     U84180.1  GI:2344953
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 521)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
   PUBMED   8977195
REFERENCE   2  (bases 1 to 521)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
     source          1. .521
                     /organism="Homo sapiens"
                     /isolate="patient LID"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /note="CLL: chronic lymphocytic leukemia"
     gene            1. .521
                     /gene="VH1-69"
     CDS             join(1. .46,133. .>521)
                     /gene="VH1-69"
                     /note="Allele: variant 4"
                     /codon_start=1
                     /product="IgM heavy chain VH1 region precursor"
                     /protein_id="AAC51707.1"
                     /db_xref="GI:2344954"
                     /translation="MDWTWRFLFVVAAATGVQSQVQLVQSGAEVKKPGSSVKVSCKAS
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                     /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
BASE COUNT      115 a    128 c    157 g    121 t
ORIGIN

  Query Match             83.1%;  Score 305.8;  DB 9;  Length 521;
  Best Local Similarity   90.5%;  Pred. No. 1.1e-82;
  Matches  341;  Conservative    0;  Mismatches   27;  Indels    9;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              ||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 264

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        265 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 324

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 384

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||  |||| |
Db        385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGCAATCCTG 444

Qy        301 ATTATGTTTGGGG---------GAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCC 351
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Db        445 TTACGATTTTTGGAGTGGTTATTAAAACAAACTGGTTCGACCCCTGGGGCCAGGGAACCC 504

Qy        352 TGCTCATCGTCTCCTCA 368
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Db        505 TGGTCACTGTCTCCTCA 521


RESULT 9
HUMIGHDYN
LOCUS       HUMIGHDYN               528 bp    DNA     linear   PRI 09-MAY-1996
DEFINITION  Human Ig rearranged H chain gene V-region (V-D-J) hybridoma L42,
            subgroup VH-I.
ACCESSION   M65104
VERSION     M65104.1  GI:185344
KEYWORDS    V-region; immunoglobulin heavy chain subgroup VH-I; rearranged DNA.
SOURCE      Homo sapiens tonsil DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 528)
  AUTHORS   Kipps,T.J. and Duffy,S.F.
  TITLE     Relationship of the CD5 B cell to human tonsillar lymphocytes that
            express autoantibody-associated cross-reactive idiotypes
  JOURNAL   J. Clin. Invest. 87 (6), 2087-2096 (1991)
  MEDLINE   91250563
   PUBMED   1710233
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="14q32.33"
                     /cell_type="B lymphocytes"
                     /tissue_type="tonsil"
     gene            11. .528
                     /gene="IGH@"
     CDS             join(11. .56,143. .528)
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                     /codon_start=1
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                     /protein_id="AAA99225.1"
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                     SSLRSEDTAVYYCARGGMGYCSGGSCYWFDPWGQGTLVTVSS"
     sig_peptide     join(11. .56,143. .153)
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                     /note="G00-118-731"
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BASE COUNT      108 a    131 c    170 g    119 t
ORIGIN

  Query Match             83.0%;  Score 305.6;  DB 9;  Length 528;
  Best Local Similarity   90.6%;  Pred. No. 1.2e-82;
  Matches  339;  Conservative    0;  Mismatches   29;  Indels    6;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        155 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 214

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              ||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        215 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 274

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        275 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 334

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        335 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 394

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG------ 294
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Db        395 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGA 454

Qy        295 ATCCCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
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Db        455 TGGGATATTGTAGTGGTGGTAGCTGCTACTGGTTCGACCCCTGGGGCCAGGGAACCCTGG 514

Qy        355 TCATCGTCTCCTCA 368
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Db        515 TCACCGTCTCCTCA 528


RESULT 10
AF062189
LOCUS       AF062189                387 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 48u-22 immunoglobulin heavy chain variable
            region (IGH) mRNA, partial cds.
ACCESSION   AF062189
VERSION     AF062189.1  GI:3170840
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 387)
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  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
  MEDLINE   99459182
   PUBMED   10527689
REFERENCE   2  (bases 1 to 387)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1. .387
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.33"
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                     /cell_type="peripheral B lymphocyte"
                     /tissue_type="blood"
                     /note="from elderly repertoire 48u"
     gene            <1. .>387
                     /gene="IGH"
     CDS             <1. .>387
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC18225.1"
                     /db_xref="GI:3170841"
                     /translation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQG
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                     SGGSCYDIFPNWFDPWGQGTLVTVSSG"
     V_region        1. .>387
                     /gene="IGH"
BASE COUNT       84 a    100 c    124 g     79 t
ORIGIN

  Query Match             82.8%;  Score 304.6;  DB 9;  Length 387;
  Best Local Similarity   89.8%;  Pred. No. 2.4e-82;
  Matches  344;  Conservative    0;  Mismatches   24;  Indels   15;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              ||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACAAGCCG 301

Qy        301 ATTATGTTTGGGGGAGCGAC--------------AACTGGTTCGACCCCTGGGGCCAGG 345
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Db        302 ATTGTAGTGGTGGTAGCTGCTACGATATTTTCCCGAACTGGTTCGACCCCTGGGGCCAGG 361

Qy        346 GAACCCTGCTCATCGTCTCCTCA 368
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Db        362 GAACCCTGGTCACCGTCTCCTCA 384


RESULT 11
HSU84178
LOCUS       HSU84178                 515 bp    DNA     linear   PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate LAN IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84178
VERSION     U84178.1  GI:2344949
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 515)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
   PUBMED   8977195
REFERENCE   2  (bases 1 to 515)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
     source          1. .515
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /chromosome="14"
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                     /note="CLL: chronic lymphocytic leukemia"
     gene            1. .515
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     CDS             join(1. .46,133. .>515)
                     /gene="VH1-69"
                     /note="Allele: variants 1,5"
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                     /protein_id="AAC51705.1"
                     /db_xref="GI:2344950"
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                     GGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMEL
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     sig_peptide     join(1. .46,133. .143)
                     /gene="VH1-69"
     mat_peptide     144. .515
                     /gene="VH1-69"
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                     /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
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ORIGIN

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  Best Local Similarity   90.6%;  Pred. No. 4.4e-82;
  Matches  336;  Conservative    0;  Mismatches   32;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              ||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 264

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              ||||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        265 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 324

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 384

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGA---GAGATC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||    | | |
Db        385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGCTGCGGTT 444
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Qy        298 CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              | |    |  ||||       ||||||||||||||||||||||||||||||||||| |||
Db        445 CGGGGAGTTATTGGCCTTTGTGCAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA 504

Qy        358 TCGTCTCCTCA 368
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Db        505 CCGTCTCCTCA 515


RESULT 12
AB067158
LOCUS       AB067158                372 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
            partial cds, clone:ya0037h.
ACCESSION   AB067158
VERSION     AB067158.1  GI:21670372
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:ya0037h.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 372)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University,
            Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
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                     /clone="ya0037h"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1. .372
                     /gene="IGH"
     CDS             <1. .>372
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain VHDJ region"
                     /protein_id="BAC02196.1"
                     /db_xref="GI:21670373"
                     /translation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRHAPGQG
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BASE COUNT       84 a     89 c    115 g     84 t
ORIGIN

  Query Match           82.3%;  Score 303;  DB 9;  Length 372;
  Best Local Similarity   91.0%;  Pred. No. 7.5e-82;
  Matches  334;  Conservative    0;  Mismatches   30;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||| ||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACATGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        122 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA---GATC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||    ||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGATGCCATA 301

Qy        298 CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              |  ||||  | ||    |||| |    | |  || |||  |||||||||||||||||| |||
Db        302 CGTATTACGATTTTTGGAGTGGTTATTATTTTGACTACTGGGGCCAGGGAACCCTGGTCA 361

Qy        358 TCGTCTC 364
              |||||||
Db        362 CCGTCTC 368


RESULT 13
U00583
LOCUS       U00583                  363 bp    mRNA    linear   PRI 25-MAY-1994
DEFINITION  Human immunoglobulin heavy chain variable region (clone Tmu60)
            mRNA, partial cds.
ACCESSION   U00583
VERSION     U00583.1  GI:392755
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 363)
  AUTHORS   Huang,C. and Stollar,B.D.
  TITLE     A majority of Ig H chain cDNA of normal human adult blood
            lymphocytes resembles cDNA for fetal Ig and natural autoantibodies
  JOURNAL   J. Immunol. 151 (10), 5290-5300 (1993)
  MEDLINE   94044753
   PUBMED   8228225
REFERENCE   2  (bases 1 to 363)
  AUTHORS   Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-1993) Stollar B.D., Tufts University,
            Biochemistry, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /tissue_type="peripheral blood"
                     /clone_lib="Tmu"
                     /dev_stage="adult"
     CDS             <1. .>363
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                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAA18279.1"
                     /db_xref="GI:392756"
                     /translation="QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQG
                     LEWMGGIIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGDIL
                     TGLNWFDPWGQGTLVTVSS"
BASE COUNT       80 a     94 c    114 g     75 t
ORIGIN

  Query Match           82.3%;  Score 302.8;  DB 9;  Length 363;
  Best Local Similarity   91.0%;  Pred. No. 8.6e-82;
  Matches  335;  Conservative    0;  Mismatches   27;  Indels    6;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61
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Qy          61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
               |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db          62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy         121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
               |||||||||||||||||||||||||| ||||||| |||||| ||||    |||||| ||||
Db         122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy         181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
               |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 CACAAAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy         241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||      |
Db         242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCTGTGTATTACTGTGCGAGA------G 295

Qy         301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
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Db         296 GCGATATTTTGACTGGCCTTAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 355

Qy         361 TCTCCTCA 368
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Db         356 TCTCCTCA 363


RESULT 14
HSU84161
LOCUS       HSU84161                 518 bp    DNA     linear   PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate BRA IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84161
VERSION     U84161.1  GI:2344915
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
   PUBMED   8977195
REFERENCE   2  (bases 1 to 518)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
     source          1. .518
                     /organism="Homo sapiens"
                     /isolate="patient BRA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /note="CLL: chronic lymphocytic leukemia"
     gene            1. .518
                     /gene="VH1-69"
     CDS             join(1. .46,133. .>518)
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                     /codon_start=1
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                     /db_xref="GI:2344916"
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                     SSLRSEDTAVYYCARDGCSGGSCYFWGWFDPWGQGTLVTVSS"
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                     /gene="VH1-69"
     mat_peptide     144. .518
                     /gene="VH1-69"
                     /product="IgM heavy chain VH1 region"
                     /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
BASE COUNT      107 a    127 c    165 g    119 t
ORIGIN

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  Best Local Similarity   89.8%;  Pred. No. 3.6e-81;
  Matches  336;  Conservative    0;  Mismatches   32;  Indels    6;  Gaps    1;

Qy           1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db         145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy          61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
               |||||||||||||||||||||||||| || ||| |||||| ||||||||||||||||||
Db         205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAACTGGGTGCGACAGGCCC 264

Qy         121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
               |||||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db         265 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 324

Qy         181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
               |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAACACAGCCTACA 384

Qy         241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATGGTT 444

Qy         301 ATTATGTTTGGGGGAGCGAC------AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
                 | || | |  | || ||      ||||||||||||||||||||||||||||||
Db         445 GTAGTGGTGGTAGCTGCTACTTTTGGGGCTGGTTCGACCCCTGGGGCCAGGGAACCCTGG 504

Qy         355 TCATCGTCTCCTCA 368
               ||| ||||||||||
Db         505 TCACCGTCTCCTCA 518


RESULT 15
HSU84164
LOCUS       HSU84164                 518 bp    DNA     linear   PRI 27-AUG-1997
DEFINITION  Homo sapiens isolate CRA IgM heavy chain VH1 region precursor
            (VH1-69) gene, partial cds.
ACCESSION   U84164
VERSION     U84164.1  GI:2344921
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Johnson,T.A., Rassenti,L.Z. and Kipps,T.J.
  TITLE     Ig VH1 genes expressed in B cell chronic lymphocytic leukemia
            exhibit distinctive molecular features
  JOURNAL   J. Immunol. 158 (1), 235-246 (1997)
  MEDLINE   97131694
   PUBMED   8977195
REFERENCE   2  (bases 1 to 518)
  AUTHORS   Johnson,T.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1997) Medicine, UCSD, 9500 Gilman Drive, 0663, La
            Jolla, CA 92093, USA
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /note="CLL: chronic lymphocytic leukemia"
     gene            1. .518
                     /gene="VH1-69"
     CDS             join(1. .46,133. .>518)
                     /gene="VH1-69"
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                     GGTFSSYAINWVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTNTAYMEL
                     SSLRSEDTAVYYCARDGCSGGSCYFWGWFDPWGQGTLVTVSS"
     sig_peptide     join(1. .46,133. .143)
                     /gene="VH1-69"
     mat_peptide     144. .518
                     /gene="VH1-69"
                     /product="IgM heavy chain VH1 region"
                     /note="FW1/CDR1/FW2/CDR2/FW3/CDR3/FW4"
BASE COUNT      107 a    127 c    165 g    119 t
ORIGIN

  Query Match             81.7%;  Score 300.8;  DB 9;  Length 518;
  Best Local Similarity   89.8%;  Pred. No. 3.6e-81;
  Matches  336;  Conservative    0;  Mismatches   32;  Indels    6;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        145 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 204

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| |||||| ||||||||||||||||||
Db        205 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAACTGGGTGCGACAGGCCC 264

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| |||||| |||| |||||| ||||
Db        265 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 324

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||| ||||||||||
Db        325 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAACACAGCCTACA 384

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATGGTT 444

Qy        301 ATTATGTTTGGGGGAGCGAC------AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
              |  || | |  |  || ||         ||||||||||||||||||||||||||||
Db        445 GTAGTGGTGGTAGCTGCTACTTTTGGGGCTGGTTCGACCCCTGGGGCCAGGGAACCCTGG 504

Qy        355 TCATCGTCTCCTCA 368 .
              ||| ||||||||||
Db        505 TCACCGTCTCCTCA 518


Search completed: July 18, 2003, 13:47:37
Job time : 1032.02 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:16:54 ; Search time 637.709 Seconds
(without alignments)
9345.860 Million cell updates/sec

Title: US-09-627-896B-29
Perfect score: 368
Sequence: 1 aggtgcagctggtgcagtct.....ccctgctcatcgtctcctca 368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	297.4	80.8	477	12	BF975791	BF975791 602246355
2	297.4	80.8	909	12	BG397239	BG397239 602439015
3	297.4	80.8	1012	12	BF974633	BF974633 602243363
4	287.8	78.2	959	14	BQ706226	BQ706226 AGENCOURT
5	286.4	77.8	903	12	BG754936	BG754936 602711631
6	285.4	77.6	878	12	BG758459	BG758459 602712658
7	284.8	77.4	903	14	BQ706171	BQ706171 AGENCOURT
8	283	76.9	1035	14	BQ881378	BQ881378 AGENCOURT
9	282.4	76.7	980	14	BQ708591	BQ708591 AGENCOURT
10	281.6	76.5	991	14	BQ710257	BQ710257 AGENCOURT
11	279	75.8	970	14	BQ706539	BQ706539 AGENCOURT
12	278.8	75.8	417	10	AW408371	AW408371 UI-HF-BK0
13	277.2	75.3	884	14	BQ708380	BQ708380 AGENCOURT
14	277.2	75.3	937	14	BQ711877	BQ711877 AGENCOURT
15	276.6	75.2	418	10	AW401468	AW401468 UI-HF-BK0
16	276.6	75.2	920	14	BQ708488	BQ708488 AGENCOURT
17	276.6	75.2	989	14	BQ889215	BQ889215 AGENCOURT
18	275.2	74.8	937	12	BG685980	BG685980 602638543
19	275	74.7	896	14	BQ711903	BQ711903 AGENCOURT
20	273.6	74.3	516	10	AW402422	AW402422 UI-HF-BK0
21	273.2	74.2	485	10	AW403940	AW403940 UI-HF-BK0
22	272.2	74.0	477	10	AW408484	AW408484 UI-HF-BK0
23	271.6	73.8	863	14	BQ708543	BQ708543 AGENCOURT
24	271.6	73.8	939	14	BQ708868	BQ708868 AGENCOURT
25	270.8	73.6	784	13	BM007990	BM007990 603617728
26	270.8	73.6	867	14	BQ710457	BQ710457 AGENCOURT
27	270.8	73.6	931	14	BQ710875	BQ710875 AGENCOURT
28	270.8	73.6	934	14	BQ710011	BQ710011 AGENCOURT
29	270.8	73.6	948	14	BQ707622	BQ707622 AGENCOURT
30	270.8	73.6	948	14	BQ709702	BQ709702 AGENCOURT
31	270.8	73.6	989	14	BQ894399	BQ894399 AGENCOURT
32	270.6	73.5	935	14	BQ707616	BQ707616 AGENCOURT
33	270.4	73.5	858	13	BM008223	BM008223 603616843
34	270.4	73.5	1007	13	BM007307	BM007307 603616509
35	270.4	73.5	1029	14	BQ709894	BQ709894 AGENCOURT
36	270.2	73.4	885	14	BQ710560	BQ710560 AGENCOURT
37	270.2	73.4	970	14	BQ711603	BQ711603 AGENCOURT
38	269.6	73.3	649	13	BM008377	BM008377 603617356
39	269.2	73.2	790	13	BM007855	BM007855 603617544
40	269.2	73.2	821	13	BM008148	BM008148 603618039
41	269.2	73.2	930	14	BQ709430	BQ709430 AGENCOURT
42	269.2	73.2	944	14	BQ712203	BQ712203 AGENCOURT
43	269.2	73.2	959	14	BQ709701	BQ709701 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS BF975791 477 bp mRNA linear EST 22-JAN-2001
DEFINITION 602246355F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4337485 5', mRNA sequence.
ACCESSION BF975791
VERSION BF975791.1 GI:12342993
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 477)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1211 row: n column: 14
High quality sequence stop: 473.
FEATURES Location/Qualifiers
source 1. .477

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4337485"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 102 a 127 c 150 g 98 t
ORIGIN

Query Match 80.8%; Score 297.4; DB 12; Length 477;
Best Local Similarity 89.5%; Pred. No. 1.3e-73;
Matches 332; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

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Db         85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| |||||| |||| |||||| ||||
Db        205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Db        325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384

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Db        385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCA 444

Qy        358 TCGTCTCCTCA 368
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Db        445 CCGTCTCCTCA 455
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RESULT 2
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LOCUS BG397239 909 bp mRNA linear EST 12-MAR-2001
DEFINITION 602439015F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565546 5',
mRNA sequence.
ACCESSION BG397239
VERSION BG397239.1 GI:13290687
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 909)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1282 row: m column: 03
High quality sequence stop: 848.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 195 a 261 c 271 g 180 t 2 others
ORIGIN

Query Match 80.8%; Score 297.4; DB 12; Length 909;
Best Local Similarity 89.5%; Pred. No. 1.8e-73;
Matches 332; Conservative 0; Mismatches 36; Indels 3; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db         85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
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Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384

Qy        301 ATTATGTTTGGGGGAGCGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              ||| |  | |    |||  |    |||  || |||  |||||||||||||||||||| |||
Db        385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCA 444

Qy        358 TCGTCTCCTCA 368
              ||||||||||
Db        445 CCGTCTCCTCA 455
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RESULT 3
BF974633
LOCUS BF974633 1012 bp mRNA linear EST 22-JAN-2001
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mRNA sequence.
ACCESSION BF974633
VERSION BF974633.1 GI:12341848
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1012)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

```
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1204  row: m  column: 15
            High quality sequence stop: 716.
FEATURES             Location/Qualifiers
     source          1. .1012
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4334774"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      236 a    299 c    300 g    176 t      1 others
ORIGIN

  Query Match             80.8%;  Score 297.4;  DB 12;  Length 1012;
  Best Local Similarity   89.5%;  Pred. No. 1.9e-73;
  Matches  332;  Conservative    0;  Mismatches   36;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db         85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db        145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 204

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        265 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 324

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384

Qy        301 ATTATGTTTGGGGGGAGCGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
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Db        385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCA 444

Qy        358 TCGTCTCCTCA 368
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Db        445 CCGTCTCCTCA 455


RESULT 4
BQ706226
LOCUS       BQ706226                959 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8474971 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301349
            5', mRNA sequence.
ACCESSION   BQ706226
VERSION     BQ706226.1  GI:21845125
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 959)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2517  row: b  column: 06
            High quality sequence stop: 647.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6301349"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      205 a    298 c    281 g    170 t      5 others
ORIGIN

  Query Match             78.2%;  Score 287.8;  DB 14;  Length 959;
  Best Local Similarity   87.9%;  Pred. No. 9.5e-71;
  Matches  326;  Conservative    0;  Mismatches   42;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        107 AGGTCCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTCT 166

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db        167 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCCATGGTATCAGCTGGGTGCGACAGGCCC 226

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        227 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGCTACAGCAAAGTACG 286

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        287 CACAGAAGTTCCAGGGTAGAGTCACGATTAGTGCGGACGAATCCACGAGCACAGCCTACA 346

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        347 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTATATTATTGTGCGAGAGTGCCCC 406

Qy        301 ATTATGTTTGG---GGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              |   | | ||   || |       |||||||||||||||||||||||||||||| |||
Db        407 GTATGGGTCGGGGAGGTATATCGGGCTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA 466

Qy        358 TCGTCTCCTCA 368
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Db        467 CCGTCTCCTCA 477


RESULT 5
BG754936
LOCUS       BG754936                903 bp    mRNA    linear   EST 15-MAY-2001
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DEFINITION  602711631F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852039 5',
            mRNA sequence.
ACCESSION   BG754936
VERSION     BG754936.1  GI:14065589
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1695  row: n  column: 08
            High quality sequence stop: 813.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      200 a    260 c    270 g    172 t      1 others
ORIGIN

  Query Match           77.8%;  Score 286.4;  DB 12;  Length 903;
  Best Local Similarity   89.2%;  Pred. No. 2.3e-70;
  Matches  332;  Conservative    0;  Mismatches   36;  Indels    4;  Gaps    2;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db         85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGG-CC 119
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Db        145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGTCC 204

Qy        120 CCTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTAC 179
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Db        205 CCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTAC 264

Qy        180 GCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTAC 239
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        265 GCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTAC 324

Qy        240 ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCC 299
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Db        325 ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGA 384

Qy        300 GATTATGTTTGGGGGAGCGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTC 356
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Db        385 TATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 444

Qy        357 ATCGTCTCCTCA 368
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Db        445 ACCGTCTCCTCA 456


RESULT 6
BG758459
LOCUS       BG758459                878 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602712658F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852934 5',
            mRNA sequence.
ACCESSION   BG758459
VERSION     BG758459.1  GI:14069112
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 878)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1698  row: c  column: 15
            High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1. .878
                     /organism="Homo sapiens"
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                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      196 a    258 c    246 g    177 t      1 others
ORIGIN

  Query Match           77.6%;  Score 285.4;  DB 12;  Length 878;
  Best Local Similarity   89.2%;  Pred. No. 4.3e-70;
  Matches  331;  Conservative    0;  Mismatches   36;  Indels    4;  Gaps    2;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db         85 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db        145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 204

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 264

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        265 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 324

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        325 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAGAT 384

Qy        301 ATTATGTTTGGGGGAGCGAC---AACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
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Db        385 ATTGTAGTAGTACCAGCTGCCTGTACTACTTTGACTACTGGGGCCA-GGAACCCTGGTCA 443

Qy        358 TCGTCTCCTCA 368
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Db        444 CCGTCTCCTCA 454


RESULT 7
BQ706171
LOCUS       BQ706171                903 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8354485 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281064
            5', mRNA sequence.
ACCESSION   BQ706171
VERSION     BQ706171.1  GI:21845070
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2473  row: e  column: 01
            High quality sequence stop: 576.
FEATURES             Location/Qualifiers
     source          1. .903
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      202 a    272 c    246 g    181 t      2 others
ORIGIN

  Query Match           77.4%;  Score 284.8;  DB 14;  Length 903;
  Best Local Similarity   87.8%;  Pred. No. 6.5e-70;
  Matches  323;  Conservative    0;  Mismatches   42;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        102 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 161

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        162 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 221

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              ||||||||||||||||||||||| ||||||| |||||| ||||    ||||| ||||
Db        222 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACGGCAAACTACG 281

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        282 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 341

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        342 TGGAGCTGAACAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGTGGGGA 401

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              |       |    ||   |      ||| |||  |||||||||||||||||| ||| ||
Db        402 ACACACCTCCTTGGTTTG---GTGTGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCG 458

Qy        361 TCTCCTCA 368
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Db        459 TCTCCTCA 466


RESULT 8
BQ881378
LOCUS       BQ881378                1035 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8642770 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6295574
            5', mRNA sequence.
ACCESSION   BQ881378
VERSION     BQ881378.1  GI:22273386
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1035)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2502  row: a  column: 15
            High quality sequence start: 71
            High quality sequence stop: 599.
FEATURES             Location/Qualifiers
     source          1. .1035
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6295574"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      219 a    340 c    276 g    196 t      4 others
ORIGIN

  Query Match           76.9%;  Score 283;  DB 14;  Length 1035;
  Best Local Similarity   87.1%;  Pred. No. 2.3e-69;
  Matches  323;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        164 AGGTCCACCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGAAGGTCT 223

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        284 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGCTACATCAAAGTACG 343

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||.|||||| |||||||||||||   |||||| |||| ||||||||||||||||
Db        344 CACAGAAGTTCCAGGGTAGAGTCACGATTAGTGCGGACGAATCTACGAGCACAGCCTACA 403

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||| |||||||||||||||||||||||| ||||| ||||||||||   |||
Db        404 TGGAGCTGAGCACCCTGAGATCTGAGGACACGGCCGTATATTATTGTGCGAGAGTGCCCC 463

Qy        301 ATTATGTTTGG---GGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              |  | | ||   || |       |||||||||||||||||||||||||||||| |||
Db        464 GTATGGGTCGGGGAGGTATATCGGGCTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCA 523

Qy        358 TCGTCTCCTCA 368
              ||||||||||
Db        524 CCGTCTCCTCA 534
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RESULT 9
BQ708591
LOCUS BQ708591 980 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7977406 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6216047 5', mRNA sequence.
ACCESSION BQ708591
VERSION BQ708591.1 GI:21847477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 980)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2385 row: o column: 24
High quality sequence start: 24
High quality sequence stop: 594.
FEATURES Location/Qualifiers
source 1. .980
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6216047"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 224 a 311 c 276 g 169 t
ORIGIN

Query Match 76.7%; Score 282.4; DB 14; Length 980;
Best Local Similarity 87.8%; Pred. No. 3.2e-69;
Matches 323; Conservative 0; Mismatches 36; Indels 9; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         58 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 117

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db        118 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATACTATCAACTGGGTGCGACAGGCCC 177

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||| |||||  ||| ||  |||   | | || ||||
Db        178 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCTCCCCTGTCTCTGGTGCAACCAACTACG 237

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||||| |||| ||||||||| |||||
Db        238 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCGACGAGCACAGTCTACA 297

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||| |||||||||||||||||||||||||||||||| ||||||||||||||  ||
Db        298 TGGAGTTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTTTTACTGTGCGAGAGATAACG 357

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              | ||||  |          |  |||| ||| |||||||||||||||||| ||| ||
Db        358 ACTATGAACG---------AATTGGGTTTGACTCCTGGGGCCAGGGAACCCTGGTCACCG 408

Qy        361 TCTCCTCA 368
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Db        409 TCTCCTCA 416
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RESULT 10
BQ710257
LOCUS BQ710257 991 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7976230 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214702 5', mRNA sequence.
ACCESSION BQ710257
VERSION BQ710257.1 GI:21849156
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 991)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2382 row: g column: 23
High quality sequence stop: 587.
FEATURES Location/Qualifiers
source 1. .991
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6214702"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 221 a 310 c 264 g 196 t
ORIGIN

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  Query Match           76.5%;  Score 281.6;  DB 14;  Length 991;
  Best Local Similarity   86.6%;  Pred. No. 5.5e-69;
  Matches  324;  Conservative    0;  Mismatches   44;  Indels    6;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         94 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 153

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        154 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 213

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| | ||||| |||||| ||||   |||||| ||||
Db        214 CTGGACAAGGGCTTGAGTGGATGGGAGGAATCATCCCTATCTTTGGTACAGCAAACTACG 273

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||||
Db        274 CACAGAAGTTCCAGGGCAGAGTCACGATTATCGCGGACGAATCCACGAGCACAGCCTACA 333

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||   |
Db        334 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACATTACT 393

Qy        301 ATTAT------GTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
              ||  |      ||  |    |   |  ||||| | ||||||||  || ||||||
Db        394 ATGGTTCGGGGAGTTATAGAGAATATTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGG 453

Qy        355 TCATCGTCTCCTCA 368
              |||  |||||||||
Db        454 TCACTGTCTCCTCA 467
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RESULT 11
BQ706539
LOCUS       BQ706539                970 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8487914 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300622
            5', mRNA sequence.
ACCESSION   BQ706539
VERSION     BQ706539.1  GI:21845438
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 970)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2515  row: c  column: 23
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .970
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6300622"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      204 a    312 c    273 g    178 t      3 others
ORIGIN
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  Query Match           75.8%;  Score 279;  DB 14;  Length 970;
  Best Local Similarity   86.9%;  Pred. No. 3e-68;
  Matches  319;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||| |||||||||||||||||||||||||||| |||||||
Db         91 AGGTCCAGCTGGTGCAGTCTGGGACTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 150

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| |  ||| ||||||||||||||||||||||||
Db        151 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC 210

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||| ||||||| |||||| |  |  ||||||||||
Db        211 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTACGTACAGCAAATTACG 270

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||| |||| |||||||||||||||||||||||| ||||||||||||||||||||
Db        271 CACAGAATTTCCTGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 330

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||| |||||||||||||||||||||||| |  |  |
Db        331 TGGAGCTGAGCAGCCTGAGATCTGAAGACACGGCCGTGTATTACTGTGCGAGGGGCCGGG 390

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                | ||| |||    |          | |||  ||||||||||||||||| |||| |
Db        391 ---AAGTTGGGGTTCTCTCGTCGGCCGTTGACTACTGGGGCCAGGGAACCCTGATCATTG 447

Qy        361 TCTCCTC 367
              |||||||
Db        448 TCTCCTC 454
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RESULT 12
AW408371
LOCUS       AW408371                417 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-abk-c-03-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3056620 5', mRNA sequence.
ACCESSION   AW408371
VERSION     AW408371.1  GI:6927428
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 417)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .417
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3056620"
                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
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/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 91 a 106 c 130 g 90 t
ORIGIN

Query Match 75.8%; Score 278.8; DB 10; Length 417;
Best Local Similarity 88.5%; Pred. No. 2.2e-68;
Matches 317; Conservative 0; Mismatches 32; Indels 9; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         60 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 119

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||  || ||| ||||||||||||||||||||||||
Db        120 CCTGCAAGGCTTCTGGAGGCACCTTCACCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 179

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||| ||||||| |||||  |||||| ||||
Db        180 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATTCCTATCTTTGGTACAGCAAACTACG 239

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||| |||||||||||| ||||||||||||||||||||||
Db        240 CACAGAAGTTCCAGGGCAGAGTCACCATTACCGCGGACGAATCCACGAGCACAGCCTACA 299

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        300 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGCCAAT 359

Qy        301 ATTATG---------TTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAAC 349
              ||  |         | |  | |  ||||||||||||||||||||||||||||||||
Db        360 TTTTAGATATTTTGACTGGTTACAACCTCAACTGGTTCGACCCCTGGGGCCAGGGAAC 417
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RESULT 13
BQ708380
LOCUS BQ708380 884 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7983360 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215351 5', mRNA sequence.
ACCESSION BQ708380
VERSION BQ708380.1 GI:21847279
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 884)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2384 row: b column: 24
High quality sequence stop: 631.
FEATURES Location/Qualifiers
source 1. .884
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6215351"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 185 a 291 c 246 g 162 t
ORIGIN

Query Match 75.3%; Score 277.2; DB 14; Length 884;
Best Local Similarity 86.7%; Pred. No. 9.1e-68;
Matches 319; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||| || | |||||
Db         85 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGACGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| |  || ||||||| ||||||||||||||||||
Db        145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACAATGCTATCAGTTGGGTGCGACAGGCCC 204

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||| ||||||| || ||| |||    |||||| ||||
Db        205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCCATCTTTGGTTCAGCAAACTACG 264

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              | |||| ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        265 CTCAGAGGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 324

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||| ||||| |||||| |||||||||||||||||||||||||||||||||||||  ||
Db        325 TGGAGTTGAGCGGCCTGACATCTGAGGACACGGCCGTGTATTACTGTGCGCGA------C 378

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              |     ||       ||||||||||||||||||||||||||||||||||||| ||| ||
Db        379 GTGGAAGCCCGGAACAGCACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 438

Qy        361 TCTCCTCA 368
              ||||||||
Db        439 TCTCCTCA 446
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RESULT 14
BQ711877
LOCUS BQ711877 937 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7975529 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215114 5', mRNA sequence.
ACCESSION BQ711877
VERSION BQ711877.1 GI:21850776
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 937)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2383 row: i column: 03
High quality sequence stop: 516.
FEATURES Location/Qualifiers
source 1. .937

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6215114"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 222 a 279 c 266 g 170 t
ORIGIN

Query Match 75.3%; Score 277.2; DB 14; Length 937;
Best Local Similarity 86.7%; Pred. No. 9.4e-68;
Matches 319; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||| || | |||||
Db         85 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCAGTGACGGTCT 144

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| |   || ||||||| ||||||||||||||||
Db        145 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACAATGCTATCAGTTGGGTGCGACAGGCCC 204

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| || ||| ||||   |||||| ||||
Db        205 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCCATCTTTGGTTCAGCAAACTACG 264

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              | |||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        265 CTCAGAGGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 324

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||| ||||| |||||| |||||||||||||||||||||||||||||| ||
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Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
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Db        379 GTGGAAGCCCGGAACAGCACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCG 438

Qy        361 TCTCCTCA 368
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Db        439 TCTCCTCA 446
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RESULT 15
AW401468
LOCUS AW401468 418 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BK0-aad-f-06-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053339 5', mRNA sequence.
ACCESSION AW401468
VERSION AW401468.1 GI:6920051
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 418)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES Location/Qualifiers
source 1. .418
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3053339"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 95 a 117 c 122 g 84 t
ORIGIN

Query Match 75.2%; Score 276.6; DB 10; Length 418;
Best Local Similarity 86.0%; Pred. No. 9.3e-68;
Matches 319; Conservative 0; Mismatches 49; Indels 3; Gaps 1;

```
Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db         15 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGATCCTCGGTGAAGGTCT 74

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Db        135 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGATATAACAAACTACG 194

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Db       -195 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCGACGAGCACAGGCTACA 254

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||
Db        255 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACTTCGTT 314

Qy        301 ATTATGTTTGGG---GGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              |  |    | |      | || |||   | |||  ||||||| | || |||  | |||
Db        315 ACAGTAACCGCGACTACTTCTACTACTACATGGACGTCTGGGGCAAAGGGACCACGGTCA 374

Qy        358 TCGTCTCCTCA 368
              ||||||||||
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Job time : 639.709 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:14:58 ; Search time 95.4001 Seconds
(without alignments)
8686.944 Million cell updates/sec

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Perfect score: 368
Sequence: 1 aggtgcagctggtgcagtct.....ccctgctcatcgtctcctca 368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	293.2	79.7	2287	13	AAQ25443	Sequence encoding
2	293.2	79.7	2287	18	AAT60739	IgG1 gene. Homo s
3	289.6	78.7	378	22	AAF29080	Human HIV-1 monocl
4	286.4	77.8	747	21	AAC67868	Recombinant human
5	284.8	77.4	354	21	AAA48411	Human LH13 monoclo
6	282.8	76.8	1517	22	AAF29714	G71-1 immunoconjug
7	280.8	76.3	812	13	AAQ22419	Human heavy chain
8	280.8	76.3	812	14	AAQ44185	Human heavy chain
9	280.8	76.3	812	17	AAT37243	DNA fragment vh49.
10	280.8	76.3	812	18	AAV12538	Human VHI family g
11	280.8	76.3	812	18	AAT70522	Human immunoglobul
12	280.8	76.3	812	18	AAT73471	Human VH1 gene VH4
13	280.8	76.3	812	20	AAZ21897	Nucleotide sequenc
14	280.8	76.3	812	20	AAX06042	Sequence of human
15	278.6	75.7	294	16	AAQ89328	HV1263 VH gene. H
16	277.6	75.4	495	21	AAC98082	Human colon cancer
17	275.8	74.9	375	22	AAS03455	DNA encoding anti-
18	275.2	74.8	488	21	AAZ42325	Human 5' EST isola
19	274.8	74.7	354	15	AAX79685	Human cancer cell
20	274	74.5	1599	24	ABK64550	Human benign prost
21	274	74.5	1599	24	ABL62673	Colon adenocarcino
22	274	74.5	1599	24	ABL65479	Lung cancer relate
23	274	74.5	1599	24	ABL66294	Lung cancer relate
24	273.8	74.4	294	16	AAQ89327	DP10 VH gene. Hom
25	273.4	74.3	360	22	AAS03466	DNA encoding anti-
26	273.2	74.2	295	21	AAZ43860	Human anti-factor
27	273.2	74.2	357	22	AAS03456	DNA encoding anti-
28	272.8	74.1	369	18	AAT72131	CEA-specific antib
29	272.4	74.0	1617	14	AAQ35099	Antibody D heavy c
30	272.2	74.0	1884	24	ABA05279	Human Ig-M heavy c
c 31	272	73.9	3229	22	AAS22828	Human cDNA encodin
c 32	272	73.9	3229	22	AAS22829	Human cDNA encodin
33	269.2	73.2	363	22	AAS03498	DNA encoding anti-
34	268.8	73.0	3229	22	AAS22828	Human cDNA encodin
35	268.8	73.0	3229	22	AAS22829	Human cDNA encodin
36	266.6	72.4	492	21	AAC00054	Human secreted pro
37	266.4	72.4	786	20	AAX05452	CEA6 antibody sing
38	266	72.3	363	22	AAS03473	DNA encoding anti-
39	265.6	72.2	354	22	AAH26788	Anti-human CD154 a
40	265.4	72.1	396	24	AAK98400	Humanised murine a
41	265.4	72.1	782	24	AAK98405	Anti-FAPalpha anti
42	264.6	71.9	366	20	AAV72234	Human anti-GPIIb/I
43	264.2	71.8	378	22	AAS03450	DNA encoding anti-
44	263.4	71.6	342	21	AAZ43867	Human FVIII antibo
45	260	70.7	425	21	AAC00055	Human secreted pro

ALIGNMENTS

RESULT 1
AAQ25443
ID AAQ25443 standard; DNA; 2287 BP.
XX
AC AAQ25443;
XX
DT 02-JAN-1992 (first entry)
XX
DE Sequence encoding antibody molecule IgG1.
XX
KW Antibody; immunoglobulin G1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT exon 1..453
FT /*tag= a
FT exon 619..972
FT /*tag= b
FT exon 1361..1405
FT /*tag= c
FT exon 1524..1853
FT /*tag= d
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XX
PN WO9209293-A.
XX
PD 11-JUN-1992.
XX
PF 18-NOV-1991; 91WO-US08605.
XX

PR 23-NOV-1990; 90US-0618314.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Seed B, Walz G;
XX
DR WPI; 1992-216789/26.
DR P-PSDB; AAR24442.
XX
PT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
PT - used in treating chronic inflammation, rheumatoid arthritis,
PT psoriasis, etc.
XX
PS Disclosure; Fig 1; 46pp; English.
XX
CC The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
CC inventors designed a molecule including several such sites for
CC attachment of sialyl-Lex side chains (see AAR24442, FT). The
CC additional N-linked glycosylation sites are introduced at locations
CC which impair complement fixing and Fc receptor binding ability. They
CC are preferably located in the CH2 region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for
CC disrupting undesirable interactions between cells or proteins.
CC Disrupting this interaction has therapeutic applications, for
CC example, in minimising inflammation following tissue injury.
XX
SQ Sequence 2287 BP; 483 A; 753 C; 652 G; 399 T; 0 other;

Query Match 79.7%; Score 293.2; DB 13; Length 2287;
Best Local Similarity 88.2%; Pred. No. 5.6e-75;
Matches 335; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

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Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
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              |||||||||||||||||||||||||| ||||||| |||||| |||| |||||| ||||
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              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy        301 ------------ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                         |  || | |  |    |      ||||||||||||||||||||||||||
Db        374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy        349 CCCTGCTCATCGTCTCCTCA 368
              ||||| ||| |||||| |||
Db        434 CCCTGGTCACCGTCTCTTCA 453
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RESULT 2
AAT60739
ID AAT60739 standard; DNA; 2287 BP.
XX
AC AAT60739;
XX
DT 22-APR-1997 (first entry)
XX
DE IgG1 gene.
XX
KW IgG1; P-selectin ligand; PSGL-1; counter-receptor; E-selectin;
KW sialyl-Lewis X; antiinflammatory; inflammation;
KW extravasation-dependent adverse reaction; organ damage; clotting;
KW adult respiratory distress syndrome; glomerular nephritis;
KW ischaemic myocardial injury; immune reaction; septic shock;
KW septicaemia; therapy; diagnosis; ds.
XX
OS Homo sapiens.
XX
PN WO9700079-A1.
XX
PD 03-JAN-1997.
XX
PF 11-JUN-1996; 96WO-US10043.
XX
PR 14-JUN-1995; 95US-0000213.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Pouyani T, Seed B;
XX
DR WPI; 1997-077356/07.
DR P-PSDB; AAW10550.
XX
PT P-selectin and opt. E-selectin binding organic mol. - having
PT sialyl-Le(x) and sulphated determinant, useful for protecting
PT against inflammatory or immune reactions
XX
PS Disclosure; Page 40-41; 81pp; English.
XX
CC The gene (AAT60739) encoding IgG1 (AAW10550) can be subjected to site-
CC directed mutagenesis in order to introduce one or more N-linked
CC glycan addition sites into the IgG1 molecule (see also AAW10551).
CC Eukaryotic host cells co-transfected with a vector carrying the
CC the mutated IgG1 gene and with a vector that expresses an alpha-
CC (1,3)fucosyltransferase capable of attaching sialyl-Le(x) groups at
CC the glycosylation sites of the antibody molecule can be used in the
CC prodn. of sialyl-Le(x)-modified antibody. Such an antibody has
CC therapeutic applns., e.g. in minimising inflammation and
CC decreasing extravasation-dependent organ damage and/or clotting.
XX
SQ Sequence 2287 BP; 483 A; 758 C; 648 G; 398 T; 0 other;

Query Match 79.7%; Score 293.2; DB 18; Length 2287;
Best Local Similarity 88.2%; Pred. No. 5.6e-75;
Matches 335; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 193

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||| |||| |||||| ||||
Db        194 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy        301 ------------ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                         |  || | |  |    |      ||||||||||||||||||||||||||
Db        374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy        349 CCCTGCTCATCGTCTCCTCA 368
              ||||| ||| |||||| |||
Db        434 CCCTGGTCACCGTCTCTTCA 453
```

```
RESULT 3
AAF29080
ID   AAF29080 standard; DNA; 378 BP.
XX
AC   AAF29080;
XX
DT   03-APR-2001  (first entry)
XX
DE   Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 36.
XX
KW   Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW   envelope glycoprotein; gp120; diagnosis; ds.
XX
OS   Homo sapiens.
XX
PN   WO200100678-A1.
XX
PD   04-JAN-2001.
XX
PF   23-JUN-2000; 2000WO-US17327.
XX
PR   30-JUN-1999;   99US-0141701.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Watkins BA,  Reitz MS;
XX
DR   WPI; 2001-112438/12.
DR   P-PSDB; AAB62779.
XX
PT   Novel human monoclonal antibody immunoreactive with human
PT   immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
PT   in biological sample and providing passive immunotherapy to HIV-1
PT   infected mammal  -
XX
PS   Claim 4; Page 47; 81pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   variable regions of human monoclonal antibodies which are immunoreactive
CC   with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC   These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ   Sequence 378 BP; 81 A; 93 C; 122 G; 82 T; 0 other;

  Query Match             78.7%;  Score 289.6;  DB 22;  Length 378;
  Best Local Similarity   88.0%;  Pred. No. 3.9e-74;
  Matches  329;  Conservative    0;  Mismatches   39;  Indels    6;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db          5 AGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 64

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
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Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        125 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTATAGCAAACTACG 184

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        185 CACAGAAGTTCCAGGGCAGAGTCTCGATTACCGCGGACAAATCCACGAGCACAGCCTACA 244

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG------ 294
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Qy        295 ATCCCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
              |       | || | | |  | |.|  |  || |||  ||||||||||||||||||
Db        305 GTATGACGATTTTTGGAGTGGTCTCCACGTTCTTTGACTACTGGGGCCAGGGAACCCTGG 364

Qy        355 TCATCGTCTCCTCA 368
              ||| ||||||||||
Db        365 TCACCGTCTCCTCA 378


RESULT 4
AAC67868
ID   AAC67868 standard; DNA; 747 BP.
XX
AC   AAC67868;
XX
DT   16-FEB-2001  (first entry)
XX
DE   Recombinant human antibody scFv TN11 nucleotide sequence.
XX
KW   Human; antibody scFv; TN11; Tenascin-C; TN-C; domain C-containing TNC;
KW   cTN-C; ds.
XX
OS   Homo sapiens.
XX
PN   WO200063699-A1.
XX
PD   26-OCT-2000.
XX
PF   19-APR-2000; 2000WO-EP03550.
XX
PR   20-APR-1999;   99IT-FI00094.
XX
PA   (PHIL-) PHILOGEN SRL.
XX
PI   Zardi L;
XX
DR   WPI; 2000-687225/67.
DR   P-PSDB; AAB36083.
XX
PT   Ligands used for diagnosis and treatment of human neoplasias, are
PT   capable of identifying the tenascin-C isoform containing domain C of
PT   tenascin-C -
XX
PS   Claim 8; Page 5-6; 31pp; English.
XX
CC   The present sequence encodes a recombinant human antibody scFv. Antibody
CC   TN11 reacts with the long form of human Tenascin-C (TN-C). The epitope
CC   recognised by TN11 is located inside domain C of TN-C. TN11 is therefore
CC   only capable of recognising TN-C isoforms containing domain C (cTN-C).
CC   TN11 is useful for detecting the presence of TN-C isoforms in vitro or
CC   in vivo for diagnosing pathologies expressing the cTN-C isoforms of TN-C.
CC   It is useful for the preparation of formulations for the treatment of
CC   human neoplasias.
XX
SQ   Sequence 747 BP; 157 A; 197 C; 231 G; 162 T; 0 other;

  Query Match             77.8%;  Score 286.4;  DB 21;  Length 747;
  Best Local Similarity   86.1%;  Pred. No. 3.9e-73;
  Matches  317;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGATCGAGAC 301

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                | |         | |       |||||   |||||||  || ||| || ||| ||
Db        302 GTATTACGATTTTTGGAGGAGGTGCTTTCGATATCTGGGGCCGAGGCACCATGGTCACCG 361

Qy        361 TCTCCTCA 368
                |||| |||
Db        362 TCTCTTCA 369


RESULT 5
AAA48411
ID   AAA48411 standard; cDNA; 354 BP.
XX
AC   AAA48411;
XX
DT   20-SEP-2000  (first entry)
XX
DE   Human LH13 monoclonal antibody heavy chain variable region cDNA.
XX
KW   Human; LH13 monoclonal antibody; hybridoma; tumour-specific; cancer;
KW   cytostatic; cytotoxic; heavy chain variable region; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..354
FT                   /*tag=  a
FT                   /partial
FT                   /product= "LH13 antibody heavy chain variable region"
XX
PN   WO200032635-A2.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US28485.
XX
PR   02-DEC-1998;   98US-0203768.
XX
PA   (IXSY-) IXSYS INC.
XX
PI   Watkins JD,  Huse WD;
XX
DR   WPI; 2000-412293/35.
DR   P-PSDB; AAY99558.
XX
PT   New tumor-specific human monoclonal antibody, useful for the treatment
PT   and diagnosis of cancer, comprises at least one complementarity
PT   determining region -
XX
PS   Claim 16; Page 82; 84pp; English.
XX
CC   The present sequence encodes the heavy chain variable region of a human
CC   tumour-specific monoclonal antibody. Neoplastic cells selectively express
CC   antigens which are not present on normal cells. Thus monoclonal
CC   antibodies can be produced that are specifically directed against
CC   tumour-specific antigens. The antibodies can be conjugated to cytotoxic
CC   or cytostatic agents and used to selectively target cancer cells for the
CC   elimination of tumours. They can also be linked to diagnostic moieties
CC   that allow the imaging of neoplastic cells. Nucleic acids encoding human
CC   tumour-specific monoclonal antibodies can be used to express the
CC   antibodies and can be recombinantly engineered to produced modified
CC   antibodies with higher affinity or higher selectivity for tumour cells.
CC   Tumour-specific antibodies were produced by hybridomas that were
CC   generated by in vitro immunisation of human spleen cell cultures with
CC   breast carcinoma cells. The nucleic acid encoding the monoclonal antibody
CC   was then isolated from the hybridoma by RT-PCR. The present sequence
CC   encodes a human monoclonal antibody heavy chain variable region which was
CC   produced by LH13 hybridoma cell line.
XX
SQ   Sequence 354 BP; 80 A; 90 C; 115 G; 69 T; 0 other;

  Query Match             77.4%;  Score 284.8;  DB 21;  Length 354;
  Best Local Similarity   88.6%;  Pred. No. 9.5e-73;
  Matches  326;  Conservative    0;  Mismatches   27;  Indels   15;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| ||||| ||||  |||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGA----- 296

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                          | |||     |||||   ||  |||||||||||||||||| ||| ||
Db        297 ----------AGATAGCAGTGGCTGGTATCACTACTGGGGCCAGGGAACCCTGGTCACCG 346

Qy        361 TCTCCTCA 368
                ||||||||
Db        347 TCTCCTCA 354


RESULT 6
AAF29714
ID   AAF29714 standard; DNA; 1517 BP.
XX
AC   AAF29714;
XX
DT   05-APR-2001  (first entry)
XX
DE   G71-1 immunoconjugate coding sequence.
XX
KW   Mouse; scFv; immunoconjugate; IgG1 effector domain; cancer;
KW   atherosclerosis; tissue factor; macular degeneration;
KW   rheumatoid arthritis; ds.
XX
OS   Synthetic.
XX
PN   WO200102439-A1.
XX
PD   11-JAN-2001.
XX
PF   14-JUN-2000; 2000WO-US16481.
XX
PR   01-JUL-1999;   99US-0142161.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Garen A;
XX
DR   WPI; 2001-123105/13.
XX
PT   Immunoconjugate protein for treatment of neovascularization, comprises
PT   protein comprising Fc region of human immunoglobulin (Ig)GI conjugated
PT   to the targeting domain which comprises factor VII mutant -
XX
PS   Example 2; Page 65-66; 69pp; English.
XX
CC   The present invention provides a composition comprising a homodimeric
CC   immunoconjugate protein made up of two chains, each containing an IgG1 Fc
CC   effector domain and a targeting domain. The targeting domain may be
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CC   either the human IgG1 Fc region or a mutant form of human factor VII. The
CC   immunoconjugate is targeted at the transmembrane receptor tissue factor.
CC   This enables the composition to be used in the treatment of diseases
CC   associated with neovascularisation, including cancer, atherosclerosis,
CC   rheumatoid arthritis and macular degeneration.
XX
SQ   Sequence 1517 BP; 338 A; 444 C; 441 G; 294 T; 0 other;

  Query Match            76.8%;  Score 282.8;  DB 22;  Length 1517;
  Best Local Similarity  88.0%;  Pred. No. 5.2e-72;
  Matches  324;  Conservative    0;  Mismatches   32;  Indels   12;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         65 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 124

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        125 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 184

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        185 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 244

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 304

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA------- 357

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              |   | |||||  |  |    || ||   |||||||| ||||| ||| ||| ||
Db        358 -----GGAGGAGGGAGATATGATGCTTTTGATATCTGGGGCCAAGGAACACTGGTCACCG 412

Qy        361 TCTCCTCA 368
              |||| |||
Db        413 TCTCTTCA 420


RESULT 7
AAQ22419
ID   AAQ22419 standard; DNA; 812 BP.
XX
AC   AAQ22419;
XX
DT   17-AUG-1992  (first entry)
XX
DE   Human heavy chain V region gene VH49.8.
XX
KW   Heavy chain; variable region; VH1 family; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..286
FT                   /*tag=  a
FT   intron          287..373
FT                   /*tag=  b
FT   exon            373..812
FT                   /*tag=  c
FT   CDS             241..689
FT                   /*tag=  d
FT   misc_recomb     678..686
FT                   /*tag=  e
FT                   /note= "recombination signal"
FT   misc_recomb     709..718
FT                   /*tag=  f
FT                   /note= "recombination signal"
XX
PN   WO9203918-A.
XX
PD   19-MAR-1992.
XX
PF   28-AUG-1991;   91WO-US06185.
XX
PR   31-AUG-1990;   90US-0575962.
PR   29-AUG-1990;   90US-0574748.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Kay R;
XX
DR   WPI; 1992-113962/14.
DR   P-PSDB; AAR22358.
XX
PT   Immunoglobulin trans:genes - for prodn. of heterologous
PT   non-rearranged and/or rearranged Ig chains
XX
PS   Example 14; Page 87; 172pp; English.
XX
CC   The human placental genomic DNA library cloned into the phage
CC   vector lambda FIX II was screened with the human VH1 family
CC   specific oligonucleotide (see AAQ22418).  Phage clone lambda
CC   49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
CC   segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
CC   An 800 bp region of this insert was sequenced.  VH49.8 was found
CC   to have an open reading frame and intact splicing and recombination
CC   signals, thus indicating that the gene is functional.
CC   See also AAQ23419-49, AAQ22417-30.
XX
SQ   Sequence 812 BP; 204 A; 189 C; 222 G; 197 T; 0 other;

  Query Match            76.3%;  Score 280.8;  DB 13;  Length 812;
  Best Local Similarity  96.0%;  Pred. No. 1.7e-71;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||| |||||||||||  ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 8
AAQ44185
ID   AAQ44185 standard; DNA; 812 BP.
XX
AC   AAQ44185;
XX
DT   10-NOV-1993  (first entry)
XX
DE   Human heavy chain V region gene VH49.8.
XX
KW   Immunoglobulin; IgG; heavy chain; minilocus transgene;
KW   isotype switching; H chain variable region; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            1..286
```

```
FT                   /*tag=  a
FT                   /number= 1
FT   intron          287..372
FT                   /*tag=  b
FT                   /number= 1
FT   exon            373..812
FT                   /*tag=  c
FT                   /number= 2
FT   CDS             241..689
FT                   /*tag=  d
FT                   /note= "CDS is interrupted by intron #1; the
FT                          last three codons of the CDS are not
FT                          translated in the amino acid sequence
FT                          AAR38623"
XX
PN   WO9312227-A.
XX
PD   24-JUN-1993.
XX
PF   17-DEC-1992;   92WO-US10983.
XX
PR   17-DEC-1991;   91US-0810279.
PR   18-MAR-1992;   92US-0853408.
PR   23-JUN-1992;   92US-0904068.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM,  Lonberg N;
XX
DR   WPI; 1993-214169/26.
DR   P-PSDB; AAR38623.
XX
PT   Transgenic non-human animals contg. immunoglobulin heavy chain
PT   trans gene - used to produce useful antibodies by isotype
PT   switching
XX
PS   Example 12; Page 96; 196pp; English.
XX
CC   A human placental genomic DNA library cloned into the phage vector
CC   lambda FIX II was screened with the human VH1 family specific
CC   oligonucleotide AAQ44184. Phage clone lambda 49.8 was isolated and a
CC   6.1kb XbaI fragment containing the variable segment VH49.8 was
CC   subcloned into pNNO3 to generate plasmid pVH49.8. An 800bp
CC   region of this insert was sequenced (AAQ44185) and VH49.8 found to
CC   have an open reading frame and intact splicing and recombination
CC   signals, indicating that the gene is functional.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

  Query Match             76.3%;  Score 280.8;  DB 14;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||| ||||||||||  ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||  | | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
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```
RESULT 9
AAT37243
ID   AAT37243 standard; DNA; 812 BP.
XX
AC   AAT37243;
XX
DT   21-APR-1997  (first entry)
XX
DE   DNA fragment vh49.8, containing variable heavy chain gene.
XX
KW   Variable; heavy chain; gene segment; human; DNA fragment; vh49.8;
KW   unrearranged; minilocus; transgene; transgenic; mouse;
KW   production; heterologous; antibody; gamma; immunoglobulin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            241..286
FT                   /*tag=  a
FT   exon            373..677
FT                   /*tag=  b
XX
PN   US5545806-A.
XX
PD   13-AUG-1996.
XX
PF   29-AUG-1990;   90US-0574748.
XX
PR   16-DEC-1992;   92US-0990860.
PR   29-AUG-1990;   90US-0574748.
PR   31-AUG-1990;   90US-0575962.
PR   17-DEC-1991;   91US-0810279.
PR   18-MAR-1992;   92US-0853408.
PR   23-JUN-1992;   92US-0904068.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM,  Lonberg N;
XX
DR   WPI; 1996-383736/38.
DR   P-PSDB; AAW03950.
XX
PT   Prodn. of heterologous human immunoglobulin(s) - by immunising
PT   transgenic mice
XX
PS   Example 12; Columns 61-62; 94pp; English.
XX
CC   The present sequence is the variable heavy chain gene segment
CC   containing human DNA fragment, vh49.8, which was injected into half
CC   day mouse embryo pronuclei, to generate an unrearranged heavy chain
CC   minilocus transgene. The resulting transgenic mice can be used for
CC   the production of heterologous (i.e. human) antibodies against
CC   specific antigens, this comprises immunising a mouse with a
CC   preselected antigen and collecting antigen binding heterologous
CC   human gamma immunoglobulins.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

  Query Match             76.3%;  Score 280.8;  DB 17;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||| ||||||||||  ||||||| ||||
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```
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
```

RESULT 10
AAV12538
ID AAV12538 standard; DNA; 812 BP.
XX
AC AAV12538;
XX
DT 26-MAY-1998 (first entry)
XX
DE Human VHI family gene VH49.8.
XX
KW Transgenic mouse; human; immunoglobulin; heavy chain segment; J region;
KW joining region; constant region; VH family; variable gene; gamma isotype;
KW diversity gene; isotype switching sequence; mu isotype; Ig production;
KW monoclonal antibody; MAb production; antigen; heavy chain isotype;
KW antigenic stimulation; ss.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	241..678
FT		/*tag= a
FT		/note= "contains an intron, no stop codon given"
FT	exon	241..286
FT		/*tag= b
FT		/number= 1
FT	intron	287..372
FT		/*tag= c
FT		/number= 1
FT	exon	373..678
FT		/*tag= d
FT		/number= 2

XX
PN US5625126-A.
XX
PD 29-APR-1997.
XX
PF 07-DEC-1994; 94US-0352322.
XX
PR 07-DEC-1994; 94US-0352322.
PR 29-AUG-1990; 90US-0574748.
PR 31-AUG-1990; 90US-0575962.
PR 17-DEC-1991; 91US-0810279.
PR 05-FEB-1992; 92US-0834539.
PR 18-MAR-1992; 92US-0853408.
PR 23-JUN-1992; 92US-0904068.
PR 16-DEC-1992; 92US-0990860.
PR 26-APR-1993; 93US-0053131.
PR 22-JUL-1993; 93US-0096762.
PR 18-NOV-1993; 93US-0155301.
PR 03-DEC-1993; 93US-0161739.
PR 10-DEC-1993; 93US-0165699.
PR 09-MAR-1994; 94US-0209741.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1997-258277/23.
DR P-PSDB; AAW41113.
XX
PT Human antibody producing transgenic mouse - containing transgene
PT comprising human V, D and J genes and sequences to provide isotype
PT switching in lymphocytes
XX
PS Example 12; Column 73-74; 153pp; English.
XX
CC This sequence represents the human VHI family gene VH49.8. This DNA
CC sequence can be used in a plasmid, which is used to develop the
CC transgenic mouse of the invention. The transgenic mouse of the invention
CC contains in its genome a transgene comprising in operable linkage human
CC variable (V), diversity (D) and junction (J) genes, a human mu constant
CC region gene (muCH), at least 2 different non-mu human CH genes and
CC associated isotype switching sequences, where human mu and gamma switch
CC sequences are located in closer proximity to each other than in the
CC naturally occurring human immunoglobulin (Ig) locus, and where in
CC lymphocytes of the mouse the transgene undergoes productive VDJ
CC rearrangement and mu to gamma isotype switching by recombination between
CC the human mu and gamma sequences, so that the mouse produces a serum
CC containing Ig of at least 3 human heavy chain isotypes in response to
CC antigenic stimulation. The transgenic mice can be used to produce human
CC Ig and monoclonal antibodies (MAb), which are specifically reactive with
CC human antigens. The MAb can be used in therapeutic or diagnostic
CC applications. The transgenic mice can produce human MAb of multiple
CC isotypes by undergoing isotype switching.
XX
SQ Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

Query Match 76.3%; Score 280.8; DB 18; Length 812;
Best Local Similarity 96.0%; Pred. No. 1.7e-71;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||| |||||||||||  ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
```

RESULT 11
AAT70522
ID AAT70522 standard; DNA; 812 BP.
XX
AC AAT70522;
XX
DT 09-MAR-1998 (first entry)
XX
DE Human immunoglobulin VH1 family VH49-8 gene.
XX
KW Immunoglobulin heavy chain; variable region; V region; VH1 family;
KW transgene; monoclonal antibody; heterologous antibody; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	241..677
FT		/*tag= a
FT		/product= VH49.8
FT		/note= "heavy chain V region gene"
FT	intron	287..372
FT		/*tag= b

```
FT   misc_feature     680..684
FT                    /*tag=  c
FT                    /note= "mentioned in specification"
FT   misc_feature     710..718
FT                    /*tag=  d
FT                    /note= "Mentioned in specification"
XX
PN   US5633425-A.
XX
PD   27-MAY-1997.
XX
PF   05-FEB-1992;   92US-0834539.
XX
PR   29-AUG-1990;   90US-0574448.
PR   31-AUG-1990;   90US-0575962.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM,  Lonberg N;
XX
DR   WPI; 1997-297410/27.
DR   N-PSDB; AAW18840; AAW18841.
XX
PT   Transgenic mouse for heterologous antibody production - containing
PT   DNA encoding human immunoglobulin components
XX
PS   Example 14; Column 54; 90pp; English.
XX
CC   This sequence encodes the VH49.8 gene from the human heavy chain
CC   V region and a member of the VH1 family. This gene was sequenced from the
CC   plasmid pVH49.8 which is used in a novel method of developing transgenic
CC   non-human animals capable of producing heterologous antibodies encoded by
CC   human immunoglobulin genes. Such transgenically produced monoclonal
CC   antibodies should alleviate the intrinsic immunogenicity of non-human
CC   immunoglobulins allowing the development of new in vivo applications.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;
```

Query Match 76.3%; Score 280.8; DB 18; Length 812;
Best Local Similarity 96.0%; Pred. No. 1.7e-71;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684
```

```
RESULT 12
AAT73471
ID   AAT73471 standard; DNA; 812 BP.
XX
AC   AAT73471;
XX
DT   23-JAN-1998  (first entry)
XX
DE   Human VH1 gene VH49.8.
XX
KW   Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW   transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW   transplant rejection; immunoglobulin; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            241..286
FT                   /*tag=  a
FT                   /number= 1
FT   intron          287..372
FT                   /*tag=  b
FT                   /anticodon= 1
FT                   /note= "DNA sequence in the specification is unclear,
FT                         so this is the best estimate of the sequence"
FT   exon            373..812
FT                   /*tag=  c
FT                   /number= 2
FT                   /note= "The protein shown in the specification ends at
FT                         position 677, not at the stop codon ending at
FT                         position 689"
XX
PN   WO9713852-A1.
XX
PD   17-APR-1997.
XX
PF   10-OCT-1996;   96WO-US16433.
XX
PR   10-OCT-1995;   95US-0544404.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM,  Lonberg N;
XX
DR   WPI; 1997-235888/21.
DR   P-PSDB; AAW24777.
XX
PT   Novel anti-CD4 antibody produced by transgenic mice - used in the
PT   treatment of auto-immune disease etc.
XX
PS   Example 12; Page 138; 396pp; English.
XX
CC   A novel composition has been developed which comprises an immunoglobulin
CC   (Ig) having an affinity constant (Ka) of at least 2 multiply
CC   1000000000 M-1 for binding to a predetermined human antigen. The
CC   present sequence represents the human VH1 gene VH49.8 isolated from
CC   a human placental genomic library lambda. Anti-CD4 antibodies
CC   may be used in therapeutic and diagnostic applications, especially
CC   for the treatment of human diseases. These antibodies reduce
CC   activity of CD4 cells and reduce undesirable autoimmune reactions,
CC   inflammatory response and transplant rejection. Transgenic animals are
CC   capable of producing heterologous antibodies of multiple isotypes by
CC   undergoing isotype switching. These animals produce a first Ig type that
CC   is necessary for antigen-stimulated B-cell maturation and can switch to
CC   encode and produce one or more subsequent heterologous isotypes.
XX
SQ   Sequence 812 BP; 203 A; 194 C; 223 G; 192 T; 0 other;
```

Query Match 76.3%; Score 280.8; DB 18; Length 812;
Best Local Similarity 96.0%; Pred. No. 1.7e-71;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```
Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564
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```
Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 13
AAZ21897
ID   AAZ21897 standard; DNA; 812 BP.
XX
AC   AAZ21897;
XX
DT   24-NOV-1999  (first entry)
XX
DE   Nucleotide sequence of human heavy chain V region gene VH49.8.
XX
KW   Transgenic animal; heterologous antibody; hybridoma; B cell;
KW   transgenic mouse; human heavy chain transgene; digoxin;
KW   human light chain transgene; immortalized cell; immunoglobulin;
KW   Shinga-like toxin; autoimmune disease; cancer; infectious disease;
KW   transplant rejection; blood disorder; coagulation disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO9945962-A1.
XX
PD   16-SEP-1999.
XX
PF   12-MAR-1999;   99WO-US05535.
XX
PR   13-MAR-1998;   98US-0042353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Lonberg N,  Fishwild DM,  Ball WJ;
XX
DR   WPI; 1999-551219/46.
DR   P-PSDB; AAY40381.
XX
PT   Novel transgenic non-human animals used to produce heterologous
PT   antibodies
XX
PS   Example 12; Page 168; 484pp; English.
XX
CC   The specification describes transgenic animals that are capable of
CC   producing a heterologous antibody. The antibodies are isolated form a
CC   hybridoma, comprising B cells, that is obtained from a transgenic mouse
CC   having a genome comprising a human heavy chain transgene and a human
CC   light chain transgene. The B cells are fused to immortalized cells
CC   suitable for generating a hybridoma, which produces a detectable
CC   amount of an immunoglobulin that specifically binds digoxin or
CC   Shinga-like toxin. B cells from transgenic animals can be used to
CC   generate hybridomas expressing monoclonal high affinity human sequence
CC   antibodies. Antibodies produced from the transgenic animals of the
CC   invention can be used to treat human diseases, e.g. autoimmune
CC   diseases, cancer, infectious disease, transplant rejection, blood
CC   disorders such as coagulation disorders and other diseases. The
CC   present sequence represents human heavy chain V region gene VH49.8,
CC   which is used in the course of the invention.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 196 T; 1 other;

  Query Match             76.3%;  Score 280.8;  DB 20;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||| ||||||||||  ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 14
AAX06042
ID   AAX06042 standard; DNA; 812 BP.
XX
AC   AAX06042;
XX
DT   10-MAY-1999  (first entry)
XX
DE   Sequence of human VH1 family gene VH 49.8.
XX
KW   Human; Immunoglobulin transgene; Ig; VH gene; D gene; JH gene; mu gene;
KW   switch sequence; gamma gene; IgM; IgG; ss.
XX
OS   Homo sapiens.
XX
PN   US5874299-A.
XX
PD   23-FEB-1999.
XX
PF   14-FEB-1997;   97US-0800353.
XX
PR   05-FEB-1992;   92US-0834539.
PR   29-AUG-1990;   90US-0574748.
PR   31-AUG-1990;   90US-0575962.
PR   28-AUG-1991;   91WO-US06185.
PR   14-FEB-1997;   97US-0800353.
XX
PA   (GENP-) GENPHARM INT INC.
XX
PI   Kay RM,  Lonberg N;
XX
DR   WPI; 1999-179989/15.
DR   P-PSDB; AAW94854, AAW94855.
XX
PT   Human immunoglobulin transgene - with mu and gamma isotype switching
PT   segments
XX
PS   Example 14; Column 53-54; 88pp; English.
XX
CC   The invention relates to a heavy chain (human) immunoglobulin (Ig)
CC   transgene. The transgene comprises: (i) human VH gene segments; (ii)
CC   human D gene segments; (iii) human JH gene segments; and either (iv) a
CC   mu constant region comprising a mu switch sequence upstream from a mu
CC   coding segment; (v) a gamma constant region comprising a gamma switch
CC   sequence upstream from a human gamma coding segment; where (vi) the mu
CC   and gamma constant regions are closer than in wild type human Ig heavy
CC   chain loci; or (vii) a heavy chain enhancer; (viii) a mu constant region
CC   comprising a mu switch sequence upstream from a mu coding segment; (ix) a
CC   gamma constant region comprising a gamma switch sequence upstream from a
CC   human gamma coding segment; and (x) at least one discontinuity of at
CC   least 2 kb between the mu and gamma gene segments as compared to a human
CC   germ-line heavy chain locus; or (xi) a human mu CH gene and at least two
CC   non-mu human CH genes and their associated isotype switching sequences;
CC   where (xii) the human mu and human gamma switch sequences are closer than
CC   in wild type human Ig heavy chain loci. The transgenes allow non-human
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CC   animals to produce heterologous (human) Ig's with varying specificities.
CC   The presence of mu and gamma switch segments allows isotype switching of
CC   the human heavy chain mini-locus from IgM (for maturation) to IgG.
XX
SQ   Sequence 812 BP; 204 A; 188 C; 223 G; 197 T; 0 other;

  Query Match             76.3%;  Score 280.8;  DB 20;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 1.7e-71;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| | | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 15
AAQ89328
ID   AAQ89328 standard; DNA; 294 BP.
XX
AC   AAQ89328;
XX
DT   26-SEP-1995  (first entry)
XX
DE   HV1263 VH gene.
XX
KW   Graves ophthalmopathy associated immunoglobulin protein;
KW   orbital antigen; monoclonal antibody; heavy chain; H chain;
KW   variable region; VH; autoimmunity; ss.
XX
OS   Homo sapiens.
XX
PN   WO9508336-A.
XX
PD   30-MAR-1995.
XX
PF   22-SEP-1994;   94WO-US10756.
XX
PR   22-SEP-1993;   93US-0124469.
XX
PA   (NICH-) NICHOLS INST DIAGNOSTICS.
XX
PI   Mclachlan SM,  Rapoport B;
XX
DR   WPI; 1995-139383/18.
DR   P-PSDB; AAR72069.
XX
PT   Graves' ophthalmopathy-associated monoclonal antibody - produced
PT   by molecular cloning of immunoglobulin genes by PCR
XX
PS   Disclosure; Page 68; 94pp; English.
XX
CC   L- and H-chain DNA was amplified by PCR from Graves' orbital
CC   tissue and clones encoding autoimmune-associated immunoglobulin
CC   fragments were obtained.  13/15 clones of H chain (IgG1) genes
CC   showed homology to the closest germline genes, DP10 (AAQ89327) and
CC   HV1263 (AAQ89328).  The DNA (AAQ89329) and corresp. amino acid
CC   (AAR72070) sequences of the VH region of a representative clone,
CC   OF7H1.2, are provided.
XX
SQ   Sequence 294 BP; 69 A; 74 C; 94 G; 57 T; 0 other;

  Query Match             75.7%;  Score 278.6;  DB 16;  Length 294;
  Best Local Similarity   96.9%;  Pred. No. 5.6e-71;
  Matches  284;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 294


Search completed: July 18, 2003, 06:44:06
Job time : 96.4001 secs
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 06:19:39 ; Search time 88.9613 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	277.6	75.4	495	10	US-09-925-299-92	Sequence 92, Appl
	2	277.6	75.4	495	12	US-09-925-299-92	Sequence 92, Appl
	3	276.8	75.2	723	15	US-10-151-882-9	Sequence 9, Appli
	4	276	75.0	375	15	US-10-091-300-19	Sequence 19, Appl
	5	274	74.5	1599	11	US-09-954-456-789	Sequence 789, App
	6	274	74.5	1599	11	US-09-954-456-1604	Sequence 1604, Ap
	7	272.2	74.0	1884	15	US-10-047-542-61	Sequence 61, Appl
	8	272.2	74.0	2213	15	US-10-047-542-46	Sequence 46, Appl
	9	268	72.8	735	15	US-10-151-882-3	Sequence 3, Appli
	10	267.6	72.7	720	15	US-10-151-882-10	Sequence 10, Appl
	11	265.4	72.1	396	10	US-09-811-737-12	Sequence 12, Appl
	12	265.4	72.1	782	10	US-09-811-737-22	Sequence 22, Appl
	13	263.6	71.6	717	15	US-10-151-882-11	Sequence 11, Appl
	14	263.6	71.6	744	15	US-10-151-882-7	Sequence 7, Appli
	15	262.8	71.4	744	15	US-10-151-882-5	Sequence 5, Appli
	16	251	68.2	396	10	US-09-811-737-13	Sequence 13, Appl
	17	251	68.2	782	10	US-09-811-737-21	Sequence 21, Appl
	18	250.4	68.0	699	15	US-10-006-593-54	Sequence 54, Appl
	19	249.2	67.7	726	15	US-10-151-882-4	Sequence 4, Appli
	20	248.4	67.5	372	8	US-08-844-215-24	Sequence 24, Appl
	21	248.2	67.4	378	8	US-08-844-215-27	Sequence 27, Appl
	22	247.8	67.3	762	15	US-10-151-882-12	Sequence 12, Appl
	23	247.6	67.3	750	15	US-10-151-882-8	Sequence 8, Appli
	24	246	66.8	376	11	US-09-828-708-122	Sequence 122, App
	25	244.2	66.4	369	10	US-09-905-243-8	Sequence 8, Appli
	26	242.8	66.0	415	15	US-10-160-232-35	Sequence 35, Appl
	27	242	65.8	1449	11	US-09-747-669-1	Sequence 1, Appli
c	28	242	65.8	1449	11	US-09-747-669-2	Sequence 2, Appli
	29	242	65.8	1449	15	US-10-290-703-1	Sequence 1, Appli
c	30	242	65.8	1449	15	US-10-290-703-2	Sequence 2, Appli
	31	240.4	65.3	1563	11	US-09-822-830A-505	Sequence 505, App
	32	237.8	64.6	510	15	US-10-106-698-2502	Sequence 2502, Ap
	33	237.6	64.6	747	15	US-10-151-882-6	Sequence 6, Appli
	34	237.2	64.5	409	15	US-10-160-232-42	Sequence 42, Appl
	35	236	64.1	317	10	US-09-864-761-31160	Sequence 31160, A
	36	236	64.1	463	10	US-09-925-299-277	Sequence 277, App
	37	236	64.1	463	12	US-09-925-299-277	Sequence 277, App
	38	232.4	63.2	409	15	US-10-160-232-78	Sequence 78, Appl
	39	232	63.0	1616	11	US-09-859-053-27	Sequence 27, Appl
	40	230	62.5	395	10	US-09-753-436-85	Sequence 85, Appl
	41	229.8	62.4	690	12	US-09-791-153A-52	Sequence 52, Appl
	42	229.8	62.4	690	12	US-09-791-153A-54	Sequence 54, Appl
	43	229.6	62.4	789	15	US-10-060-585-10	Sequence 10, Appl
	44	228	62.0	947	15	US-10-158-646-53	Sequence 53, Appl
	45	226.4	61.5	418	10	US-09-760-723-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-925-299-92
; Sequence 92, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (402)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-92

Query Match 75.4%; Score 277.6; DB 10; Length 495;
Best Local Similarity 85.7%; Pred. No. 3.3e-84;
Matches 318; Conservative 3; Mismatches 43; Indels 7; Gaps 1;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        125 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 184

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        185 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 244

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
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Db        245 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 304

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240

Db        305 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 364

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db        365 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCATNTATTACTGTGCGARAAGKCCCT 424

Qy        301 ATTATGTTT-------GGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTG 353

Db        425 MAGCGGGTTATCTATCCCAACTACTACCACGGTATGGACGTCTGGGGCCAAGGGACCACG 484

Qy        354 CTCATCGTCTC 364

Db        485 GTCACCGTCTC 495


RESULT 2
US-09-925-299-92
; Sequence 92, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
;   LENGTH: 495
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (402)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-92

  Query Match             75.4%;  Score 277.6;  DB 12;  Length 495;
  Best Local Similarity   85.7%;  Pred. No. 3.3e-84;
  Matches  318;  Conservative    3;  Mismatches   43;  Indels    7;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

Db        125 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 184

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120

Db        185 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 244

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180

Db        245 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 304

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240

Db        305 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 364

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db        365 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCATNTATTACTGTGCGARAAGKCCCT 424

Qy        301 ATTATGTTT-------GGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTG 353

Db        425 MAGCGGGTTATCTATCCCAACTACTACCACGGTATGGACGTCTGGGGCCAAGGGACCACG 484

Qy        354 CTCATCGTCTC 364

Db        485 GTCACCGTCTC 495


RESULT 3
US-10-151-882-9
; Sequence 9, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;  FILE REFERENCE: PF554
;  CURRENT APPLICATION NUMBER: US/10/151,882
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293,100
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
;   LENGTH: 723
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A010D09 scFv
US-10-151-882-9

  Query Match             75.2%;  Score 276.8;  DB 15;  Length 723;
  Best Local Similarity   87.2%;  Pred. No. 6.8e-84;
  Matches  321;  Conservative    0;  Mismatches   32;  Indels   15;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCTTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120

Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180

Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240

Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCAAGAGATC--- 298

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360

Db        299 ------------TGAGCAGGCTCGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCG 346

Qy        361 TCTCCTCA 368

Db        347 TCTCCTCA 354


RESULT 4
US-10-091-300-19
; Sequence 19, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
;  APPLICANT: Rockwell, Patricia
;  APPLICANT:  Goldstein, Neil I.
;  TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth With a Vascular
;  TITLE OF INVENTION:  Endothelial Growth Factor Receptor Antagonist
;  FILE REFERENCE: 11245/46211
;  CURRENT APPLICATION NUMBER: US/10/091,300
;  CURRENT FILING DATE:  2002-03-04
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;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 19
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Human
US-10-091-300-19

  Query Match             75.0%;  Score 276;  DB 15;  Length 375;
  Best Local Similarity   86.2%;  Pred. No. 1.1e-83;
  Matches  319;  Conservative    0;  Mismatches   45;  Indels    6;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||| |||| || |||||||
Db          2 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||| ||||||| ||||| |||| |||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||  |||||||||||||||||||||| |||||||| |
Db        182 CACAGAAGTTCCAGGGCAGAGTCACTTTTACCGCGGACAAATCCACGAGTACAGCCTATA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA------G 294
              ||||| |||| |||||||||||||| ||||||||||||||||||||||||       |
Db        242 TGGAGTTGAGGAGCCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAGGATACG 301

Qy        295 ATCCCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGC 354
              ||  | || ||  | | ||     |     |   || |||  ||||||||||||||||||
Db        302 ATTACTATGATAGTAGTGGCGTGGCTTCCCCCTTTGACTACTGGGGCCAGGGAACCCTGG 361

Qy        355 TCATCGTCTC 364
              ||| ||||||
Db        362 TCACCGTCTC 371


RESULT 5
US-09-954-456-789
; Sequence 789, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 789
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-789

  Query Match             74.5%;  Score 274;  DB 11;  Length 1599;
  Best Local Similarity   85.0%;  Pred. No. 7.5e-83;
  Matches  323;  Conservative    0;  Mismatches   45;  Indels   12;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              || ||||| |||||||||||||||||||| || |||||||||||||||||| | |||||
Db         93 AGATGCAGGTGGTGCAGTCTGGGGCTGAAGTAAAGAAGCCTGGGTCCTCGGTGACGGTCT 152

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              ||||||||| |||||||||||||||| |  ||| ||||||||||||||||||||||||
Db        153 CCTGCAAGGCATCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC 212

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| ||| |  ||||  | |||  |||
Db        213 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCTTTTTGGTACACCAACCTACT 272

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||| |||||||||||||||||||||||||||||||||||||||| ||||||||| |||
Db        273 CACAGAACTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACCAGCACAGCCCACA 332

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATC--- 297
              ||||||||| |||||||||||||||||||||||||||||||||||||||||| |||||
Db        333 TGGAGCTGATCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGACAGATCGCT 392

Qy        298 ---------CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                      |  ||| ||  |||  | |    |||||||||||||||||||||||| |
Db        393 ACAGGCAGGCAAATTTTGACCGGGCCCGGGTTGGCTGGTTCGACCCCTGGGGCCAGGGCA 452

Qy        349 CCCTGCTCATCGTCTCCTCA 368
              ||||| ||| ||||||||||
Db        453 CCCTGGTCACCGTCTCCTCA 472


RESULT 6
US-09-954-456-1604
; Sequence 1604, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 1604
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-1604

  Query Match             74.5%;  Score 274;  DB 11;  Length 1599;
  Best Local Similarity   85.0%;  Pred. No. 7.5e-83;
  Matches  323;  Conservative    0;  Mismatches   45;  Indels   12;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              || ||||| |||||||||||||||||| || ||||||||||||||||||| | |||||
Db         93 AGATGCAGGTGGTGCAGTCTGGGGCTGAAGTAAAGAAGCCTGGGTCCTCGGTGACGGTCT 152

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||| |||||||||||||||| |  ||| ||||||||||||||||||||||||
Db        153 CCTGCAAGGCATCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC 212

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| ||| |  ||||  | |||  |||
Db        213 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCTTTTTGGTACACCAACCTACT 272

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||| |||||||||||||||||||||||||||||||||||| |||||||||  |||
Db        273 CACAGAACTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACCAGCACAGCCCACA 332

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATC--- 297
              |||||||| |||||||||||||||||||||||||||||||||||| |||||
Db        333 TGGAGCTGATCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGACAGATCGCT 392

Qy        298 ---------CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                      |  ||| ||   |||   | |    |||||||||||||||||||||| |
Db        393 ACAGGCAGGCAAATTTTGACCGGGCCCGGGTTGGCTGGTTCGACCCCTGGGGCCAGGGCA 452

Qy        349 CCCTGCTCATCGTCTCCTCA 368
              ||||| ||| ||||||||||
Db        453 CCCTGGTCACCGTCTCCTCA 472


RESULT 7
US-10-047-542-61
; Sequence 61, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
;  APPLICANT: LARRICK, JAMES W.
;  APPLICANT:  WYCOFF, KEITH L.
;  TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
;  TITLE OF INVENTION:  AND BACTERIAL DISEASES
;  FILE REFERENCE: 030905.0004.CIP1
;  CURRENT APPLICATION NUMBER: US/10/047,542
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: PCT/US01/13932
;  PRIOR FILING DATE: 2001-04-28
;  PRIOR APPLICATION NUMBER: 60/200,298
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
;   LENGTH: 1884
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-047-542-61

  Query Match             74.0%;  Score 272.2;  DB 15;  Length 1884;
  Best Local Similarity   95.6%;  Pred. No. 3.2e-82;
  Matches  280;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 118

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||| |||||||||||||||| || ||| ||||||||||||||||||||||||
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Db        119 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 178

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        179 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 238

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        239 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 298

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        299 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAAA 351


RESULT 8
US-10-047-542-46
; Sequence 46, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
;  APPLICANT: LARRICK, JAMES W.
;  APPLICANT:  WYCOFF, KEITH L.
;  TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
;  TITLE OF INVENTION:  AND BACTERIAL DISEASES
;  FILE REFERENCE: 030905.0004.CIP1
;  CURRENT APPLICATION NUMBER: US/10/047,542
;  CURRENT FILING DATE:  2001-10-26
;  PRIOR APPLICATION NUMBER: PCT/US01/13932
;  PRIOR FILING DATE: 2001-04-28
;  PRIOR APPLICATION NUMBER: 60/200,298
;  PRIOR FILING DATE: 2000-04-28
;  NUMBER OF SEQ ID NOS: 101
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
;   LENGTH: 2213
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-047-542-46

  Query Match             74.0%;  Score 272.2;  DB 15;  Length 2213;
  Best Local Similarity   95.6%;  Pred. No. 3.4e-82;
  Matches  280;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        131 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 190

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        191 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 250

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        251 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 310

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        311 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 370

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGA 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        371 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAAA 423


RESULT 9
US-10-151-882-3
; Sequence 3, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;  FILE REFERENCE: PF554
;  CURRENT APPLICATION NUMBER: US/10/151,882
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;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293,100
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 735
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A004G02 scFv
US-10-151-882-3

  Query Match             72.8%;  Score 268;  DB 15;  Length 735;
  Best Local Similarity   94.9%;  Pred. No. 6.6e-81;
  Matches  277;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              ||||||||||||||||||||||||||| ||||||  |||||| ||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGTTATGGTATCAGGTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              ||||||||||||||||||||||||||| ||||||| |||||| ||||   |||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||| |
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATACACGAGCACAGCCTATA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAG 292
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAG 293


RESULT 10
US-10-151-882-10
; Sequence 10, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;  FILE REFERENCE: PF554
;  CURRENT APPLICATION NUMBER: US/10/151,882
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293,100
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A027B01 scFv
US-10-151-882-10

  Query Match             72.7%;  Score 267.6;  DB 15;  Length 720;
  Best Local Similarity   85.9%;  Pred. No. 9e-81;
  Matches  316;  Conservative    0;  Mismatches   34;  Indels   18;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||| ||||||||| ||||||||||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGTTGCAGTCTGCGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||| |||||||||||||||||| | | || ||||||| ||||||||||||||||
Db         62 CCTGCAAGACTTCTGGAGGCACCTTCAGAAATCATGCTATCAGTTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGA--------- 292

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
                          ||||||          |  | |||  ||||||||  |||||||| ||| ||
Db        293 ---------GGGGGATATCGGCTGGTATGGACGTCTGGGGCCGAGGAACCCTGGTCACCG 343

Qy        361 TCTCCTCA 368
              ||||||||
Db        344 TCTCCTCA 351


RESULT 11
US-09-811-737-12
; Sequence 12, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Human FAP-alpha-specific antibodies
;  FILE REFERENCE: 1-1129
;  CURRENT APPLICATION NUMBER: US/09/811,737
;  CURRENT FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Humanised Antibody
US-09-811-737-12

  Query Match             72.1%;  Score 265.4;  DB 10;  Length 396;
  Best Local Similarity   84.1%;  Pred. No. 4.3e-80;
  Matches  312;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||  |||||| ||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| |   ||||||||| ||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCACCCATACTATCAACTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||| |||||   |||||  ||||   |||||| ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCGCCCCTATGTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACAATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGC---GAGAGATC 297
              ||||| |||||||||||||||||| |||||||| |||||||||||||    |||
Db        242 TGGAGATGAGCAGCCTGAGATCTGACGACACGGCTGTGTATTACTGTGCAAGAAGAAGAA 301

Qy        298 CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              ||  || | ||  |     | | |     | |||  |||||| || ||||||||  |||
Db        302 TCGCGTACGGTTACGACGAGGGCCATGCTATGGACTACTGGGGTCAAGGAACCCTTGTCA 361

Qy        358 TCGTCTCCTCA 368
              ||||||||||
Db        362 CCGTCTCCTCA 372
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RESULT 12
US-09-811-737-22
; Sequence 22, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Human FAP-alpha-specific antibodies
;  FILE REFERENCE: 1-1129
;  CURRENT APPLICATION NUMBER: US/09/811,737
;  CURRENT FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 782
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Humanised Antibody
US-09-811-737-22

  Query Match             72.1%;  Score 265.4;  DB 10;  Length 782;
  Best Local Similarity   84.1%;  Pred. No. 5.2e-80;
  Matches  312;  Conservative    0;  Mismatches   56;  Indels    3;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||  |||||| ||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| |   ||||||||| ||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCACCCATACTATCAACTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| |||||   |||||  ||||   ||||||  ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCGCCCCTATGTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACAATTACCGCGGACAAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGC---GAGAGATC 297
              |||||  |||||||||||||||||||  ||||||||  ||||||||||||    |||
Db        242 TGGAGATGAGCAGCCTGAGATCTGACGACACGGCTGTGTATTACTGTGCAAGAAGAAGAA 301

Qy        298 CCGATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCA 357
              ||  ||| |  ||  |    | | |     | |||  |||||| || ||||||||  |||
Db        302 TCGCGTACGGTTACGACGAGGGCCATGCTATGGACTACTGGGGTCAAGGAACCCTTGTCA 361

Qy        358 TCGTCTCCTCA 368
              ||||||||||
Db        362 CCGTCTCCTCA 372


RESULT 13
US-10-151-882-11
; Sequence 11, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;  FILE REFERENCE: PF554
;  CURRENT APPLICATION NUMBER: US/10/151,882
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293,100
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 717
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A027H08 scFv
US-10-151-882-11

  Query Match             71.6%;  Score 263.6;  DB 15;  Length 717;
  Best Local Similarity   93.5%;  Pred. No. 2.1e-79;
  Matches  275;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db          2 AGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||| |||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGACCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| |||||||  |||||  ||||   ||||||  ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTGCAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCCACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG 294
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGCGCGAGAG 295


RESULT 14
US-10-151-882-7
; Sequence 7, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;  FILE REFERENCE: PF554
;  CURRENT APPLICATION NUMBER: US/10/151,882
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293,100
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A053H04 scFv
US-10-151-882-7

  Query Match             71.6%;  Score 263.6;  DB 15;  Length 744;
  Best Local Similarity   93.5%;  Pred. No. 2.1e-79;
  Matches  275;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| |   ||| ||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| |||||||  ||| ||  |||    | | || ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCTCTTTGACACACCTAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAG 294
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGCGCGAGAG 295
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Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAGAG 295

RESULT 15
US-10-151-882-5
; Sequence 5, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
;  FILE REFERENCE: PF554
;  CURRENT APPLICATION NUMBER: US/10/151,882
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293,100
;  PRIOR FILING DATE: 2001-05-24
;  NUMBER OF SEQ ID NOS: 48
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 744
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA encoding A034G03 scFv
US-10-151-882-5

  Query Match             71.4%;  Score 262.8;  DB 15;  Length 744;
  Best Local Similarity   85.2%;  Pred. No. 3.9e-79;
  Matches  310;  Conservative    0;  Mismatches   42;  Indels   12;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||  |||||| ||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTACAGCTGCAGCAGTCAGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| |  ||| ||||||||||||||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTATGCTATCAGCTGGGTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||| ||||||| ||| || |||    | | || ||||
Db        122 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTCTCTTTGACACACCTAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        182 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTCTATTACTGTGCGAGAGGAAATA 301

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
               |            ||   |     |||||||||||||||| || |||||| ||| ||
Db        302 CT------------GGCCCGAGACCCTTCGACCCCTGGGGCCAAGGCACCCTGGTCACCG 349

Qy        361 TCTC 364
              ||||
Db        350 TCTC 353


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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 153338381 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
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SUMMARIES

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2	293.2	79.7	2287	1	US-08-461-968A-1	Sequence 1, Appli
3	293.2	79.7	2287	2	US-08-462-571-1	Sequence 1, Appli
4	293.2	79.7	2287	5	PCT-US96-10043-8	Sequence 8, Appli
5	282.4	76.7	369	2	US-08-652-816A-46	Sequence 46, Appl
6	280.8	76.3	369	2	US-08-652-816A-44	Sequence 44, Appl
7	280.8	76.3	812	1	US-07-834-539A-53	Sequence 53, Appl
8	280.8	76.3	812	2	US-08-800-353-53	Sequence 53, Appl
9	280.8	76.3	812	4	US-09-042-353-231	Sequence 231, App
10	280.8	76.3	812	4	US-08-758-417A-79	Sequence 79, Appl
11	280.8	76.3	812	5	PCT-US92-06185-53	Sequence 53, Appl
12	280.8	76.3	813	1	US-08-053-131-61	Sequence 61, Appl
13	280.8	76.3	813	1	US-08-645-641-61	Sequence 61, Appl
14	280.8	76.3	813	1	US-07-853-408B-61	Sequence 61, Appl
15	280.8	76.3	813	1	US-08-096-762-61	Sequence 61, Appl
16	280.8	76.3	813	2	US-08-308-865-61	Sequence 61, Appl
17	280.8	76.3	813	5	PCT-US92-10983-61	Sequence 61, Appl
18	279.2	75.9	369	2	US-08-652-816A-45	Sequence 45, Appl
19	277.6	75.4	369	2	US-08-652-816A-47	Sequence 47, Appl
20	272.8	74.1	369	2	US-08-652-816A-25	Sequence 25, Appl
21	272.4	74.0	1617	2	US-08-378-939-9	Sequence 9, Appli
22	250.4	68.0	4691	4	US-08-591-632-43	Sequence 43, Appl
23	250.4	68.0	4691	4	US-09-611-451-43	Sequence 43, Appl
24	250.4	68.0	6166	4	US-08-591-632-51	Sequence 51, Appl
25	250.4	68.0	6166	4	US-09-611-451-51	Sequence 51, Appl
26	250.2	68.0	441	1	US-08-217-918-3	Sequence 3, Appli
27	248	67.4	687	1	US-08-300-386A-1	Sequence 1, Appli
28	248	67.4	687	3	US-08-931-645-1	Sequence 1, Appli
29	248	67.4	687	5	PCT-US94-01258-1	Sequence 1, Appli
30	248	67.4	687	5	PCT-US95-11235-1	Sequence 1, Appli
31	243.6	66.2	363	1	US-08-264-093-1	Sequence 1, Appli
32	236.4	64.2	564	3	US-08-545-809A-8	Sequence 8, Appli
33	236	64.1	539	3	US-08-545-809A-18	Sequence 18, Appl
34	234.4	63.7	799	3	US-08-545-809A-46	Sequence 46, Appl
35	233.2	63.4	246	4	US-09-042-353-146	Sequence 146, App
36	233.2	63.4	246	4	US-08-758-417A-410	Sequence 410, App
37	232.8	63.3	936	3	US-09-049-672A-26	Sequence 26, Appl
38	231.2	62.8	512	3	US-08-545-809A-2	Sequence 2, Appli
39	230	62.5	395	1	US-08-482-882-85	Sequence 85, Appl
40	230	62.5	395	1	US-08-483-389-85	Sequence 85, Appl
41	230	62.5	395	2	US-08-487-113D-85	Sequence 85, Appl
42	230	62.5	395	2	US-08-473-503-85	Sequence 85, Appl
43	230	62.5	395	2	US-08-483-932-85	Sequence 85, Appl
44	230	62.5	395	2	US-08-720-420A-85	Sequence 85, Appl
45	230	62.5	395	3	US-08-714-017-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-480-036-1
; Sequence 1, Application US/08480036
; Patent No. 5723583
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian et al.
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.00)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,036
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/618,314C
; FILING DATE: No. 5723583ember 23, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-480-036-1

Query Match 79.7%; Score 293.2; DB 1; Length 2287;
Best Local Similarity 88.2%; Pred. No. 7.4e-83;
Matches 335; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

Qy 1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

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Db        74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy        61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120

Db       134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 193

Qy       121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180

Db       194 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy       181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240

Db       254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy       241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db       314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy       301 ------------ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348

Db       374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy       349 CCCTGCTCATCGTCTCCTCA 368

Db       434 CCCTGGTCACCGTCTCTTCA 453
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RESULT 2
US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
; GENERAL INFORMATION:
; APPLICANT: Seed et al., Brian
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 0210-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,968A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/618,314
; FILING DATE: 23-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/067003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-461-968A-1

Query Match 79.7%; Score 293.2; DB 1; Length 2287;

Best Local Similarity 88.2%; Pred. No. 7.4e-83;
Matches 335; Conservative 0; Mismatches 33; Indels 12; Gaps 1;

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Qy         1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60

Db        74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy        61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120

Db       134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 193

Qy       121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180

Db       194 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy       181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240

Db       254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy       241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300

Db       314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy       301 ------------ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348

Db       374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy       349 CCCTGCTCATCGTCTCCTCA 368

Db       434 CCCTGGTCACCGTCTCTTCA 453
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RESULT 3
US-08-462-571-1
; Sequence 1, Application US/08462571
; Patent No. 5858983
; GENERAL INFORMATION:
; APPLICANT: Seed, Brian et al.
; TITLE OF INVENTION: INHIBITION OF CELL ADHESION
; TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,571
; FILING DATE: 05 June 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/618,314
; FILING DATE: 23 No. 5858983ember 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/067002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2287
; TYPE: nucleic acid
; STRANDEDNESS: single

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;      TOPOLOGY:  linear
US-08-462-571-1

  Query Match             79.7%;  Score 293.2;  DB 2;  Length 2287;
  Best Local Similarity   88.2%;  Pred. No. 7.4e-83;
  Matches  335;  Conservative    0;  Mismatches   33;  Indels   12;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 193

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||  ||||   |||||| ||||
Db        194 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||    |
Db        314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy        301 ------------ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                         |  ||  | |  |   |     |||||||||||||||||||||||||
Db        374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy        349 CCCTGCTCATCGTCTCCTCA 368
              ||||| ||| |||||| |||
Db        434 CCCTGGTCACCGTCTCTTCA 453


RESULT 4
PCT-US96-10043-8
; Sequence 8, Application PC/TUS9610043
;  GENERAL INFORMATION:
;    APPLICANT:  The General Hospital Corporation
;    TITLE OF INVENTION:  P-SELECTIN LIGANDS AND RELATED MOLECULES
;    TITLE OF INVENTION:  AND METHODS
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/10043
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/000,213
;      FILING DATE:  14-JUN-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:  00786/284001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US96-10043-8

  Query Match             79.7%;  Score 293.2;  DB 5;  Length 2287;
  Best Local Similarity   88.2%;  Pred. No. 7.4e-83;
  Matches  335;  Conservative    0;  Mismatches   33;  Indels   12;  Gaps    1;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db         74 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 133

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        134 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 193

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||| ||||||| |||||  ||||   |||||| ||||
Db        194 CTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACAGCAAACTACG 253

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        254 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 313

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||    |
Db        314 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATAATG 373

Qy        301 ------------ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAA 348
                         |  ||  | |  |   |     |||||||||||||||||||||||||
Db        374 GAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCCTGGGGCCAGGGAA 433

Qy        349 CCCTGCTCATCGTCTCCTCA 368
              ||||| ||| |||||| |||
Db        434 CCCTGGTCACCGTCTCTTCA 453


RESULT 5
US-08-652-816A-46
; Sequence 46, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  369 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-652-816A-46

  Query Match           76.7%;  Score 282.4;  DB 2;  Length 369;
  Best Local Similarity  86.0%;  Pred. No. 9.4e-80;
  Matches  313;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||| ||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTTCAGCTGGTTCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| |   | | |||||| |||| ||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTCTCCTATCAACTGGCTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              | |||||||||||||||||||||||| ||||| ||| | ||||   |||||| ||||
Db        122 CCGGACAAGGGCTTGAGTGGATGGGAAGTATCATCCCTTCCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              | |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||
Db        182 CTCAGAAGTTCCAGGGCAGACTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGACATAATC 301

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              || ||  |  |     | || |||  | |||  |||||||||||| ||  || ||| ||
Db        302 ATAATTATGAGCTTTACTACTACTACATGGACGTCTGGGGCCAGGGGACAATGGTCACCG 361

Qy        361 TCTC 364
              ||||
Db        362 TCTC 365


RESULT 6
US-08-652-816A-44
; Sequence 44, Application US/08652816A
; Patent No. 5872215
;  GENERAL INFORMATION:
;    APPLICANT:  Osbourn, JK
;    APPLICANT:  Allen, DJ
;    APPLICANT:  McCafferty, JG
;    TITLE OF INVENTION:  Specific binding members, materials and
;    TITLE OF INVENTION:  methods.
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,816A
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.4
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9125579.8
;      FILING DATE:  02-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  23-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9525004.9
;      FILING DATE:  07-DEC-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9610824.6
;      FILING DATE:  23-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/02240
;      FILING DATE:  02-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/244,597
;      FILING DATE:  01-JUN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/33308
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  369 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-652-816A-44

  Query Match           76.3%;  Score 280.8;  DB 2;  Length 369;
  Best Local Similarity  85.7%;  Pred. No. 3e-79;
  Matches  312;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||| ||||||||||||||||||||||||||||||||||||||| |||||||
Db          2 AGGTTCAGCTGGTTCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 61

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| |   | | |||||| |||| ||||||||||||
Db         62 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAACTCTCCTATCAACTGGCTGCGACAGGCCC 121

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              | |||||||||||||||||||||||| ||||| ||| | ||||   |||||| ||||
Db        122 CCGGACAAGGGCTTGAGTGGATGGGAAGTATCATCCCTTCCTTTGGTACAGCAAACTACG 181

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              | |||||||||||||||||| |||||||||||||||| ||||||||||||||||||||||
Db        182 CTCAGAAGTTCCAGGGCAGACTCACGATTACCGCGGACGAATCCACGAGCACAGCCTACA 241
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Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| || | |
Db        242 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGGGATGTTCTC 301

Qy        301 ATTATGTTTGGGGGAGCGACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGCTCATCG 360
              || ||  |  |     | || |||   | |||  |||||||||||| ||  || ||| ||
Db        302 ATAATTATGAGCTTTACTACTACTACATGGACGTCTGGGGCCAGGGGACAATGGTCACCG 361

Qy        361 TCTC 364
              ||||
Db        362 TCTC 365


RESULT 7
US-07-834-539A-53
; Sequence 53, Application US/07834539A
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic Non-Human Animals Capable of
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/834,539A
;      FILING DATE:  1992-02-05
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  14643-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Exon
;      LOCATION:  241..335
;      OTHER INFORMATION:  Codes for peptide of SEQ ID NO 54
;    FEATURE:
;      NAME/KEY:  Exon
;      LOCATION:  372..677
;      OTHER INFORMATION:  Codes for peptide of SEQ ID NO 55
US-07-834-539A-53

  Query Match             76.3%;  Score 280.8;  DB 1;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||

Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 8
US-08-800-353-53
; Sequence 53, Application US/08800353
; Patent No. 5874299
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 5874299-Human Animals Capable of
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/800,353
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/834,539
;      FILING DATE:  1992-02-05
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  14643-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Exon
;      LOCATION:  241..335
;      OTHER INFORMATION:  Codes for peptide of SEQ ID NO 54
;    FEATURE:
;      NAME/KEY:  Exon
;      LOCATION:  372..677
;      OTHER INFORMATION:  Codes for peptide of SEQ ID NO 55
US-08-800-353-53

  Query Match             76.3%;  Score 280.8;  DB 2;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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                ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                ||||||||||||||||||||||||||  ||  |||  ||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                |||||||||||||||||||||||||||||||  ||||||||||  |||||||  ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||  | ||
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 9
US-09-042-353-231
; Sequence 231, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  231:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(241..286, 373..677)
;      OTHER INFORMATION:  /product= "human V-HI family
;      OTHER INFORMATION:  gene V-H49.8"
US-09-042-353-231

  Query Match             76.3%;  Score 280.8;  DB 4;  Length 812;
  Best Local Similarity   96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
                ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
                ||||||||||||||||||||||||||  ||  |||  ||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
                |||||||||||||||||||||||||||||||  ||||||||||  |||||||  ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||  | ||
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 10
US-08-758-417A-79
; Sequence 79, Application US/08758417A
; Patent No. 6300129
;   GENERAL INFORMATION:
;        APPLICANT: Lonberg, Nils
```

```
;               Kay, Robert M.
;       TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                           Producing Heterologous Antibodies
;       NUMBER OF SEQUENCES: 417
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Townsend and Townsend and Crew LLP
;            STREET: Two Embarcadero Center, Eighth Floor
;            CITY: San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94111-3834
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/758,417A
;            FILING DATE: 02-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/728,463
;            FILING DATE: 10-OCT-1996
;            APPLICATION NUMBER: US 08/544,404
;            FILING DATE: 10-OCT-1995
;            APPLICATION NUMBER: US 08/352,322
;            FILING DATE: 07-DEC-1994
;            APPLICATION NUMBER: US 08/209,741
;            FILING DATE: 09-MAR-1994
;            APPLICATION NUMBER: US 08/165,699
;            FILING DATE: 10-DEC-1993
;            APPLICATION NUMBER: US 08/161,739
;            FILING DATE: 03-DEC-1993
;            APPLICATION NUMBER: US 08/155,301
;            FILING DATE: 18-NOV-1993
;            APPLICATION NUMBER: US 08/096,762
;            FILING DATE: 22-JUL-1993
;            APPLICATION NUMBER: US 08/053,131
;            FILING DATE: 26-APR-1993
;            APPLICATION NUMBER: US 07/990,860
;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 79:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 812 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  join(241..286, 373..677)
;            OTHER INFORMATION:  /note= "human V-HI family gene V-H49.8"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-08-758-417A-79

  Query Match           76.3%;  Score 280.8;  DB 4;  Length 812;
  Best Local Similarity  96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||||| |||||||||  ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||  | |
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 11
PCT-US92-06185-53
; Sequence 53, Application PC/TUS9206185
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic Non-Human Animals Capable of
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06185
;      FILING DATE:  19910828
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  87654
;      REFERENCE/DOCKET NUMBER:  14643-5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  812 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  Exon
;      LOCATION:  241..335
;      OTHER INFORMATION:  Codes for peptide of SEQ ID NO 54
;    FEATURE:
;      NAME/KEY:  Exon
;      LOCATION:  372..677
;      OTHER INFORMATION:  Codes for peptide of SEQ ID NO 55
PCT-US92-06185-53

  Query Match           76.3%;  Score 280.8;  DB 5;  Length 812;
  Best Local Similarity  96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        385 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 444

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
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Db        445 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 504

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||| ||||||||||  ||||||| ||||
Db        505 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 564

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 624

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  | ||
Db        625 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 684


RESULT 12
US-08-053-131-61
; Sequence 61, Application US/08053131
; Patent No. 5661016
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 5661016-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,131
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  14643-9-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  813 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  241..285
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  373..678
US-08-053-131-61

  Query Match    76.3%;  Score 280.8;  DB 1;  Length 813;
  Best Local Similarity   96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
              |||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 445

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 505

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||| |||||||||||  ||||||| ||||
Db        506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 565

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 625

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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RESULT 13
US-08-645-641-61
; Sequence 61, Application US/08645641
; Patent No. 5719032
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 5719032-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  150
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  William M. Smith
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/645,641
;      FILING DATE:  20-MAY-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  14643-000913
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-326-2400
;      TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  813 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  241..285
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  373..678
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US-08-645-641-61

Query Match 76.3%; Score 280.8; DB 1; Length 813;
Best Local Similarity 96.0%; Pred. No. 4e-79;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db        446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 505

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 565

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 625

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Db        626 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 685
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RESULT 14
US-07-853-408B-61
; Sequence 61, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 813 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 241..285
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 373..678

US-07-853-408B-61

Query Match 76.3%; Score 280.8; DB 1; Length 813;
Best Local Similarity 96.0%; Pred. No. 4e-79;
Matches 288; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Qy          1 AGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTAAAGGTCT 60
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Db        386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 445

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||||
Db        446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 505

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 565

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Db        566 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 625

Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Db        626 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGACACAG 685
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RESULT 15
US-08-096-762-61
; Sequence 61, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:

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;       TELEPHONE:  415-326-2400
;       TELEFAX:  415-326-2422
;  INFORMATION FOR SEQ ID NO:  61:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  813 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  241..285
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  373..678
US-08-096-762-61

  Query Match             76.3%;  Score 280.8;  DB 1;  Length 813;
  Best Local Similarity   96.0%;  Pred. No. 4e-79;
  Matches  288;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

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              |||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        386 AGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGGTGAAGGTCT 445

Qy         61 CCTGCAAGGCTTCTGGAGGCACCTTCAGTAGTTATACTATCAGCTGGGTGCGACAGGCCC 120
              |||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Db        446 CCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGACAGGCCC 505

Qy        121 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATGCCTATCCTTGGACTAGCAAATTACG 180
              |||||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db        506 CTGGACAAGGGCTTGAGTGGATGGGAAGGATCATCCCTATCCTTGGTATAGCAAACTACG 565

Qy        181 CACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACAAATCCACGAGCACAGCCTACA 240
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Qy        241 TGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGATCCCG 300
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Search completed: July 18, 2003, 19:59:08
Job time : 20.5137 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:46:48 ; Search time 1002.03 Seconds
(without alignments)
10397.705 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 1 gtgcagctggtggagtctgg.....ccctggtcaccgtctcctca 358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
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37: em_htg_vrt:*
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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	267.4	74.7	357	9	HSVH3H2FG	X70485 H.sapiens D
2	264	73.7	1679	9	BC018747	BC018747 Homo sapi
3	263.8	73.7	351	9	HSVH31328	X62965 H.sapiens r
4	262.6	73.4	420	9	AF174030	AF174030 Homo sapi
5	261	72.9	420	9	AF062138	AF062138 Homo sapi
6	260.6	72.8	351	9	HSA300796	AJ300796 Homo sapi
7	259.4	72.5	409	9	HSE55314	Z14189 H.sapiens r
8	258.4	72.2	363	9	AB067237	AB067237 Homo sapi
9	258.4	72.2	372	9	HSVH3I3RM	X63850 H.sapiens D
10	257.4	71.9	351	9	HSA300786	AJ300786 Homo sapi
11	256.6	71.7	375	6	AX061464	AX061464 Sequence
12	256.2	71.6	348	9	HSU80083	U80083 Human immun
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14	255.4	71.3	354	9	HSA300785	AJ300785 Homo sapi
15	254.8	71.2	372	9	AF062188	AF062188 Homo sapi
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17	254.2	71.0	351	9	HSA300781	AJ300781 Homo sapi
18	253.4	70.8	360	9	AF062241	AF062241 Homo sapi
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26	250.6	70.0	378	9	U00487	U00487 Human immun
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29	249	69.6	378	9	HSIGVHC01	Z37291 H.sapiens r
30	248.6	69.4	373	9	AB021520	AB021520 Homo sapi
31	247.6	69.2	384	9	AF174118	AF174118 Homo sapi
32	247.4	69.1	354	9	HSA238038	AJ238038 Homo sapi
33	246.6	68.9	360	9	HSU80084	U80084 Human immun
34	246.6	68.9	390	9	AF115121	AF115121 Homo sapi
35	246.4	68.8	423	9	AF062121	AF062121 Homo sapi
36	245.8	68.7	351	9	U00584	U00584 Human immun
37	245.8	68.7	411	9	HSIGHXX14	X65896 H.sapiens m
38	245	68.4	360	9	U96279	U96279 Homo sapien
39	245	68.4	360	9	U96284	U96284 Homo sapien
40	244.8	68.4	363	9	HSVH3DJH4	X61646 Human Ig re
41	244.8	68.4	366	9	AF174095	AF174095 Homo sapi
42	244.4	68.3	405	9	AF174034	AF174034 Homo sapi
43	244	68.2	363	9	AB063913	AB063913 Homo sapi
44	243.8	68.1	357	6	AX300024	AX300024 Sequence
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ALIGNMENTS

RESULT 1
HSVH3H2FG
LOCUS HSVH3H2FG 357 bp DNA linear PRI 17-FEB-1993
DEFINITION H.sapiens DNA for anti-DNA antibody heavy chain variable region,subgroup V(H)3 (H2F IgG line).
ACCESSION X70485
VERSION X70485.1 GI:38447
KEYWORDS anti-DNA antibody; complementarity determining region; Ig heavy chain; Ig kappa light chain; Ig variable region; IgG; immunoglobulin; systemic lupus erythematosus.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 357)

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  AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
            and Diamond,B.
  TITLE     Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype
  JOURNAL   J. Exp. Med. 174 (6), 1639-1652 (1991)
  MEDLINE   92078875
   PUBMED   1660528
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                     /cell_line="EBV-transformed 3I(+) B cell line,H2F IgG"
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                     /note="IgG heavy chain variable region"
     misc_feature    88. .99
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     misc_feature    145. .198
                     /note="complementarity determining region, CDR 2"
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  Best Local Similarity   87.7%;  Pred. No. 1.6e-75;
  Matches  315;  Conservative    0;  Mismatches   41;  Indels    3;  Gaps    2;

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Db        121 GGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTCGTGGTAGTACCATATACTACGCA 180

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
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Db        299 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 357


RESULT 2
BC018747
LOCUS       BC018747               1679 bp    mRNA    linear   PRI 11-DEC-2001
DEFINITION  Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m
            marker), clone MGC:31937 IMAGE:4851063, mRNA, complete cds.
ACCESSION   BC018747
VERSION     BC018747.1  GI:17511791
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1679)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 40 Row: i Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: Hexamer frequency ORF
            analysis, GenomeScan gene prediction, Similarity but not identity
            to protein.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="Primary B-Cells from Tonsils"
                     /clone_lib="NIH_MGC_48"
                     /lab_host="DH10B-R"
                     /note="Vector: pOTB7"
     CDS             63. .1475
                     /codon_start=1
                     /product="Similar to immunoglobulin heavy constant gamma 3
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                     /protein_id="AAH18747.1"
                     /db_xref="GI:17511792"
                     /translation="MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCVVS
                     GFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
                     NSLRAEDTAVYYCARDGSSWYRDWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG
                     GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT
                     QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
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ORIGIN

  Query Match             73.7%;  Score 264;  DB 9;  Length 1679;
  Best Local Similarity   86.9%;  Pred. No. 2.4e-74;
  Matches  313;  Conservative    0;  Mismatches   45;  Indels    2;  Gaps    2;

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Db        123 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 182

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| || ||| |||||||||||||| ||| ||    | |||||||| ||||||||||||
Db        183 TGTGTAGTCTCTGGATTCACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA 242

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        243 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 302

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        303 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 362

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
              |||||||||||||||||||||||||||||||| ||||||||||||||||||     | |
Db        363 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGCAGC 422
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Qy        299 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |   |||| | ||  || |||  ||||||||||||||||||||||||||||||||||||
Db        423 AGCTGGTACAGGGACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 482


RESULT 3
HSVH31328
LOCUS       HSVH31328               351 bp    mRNA    linear   PRI 02-JUN-1992
DEFINITION  H.sapiens rearranged mRNA for fetal IG heavy chain Vh3, an
            unidentified D (or N) region and Jh4 (clone FL13-28).
ACCESSION   X62965
VERSION     X62965.1  GI:37680
KEYWORDS    Ig CDR3 region; Ig heavy chain; Jh element; rearranged gene; Vh
            element.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Raaphorst,F.M., Timmers,E., Kenter,M.J., Van Tol,M.J., Vossen,J.M.
            and Schuurman,R.K.
  TITLE     Restricted utilization of germ-line VH3 genes and short diverse
            third complementarity-determining regions (CDR3) in human fetal B
            lymphocyte immunoglobulin heavy chain rearrangements
  JOURNAL   Eur. J. Immunol. 22 (1), 247-251 (1992)
  MEDLINE   92111633
   PUBMED   1730252
REFERENCE   2  (bases 1 to 351)
  AUTHORS   Raaphorst,F.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-OCT-1991) F.M. Raaphorst, Division of Immunology,
            Dept. of Immunohematology and Bloodbank, Academic Hospital Leiden,
            Building 1, E3-Q, P.O.Box 9600, 2300 Leiden, THE NETHERLANDS
COMMENT     For related sequences see X62954-X62972, X53612-3, M37277,
            Schroeder H.W. Jr. et al, Proc.Natl.Acad.Sci.USA, 87:6149(1990) &
            Ichihara y. et al, Eur. J. Immunol. 18:649(1988).
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Homo sapiens"
                     /isolate="Clone FL13-28"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32"
                     /cell_type="B lymphocyte"
                     /tissue_type="liver"
                     /dev_stage="13 week old foetus"
     misc_feature    1. .296
                     /note="Vh element"
     misc_feature    297. .310
                     /note="CDR3"
     misc_feature    311. .351
                     /note="Jh element"
BASE COUNT       78 a     83 c    118 g     72 t
ORIGIN

  Query Match            73.7%;  Score 263.8;  DB 9;  Length 351;
  Best Local Similarity  87.7%;  Pred. No. 2.4e-74;
  Matches  315;  Conservative    0;  Mismatches   32;  Indels   12;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||  |||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCGGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||| |||   ||    | |||||||| ||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------- 295

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |||  || || | | ||||||||||||||||||||||||||||||||||||||||||||
Db        296 ---ATGGGAGGGGATCCCTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351


RESULT 4
AF174030
LOCUS       AF174030                420 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 77u-c17 immunoglobulin heavy chain variable
            region precursor (IgH) mRNA, partial cds.
ACCESSION   AF174030
VERSION     AF174030.1  GI:5834019
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 420)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
  MEDLINE   99459182
   PUBMED   10527689
REFERENCE   2  (bases 1 to 420)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-1999) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1. .420
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.33"
                     /clone="77u-c17"
                     /cell_type="peripheral blood B lymphocyte"
                     /clone_lib="77u"
     gene            1. .>420
                     /gene="IgH"
     CDS             1. .>420
                     /gene="IgH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region
                     precursor"
                     /protein_id="AAD53776.1"
                     /db_xref="GI:5834020"
                     /translation="MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAAS
                     GFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
                     NSLRAEDTAVYYCARDGDIGDWWFDPWGQGTLVTVSSG"
     sig_peptide     1. .57
                     /gene="IgH"
     mat_peptide     58. .>420
                     /gene="IgH"
                     /product="immunoglobulin heavy chain variable region"
     V_region        58. .420
                     /gene="IgH"
BASE COUNT       88 a     92 c    143 g     97 t
ORIGIN

  Query Match            73.4%;  Score 262.6;  DB 9;  Length 420;
  Best Local Similarity  86.9%;  Pred. No. 6e-74;
  Matches  312;  Conservative    0;  Mismatches   44;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 120
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Qy          61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
               |||||||||| |||||||||||| |||  ||    | |||||||| ||||||||||
Db         121 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 180

Qy         120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
               |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db         181 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 240

Qy         180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
               ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         241 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 300

Qy         240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
               |||||||||||||||||||||||||||||||| ||||||||||||||||  ||| |
Db         301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA--GATGGGG 358

Qy         300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                 |   |       | |  || |||  ||||||||||||||||||||||||||||||||
Db         359 ATATCGGTGACTGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 417
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RESULT 5
AF062138
LOCUS       AF062138                420 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 45u-11 immunoglobulin heavy chain variable
            region (IGH) mRNA, partial cds.
ACCESSION   AF062138
VERSION     AF062138.1  GI:3170738
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 420)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
  MEDLINE   99459182
   PUBMED   10527689
REFERENCE   2  (bases 1 to 420)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
            School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1. .420
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32.33"
                     /clone="45u-11"
                     /cell_type="peripheral B lymphocyte"
                     /tissue_type="blood"
                     /note="from elderly repertoire 45u"
     gene            1. .>420
                     /gene="IGH"
     CDS             1. .>420
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC18174.1"
                     /db_xref="GI:3170739"
                     /translation="MELGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLKLSCAAS
                     GFTFGSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQM
                     NSLRAEDTAVYYCAVTIVVVPAAPDYWGQGTLVTVSSG"
     sig_peptide     1. .57
                     /gene="IGH"
     V_region        58. .>420
                     /gene="IGH"
BASE COUNT      89 a     97 c    137 g     97 t
ORIGIN
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  Query Match           72.9%;  Score 261;  DB 9;  Length 420;
  Best Local Similarity  86.6%;  Pred. No. 2e-73;
  Matches  311;  Conservative    0;  Mismatches   45;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||||||| ||||||| |||||||||| |||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAAACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||    | |||||||| ||||||||||||
Db        121 TGTGCAGCCTCTGGATTCACCTTTGGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        181 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        241 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||||||||||||||||||||  |  ||
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCCGTAACCATTGTA 360

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
               |  |  |||  ||  |  ||||||||||||||||||||||||||||||||||||||
Db        361 GTAGTACCAGCTGCGCC--TGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 417
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RESULT 6
HSA300796
LOCUS       HSA300796               351 bp    mRNA    linear   PRI 10-APR-2001
DEFINITION  Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
            variable region (IGHV3-7), clone M2-129 (m2hie129), Kawasaki
            disease patient.
ACCESSION   AJ300796
VERSION     AJ300796.1  GI:12733998
KEYWORDS    IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
            variable region.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Leucht,S., Uttenreuther-Fischer,M.M., Gaedicke,G. and Fischer,P.
  TITLE     The B cell superantigen-like interaction of intravenous
            immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
            germline gene origin cloned from a patient with Kawasaki disease is
            enhanced after IVIG therapy
  JOURNAL   Clin. Immunol. 99 (1), 18-29 (2001)
  MEDLINE   21185274
   PUBMED   11286538
REFERENCE   2  (bases 1 to 351)
  AUTHORS   Fischer,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
            Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
            Berlin, 10117, GERMANY
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Homo sapiens"
                     /isolate="Kawasaki disease patient"
                     /db_xref="taxon:9606"
                     /clone="M2-129 (m2hie129)"
                     /cell_type="B cell"
                     /rearranged
     gene            1. .351
                     /gene="IGHV3-7"
     CDS             <1. .>351
                     /gene="IGHV3-7"
                     /function="immune response"
                     /codon_start=1
                     /product="immunoglobulin gamma heavy chain variable
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                region"
                /protein_id="CAC28901.1"
                /db_xref="GI:12733999"
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                LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDDSG
                IFDYWGQGTLVTVSS"
     V_region   <1. .>351
                /gene="IGHV3-7"
                /product="immunoglobulin gamma heavy chain variable
                region"
BASE COUNT       78 a     85 c    113 g     75 t
ORIGIN

  Query Match          72.8%;  Score 260.6;  DB 9;  Length 351;
  Best Local Similarity   87.2%;  Pred. No. 2.6e-73;
  Matches  313;  Conservative    0;  Mismatches   34;  Indels   12;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | ||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| ||||||||||  |||  ||   | |||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTGGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------- 295

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                |||||   ||   ||||||||||||||||||||||||||||||||||||||||||
Db        296 ---ATGACTCTGGGATCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351


RESULT 7
HSE55314
LOCUS       HSE55314                409 bp    mRNA    linear   PRI 15-MAR-1993
DEFINITION  H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION   Z14189 X65741
VERSION     Z14189.1  GI:31005
KEYWORDS    Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig
            variable region; immunoglobulin.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 409)
  AUTHORS   Tonnelle,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie
            Marseille-Luminy, Case 906, 13288 Marseille Cedex 9, FRANCE
REFERENCE   2  (bases 1 to 409)
  AUTHORS   Cuisinier,A.M., Gauthier,L., Boubli,L., Fougereau,M. and
            Tonnelle,C.
  TITLE     Mechanisms that generate human immunoglobulin diversity operate
            from the 8th week of gestation in fetal liver
  JOURNAL   Eur. J. Immunol. 23 (1), 110-118 (1993)
  MEDLINE   93122076
   PUBMED   8419161
FEATURES             Location/Qualifiers
     source          1. .409
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="3.14"
                     /tissue_type="feral liver"
                     /clone_lib="E55"
     CDS             <1. .>409
                     /codon_start=2
                     /product="Ig heavy chain variable  region (VDJ)"
                     /protein_id="CAA78558.1"
                     /db_xref="GI:31006"
                     /translation="GLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFT
                     FSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSL
                     RAEDTAVYYCARGLTGATDAFDIWGQGTMVTVSS"
     misc_feature    1. .49
                     /note="signal peptide"
     misc_feature    50. .343
                     /note="Ig V-segment"
     misc_feature    344. .362
                     /note="Ig D-segment"
     misc_feature    363. .409
                     /note="Ig J-segment"
BASE COUNT       88 a     90 c    134 g     97 t
ORIGIN

  Query Match          72.5%;  Score 259.4;  DB 9;  Length 409;
  Best Local Similarity   86.4%;  Pred. No. 6.5e-73;
  Matches  310;  Conservative    0;  Mismatches   46;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db         53 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 112

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||   | |||||||| ||||||||||||
Db        113 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 172

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        173 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 232

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        233 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 292

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| |||||||||||||||||||||  |   |
Db        293 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCCTAACT 352

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                || || |||  |||||   ||||||||| || ||  ||||||||||||| |||
Db        353 GGGGCCACGGATGCT--TTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA 409


RESULT 8
AB067237
LOCUS       AB067237                363 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
            partial cds, clone:ya0116h.
ACCESSION   AB067237
VERSION     AB067237.1  GI:21670530
KEYWORDS    .
SOURCE      Homo sapiens cDNA to mRNA, clone_lib:AIMS4 clone:ya0116h.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 363)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
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  JOURNAL   Submitted (25-JUL-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University,
            Immunology; Kutsukake-cho, Toyoake, Aichi 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1. .363
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="ya0116h"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1. .363
                     /gene="IGH"
     CDS             <1. .>363
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain VHDJ region"
                     /protein_id="BAC02275.1"
                     /db_xref="GI:21670531"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKG
                     LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREQQL
                     GPHNWFDPWGQGTLVTVSS"
BASE COUNT       82 a     89 c    120 g     72 t
ORIGIN

  Query Match             72.2%;  Score 258.4;  DB 9;  Length 363;
  Best Local Similarity   86.5%;  Pred. No. 1.4e-72;
  Matches  308;  Conservative    0;  Mismatches   46;  Indels    2;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| |||   ||    | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||| |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGCAGCAG 303

Qy        300 CTTATGACAGA-GGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 354
              ||     |  |   ||  || |||  ||||||||||||||||||||||||||||||
Db        304 CTGGGACCTCACAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTC 359


RESULT 9
HSVH3I3RM
LOCUS       HSVH3I3RM               372 bp    DNA     linear   PRI 17-FEB-1993
DEFINITION  H.sapiens DNA for anti-DNA antibody heavy chain variable
            region,subgroup V(H)3 (III-3R IgM line).
ACCESSION   X63850
VERSION     X63850.1  GI:38346
KEYWORDS    anti-DNA antibody; complementarity determining region; Ig heavy
            chain; Ig kappa light chain; Ig variable region; IgM;
            immunoglobulin; systemic lupus erythematosus.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Manheimer-Lory,A., Katz,J.B., Pillinger,M., Ghossein,C., Smith,A.
            and Diamond,B.
  TITLE     Molecular characteristics of antibodies bearing an
            anti-DNA-associated idiotype
  JOURNAL   J. Exp. Med. 174 (6), 1639-1652 (1991)
  MEDLINE   92078875
   PUBMED   1660528
FEATURES             Location/Qualifiers
     source          1. .372
                     /organism="Homo sapiens"
                     /isolate="patient DIL(SLE)"
                     /db_xref="taxon:9606"
                     /cell_line="EBV-transformed 3I(+) B cell line,III-3R IgM"
                     /tissue_type="spleen"
     misc_feature    <1. .>372
                     /note="IgM heavy chain variable region"
     misc_feature    88. .99
                     /note="complementarity determining region, CDR 1"
     misc_feature    145. .198
                     /note="complementarity determining region, CDR 2"
BASE COUNT       81 a     90 c    126 g     75 t
ORIGIN

  Query Match             72.2%;  Score 258.4;  DB 9;  Length 372;
  Best Local Similarity   85.2%;  Pred. No. 1.4e-72;
  Matches  317;  Conservative    0;  Mismatches   41;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 60

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| |||   ||    | ||||||||| ||||||||||||
Db         61 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATCGGATGAGCTGGGTCCGCCAGGCTCCA 120

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        121 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 180

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        181 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 240

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGA----- 294
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGAAGGATG 300

Qy        295 --------TCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                      ||    ||          ||||||||||||||||||||||||||||||||||
Db        301 TGGGAGAGGTGGTTCGGGGAGTCCCCGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTC 360

Qy        347 ACCGTCTCCTCA 358
              ||||||||||||
Db        361 ACCGTCTCCTCA 372


RESULT 10
HSA300786
LOCUS       HSA300786               351 bp    mRNA    linear   PRI 10-APR-2001
DEFINITION  Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
            variable region (IGHV3-7), clone M1-45 (m1hie45), Kawasaki disease
            patient.
ACCESSION   AJ300786
VERSION     AJ300786.1  GI:12733975
KEYWORDS    IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
            variable region.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 351)
  AUTHORS   Leucht,S., Uttenreuther-Fischer,M.M., Gaedicke,G. and Fischer,P.
  TITLE     The B cell superantigen-like interaction of intravenous
            immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
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            germline gene origin cloned from a patient with Kawasaki disease is
            enhanced after IVIG therapy
  JOURNAL   Clin. Immunol. 99 (1), 18-29 (2001)
  MEDLINE   21185274
   PUBMED   11286538
REFERENCE   2  (bases 1 to 351)
  AUTHORS   Fischer,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
            Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
            Berlin, 10117, GERMANY
FEATURES             Location/Qualifiers
     source          1. .351
                     /organism="Homo sapiens"
                     /isolate="Kawasaki disease patient"
                     /db_xref="taxon:9606"
                     /clone="M1-45 (m1hie45)"
                     /cell_type="B cell"
                     /rearranged
     gene            1. .351
                     /gene="IGHV3-7"
     CDS             <1. .>351
                     /gene="IGHV3-7"
                     /function="immune response"
                     /codon_start=1
                     /product="immunoglobulin gamma heavy chain variable
                     region"
                     /protein_id="CAC28891.1"
                     /db_xref="GI:12733976"
                     /translation="EVQLLESGGGLVQPGESLRLSCAASGFTFSSYGMSWVRQAPGKG
                     LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREVAG
                     HFDYWGQGTLVTVSS"
     V_region        <1. .>351
                     /gene="IGHV3-7"
                     /product="immunoglobulin gamma heavy chain variable
                     region"
BASE COUNT       79 a     84 c    114 g     74 t
ORIGIN

  Query Match             71.9%;  Score 257.4;  DB 9;  Length 351;
  Best Local Similarity   86.6%;  Pred. No. 2.9e-72;
  Matches  311;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | |||||||||||||||||||| ||||||| | ||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGAGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| ||| ||    | ||| ||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATGGGATGAGTTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| |||||||||||||||||||| | |   |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGTGGCT 303

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ----------GGTCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351


RESULT 11
AX061464
LOCUS       AX061464                375 bp    DNA     linear   PAT 22-JAN-2001
DEFINITION  Sequence 33 from Patent WO0100678.
ACCESSION   AX061464
VERSION     AX061464.1  GI:12406599
KEYWORDS    .
SOURCE      Human immunodeficiency virus type 1.
  ORGANISM  Human immunodeficiency virus type 1
            Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate
            lentivirus group.
REFERENCE   1  (bases 1 to 375)
  AUTHORS   Watkins,B.A. and Reitz,M.S.
  TITLE     Human monoclonal antibodies to hiv-1 envelope glycoprotein gp120
  JOURNAL   Patent: WO 0100678-A 33 04-JAN-2001;
            THE GOVERNMENT OF THE UNITED STATES OF AMERICA (US)
FEATURES             Location/Qualifiers
     source          1. .375
                     /organism="Human immunodeficiency virus type 1"
                     /db_xref="taxon:11676"
                     /note="VH"
BASE COUNT       81 a     90 c    116 g     88 t
ORIGIN

  Query Match             71.7%;  Score 256.6;  DB 6;  Length 375;
  Best Local Similarity   85.1%;  Pred. No. 5.2e-72;
  Matches  314;  Conservative    0;  Mismatches   44;  Indels   11;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          7 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 66

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| ||| ||    | ||||||||| ||||||||||||
Db         67 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 126

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        127 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 186

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||| ||||  ||||||||||||||||||||||||
Db        187 GACTCTGTGAAGGGCCGATTCACCATCTTCAGAAACAACGCCAAGAACTCACTGTATCTG 246

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCT-- 297
              |||||||||||||||||||||||||||||| ||||||||||||||||  |   ||
Db        247 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGTTGCTACTAT 306

Qy        298 --------GTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC 349
                      |  |||| |       |  ||||| ||||||||||||||||||||||||||||
Db        307 GGTTCGGGGAGTTATTATTTCTACCCCTTTGCCTACTGGGGCCAGGGAACCCTGGTCACC 366

Qy        350 GTCTCCTCA 358
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Db        367 GTCTCCTCA 375


RESULT 12
HSU80083
LOCUS       HSU80083                348 bp    DNA     linear   PRI 19-FEB-1997
DEFINITION  Human immunoglobulin heavy chain variable region (V3-07) gene,
            partial cds.
ACCESSION   U80083
VERSION     U80083.1  GI:1791008
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 348)
  AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.
  TITLE     Analysis of rearranged immunoglobulin heavy chain variable region
            genes obtained from a bone marrow transplant (BMT) recipient
  JOURNAL   Clin. Exp. Immunol. 107 (2), 372-380 (1997)
  MEDLINE   97182739
   PUBMED   9030878
REFERENCE   2  (bases 1 to 348)
  AUTHORS   Glas,A.M., Nottenburg,C. and Milner,E.C.B.
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  TITLE     Direct Submission
  JOURNAL   Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
            1000 Seneca Street, Seattle, WA 98101, USA
FEATURES             Location/Qualifiers
     source          1. .348
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /map="14q32-q33"
                     /clone="3b2g11"
                     /cell_type="CD19+ B cells"
                     /tissue_type="peripheral blood"
                     /note="CD19+ peripheral blood B cells obtained from a bone
                     marrow transplant recipient 90 days post transplant; clone
                     1 in reference 1"
     gene            1. .348
                     /gene="V3-07"
     CDS             <1. .>348
                     /gene="V3-07"
                     /note="Ig VH3 heavy chain"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAC50998.1"
                     /db_xref="GI:1791009"
                     /translation="EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKG
                     LEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGSSD
                     MDYWGQGTLVTVSS"
BASE COUNT       79 a     83 c    114 g     72 t
ORIGIN

  Query Match             71.6%;  Score 256.2;  DB 9;  Length 348;
  Best Local Similarity   86.6%;  Pred. No. 7e-72;
  Matches  311;  Conservative    0;  Mismatches   33;  Indels   15;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||    | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||| |||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAAGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              ||||||||||||||||||||||||||||||| |||||||||||||||| ||    | ||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGGGCTCCAGT 303

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                ||||              ||||||||||||||||||||||||||||||||||||
Db        304 GATATG--------------GACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 348


RESULT 13
HSU76679
LOCUS       HSU76679                360 bp    mRNA    linear   PRI 14-MAY-2001
DEFINITION  Homo sapiens clone CDC-1hc IgM heavy chain variable region mRNA,
            partial cds.
ACCESSION   U76679
VERSION     U76679.1  GI:1673596
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Aguilera,I., Melero,J., Nunez-Roldan,A. and Sanchez,B.
  TITLE     Molecular structure of eight human autoreactive monoclonal
            antibodies
  JOURNAL   Immunology 102 (3), 273-280 (2001)
  MEDLINE   21195372
   PUBMED   11298825
REFERENCE   2  (bases 1 to 360)
  AUTHORS   Aguilera,I.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-OCT-1996) Hospital U. Virgen del Rocio, Immunology,
            Manuel Siurot s/n, Seville, Spain, 41013
FEATURES             Location/Qualifiers
     source          1. .360
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CDC-1hc"
                     /cell_type="hybridoma"
     CDS             <1. .>360
                     /codon_start=1
                     /product="IgM heavy chain variable region"
                     /protein_id="AAB18977.1"
                     /db_xref="GI:1673597"
                     /translation="EVQLVESGGGLVRPGGSLRLSCAASGFTFSSFWLNWVRQAPGKG
                     LEWVANIIQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRDDDTAIYYCARGSAG
                     TSPRLDYWGQGTLVTVSS"
BASE COUNT       74 a     94 c    114 g     78 t
ORIGIN

  Query Match             71.6%;  Score 256.2;  DB 9;  Length 360;
  Best Local Similarity   85.8%;  Pred. No. 7e-72;
  Matches  308;  Conservative    0;  Mismatches   48;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCGGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  |    || |||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTTTTGGCTGAACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||||   || ||||| ||||    ||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAATTCAAGACGGAAGTGAGAAGTACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||| ||| ||||||||| | ||||||||||  |||| |  |
Db        244 CAAATGAACAGCCTGAGAGACGATGACACGGCCATTTATTACTGTGC--GAGGGGTTCGG 301

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              || |  |    |  |||||||||||||||||||||||||||||||||||||||||||
Db        302 CTGGTACCTCCCCCCGCCTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 360


RESULT 14
HSA300785
LOCUS       HSA300785               354 bp    mRNA    linear   PRI 10-APR-2001
DEFINITION  Homo sapiens partial mRNA for immunoglobulin gamma heavy chain
            variable region (IGHV3-7), clone M1-40 (m1hie40), Kawasaki disease
            patient.
ACCESSION   AJ300785
VERSION     AJ300785.1  GI:12733973
KEYWORDS    IGHV3-7 gene; immunoglobulin gamma heavy chain; kawasaki disease;
            variable region.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 354)
  AUTHORS   Leucht,S., Uttenreuther-Fischer,M.M., Gaedicke,G. and Fischer,P.
  TITLE     The B cell superantigen-like interaction of intravenous
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          immunoglobin (IVIG) with Fab fragments of V(H) 3-23 and 3-30/3-30.5
          germline gene origin cloned from a patient with Kawasaki disease is
          enhanced after IVIG therapy
  JOURNAL   Clin. Immunol. 99 (1), 18-29 (2001)
  MEDLINE   21185274
   PUBMED   11286538
REFERENCE   2  (bases 1 to 354)
  AUTHORS   Fischer,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JAN-2001) Fischer P., Charite Children's Hospital,
          Molecular Biology Laboratory, Humboldt-University, Ziegelstr. 5-9,
          Berlin, 10117, GERMANY
FEATURES             Location/Qualifiers
     source          1. .354
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                     /isolate="Kawasaki disease patient"
                     /db_xref="taxon:9606"
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BASE COUNT       79 a     86 c    115 g     74 t
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  Matches  309;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    2;

Qy          3 GCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCCTG 62
              || ||| | | |||||||||||||||||||| ||||||| ||||||||||||||||||||
Db          9 GCTGCTCGAGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTG 68

Qy         63 TGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCAGG 121
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Qy        122 GAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCGGA 181
              |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |||
Db        129 GAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTGGA 188

Qy        182 CTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTGCA 241
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        189 CTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCA 248

Qy        242 AATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGTCT 301
              |||||||||||||||||||||||||||||| |||||||||||||||||| | |   |
Db        249 AATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGTGGCT-- 306

Qy        302 TATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
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Db        307 ---------GGTCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 354


RESULT 15
AF062188
LOCUS       AF062188               372 bp    mRNA    linear   PRI 08-MAY-2001
DEFINITION  Homo sapiens clone 48u-19 immunoglobulin heavy chain variable
          region (IGH) mRNA, partial cds.
ACCESSION   AF062188
VERSION     AF062188.1  GI:3170838
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 372)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Immunoglobulin VH gene expression in human aging
  JOURNAL   Clin. Immunol. 93 (2), 132-142 (1999)
  MEDLINE   99459182
   PUBMED   10527689
REFERENCE   2  (bases 1 to 372)
  AUTHORS   Wang,X. and Stollar,B.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-APR-1998) Biochemistry Department, Tufts University
          School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
FEATURES             Location/Qualifiers
     source          1. .372
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                     /db_xref="taxon:9606"
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                     /map="14q32.33"
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  Best Local Similarity   85.0%;  Pred. No. 2e-71;
  Matches  311;  Conservative    0;  Mismatches   47;  Indels    8;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||  || |||||| |||||| |||  ||    | ||||||||| ||||||||||
Db         64 TGTGCAGGATCTGGATTCCCCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||  || |||| |  ||  |||| |||   ||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        184 GACTCTGTGAAGGGCCACTTCACCATCTCCAGAGACAACGCCAAGAACTCGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Db        244 CAAATGAACAGCCTGAGAGCCGGTGACACGGCTGTGTATTACTGTGCGAGGGCGAGGGCA 303

Qy        300 CTTATGACAGAGG-------CTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 352
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Db        304 GTATTTAGAGTGGGAACTACTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 363
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Qy          353 TCCTCA 358
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Db          364 TCCTCA 369
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Search completed: July 18, 2003, 13:47:39
Job time : 1004.03 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:16:54 ; Search time 620.38 Seconds
(without alignments)
9345.860 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 1 gtgcagctggtggagtctgg.....ccctggtcaccgtctcctca 358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	262.4	73.3	704	12	BG759119	BG759119 602710759
2	261	72.9	735	9	AL551886	AL551886 AL551886
3	249	69.6	848	12	BG756291	BG756291 602713609
4	248.2	69.3	904	14	BQ709359	BQ709359 AGENCOURT
5	247.4	69.1	831	12	BG756386	BG756386 602715711
6	247.4	69.1	853	12	BG755960	BG755960 602716437
7	245	68.4	888	14	BQ706683	BQ706683 AGENCOURT
8	244	68.2	950	14	BQ711129	BQ711129 AGENCOURT
9	243.8	68.1	770	12	BG758713	BG758713 602712981
10	243.6	68.0	895	14	BQ710073	BQ710073 AGENCOURT
11	243.6	68.0	934	14	BQ708566	BQ708566 AGENCOURT
12	243.4	68.0	979	14	BQ708029	BQ708029 AGENCOURT
13	243.2	67.9	1164	12	BF974771	BF974771 602245420
14	241.8	67.5	443	10	AW401428	AW401428 UI-HF-BK0
15	241.8	67.5	540	10	AW402648	AW402648 UI-HF-BK0
16	241.8	67.5	938	14	BQ706365	BQ706365 AGENCOURT
17	241.2	67.4	750	12	BG340591	BG340591 602462161
18	240.2	67.1	669	14	BM767227	BM767227 K-EST0049
19	240.2	67.1	920	14	BQ711467	BQ711467 AGENCOURT
20	239	66.8	511	10	AW402613	AW402613 UI-HF-BK0
21	238.8	66.7	942	14	BQ710859	BQ710859 AGENCOURT
22	238.6	66.6	881	12	BG686259	BG686259 602638142
23	238.4	66.6	618	14	BM713479	BM713479 UI-E-EJ0-
24	237.4	66.3	436	10	AW402311	AW402311 UI-HF-BK0
25	237.4	66.3	928	14	BQ943156	BQ943156 AGENCOURT
26	237	66.2	999	14	BQ711203	BQ711203 AGENCOURT
27	236.6	66.1	798	12	BF128991	BF128991 601811308
28	235.8	65.9	896	14	BQ717993	BQ717993 AGENCOURT
29	235.8	65.9	984	14	BQ709776	BQ709776 AGENCOURT
30	235.2	65.7	471	10	AW403220	AW403220 UI-HF-BK0
31	235.2	65.7	907	14	BQ708724	BQ708724 AGENCOURT
32	235.2	65.7	1001	14	BM914366	BM914366 AGENCOURT
33	234.6	65.5	447	10	AW403163	AW403163 UI-HF-BK0
34	234.6	65.5	937	14	BQ707419	BQ707419 AGENCOURT
35	233.8	65.3	518	10	AW402029	AW402029 UI-HF-BK0
36	233.8	65.3	1069	14	BM914329	BM914329 AGENCOURT
37	233	65.1	669	12	BG686716	BG686716 602650678
38	232.4	64.9	810	12	BG538620	BG538620 602567352
39	232.2	64.9	834	14	BQ711497	BQ711497 AGENCOURT
40	232	64.8	958	14	BQ709987	BQ709987 AGENCOURT
41	232	64.8	962	14	BQ706534	BQ706534 AGENCOURT
42	231.4	64.6	456	10	AW403059	AW403059 UI-HF-BK0
43	230.8	64.5	518	14	BM708960	BM708960 UI-E-CI1-
44	230.2	64.3	908	12	BG686881	BG686881 602650867
45	229.4	64.1	1000	14	BQ712690	BQ712690 AGENCOURT

ALIGNMENTS

RESULT 1
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LOCUS BG759119 704 bp mRNA linear EST 15-MAY-2001
DEFINITION 602710759F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851063 5', mRNA sequence.
ACCESSION BG759119
VERSION BG759119.1 GI:14069772
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1693 row: e column: 16
High quality sequence stop: 701.
FEATURES Location/Qualifiers
source 1. .704

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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4851063"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      139 a    201 c    214 g    150 t
ORIGIN

  Query Match             73.3%;  Score 262.4;  DB 12;  Length 704;
  Best Local Similarity   86.7%;  Pred. No. 7.8e-62;
  Matches  312;  Conservative    0;  Mismatches   46;  Indels    2;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db        124 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 183

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| || ||| |||||||||||||| |||  ||    | ||||||||| ||||||||||| |
Db        184 TGTGTAGTCTCTGGATTCACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCCAGGCTCCA 243

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
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Db        244 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 303

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        304 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 363

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
              |||||||||||||||||||||||||||||| ||||||||||||||||||    | ||
Db        364 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGCAGC 423

Qy        299 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                  |    |||| | ||  || ||   ||||||||||||||||||||||||||||||||
Db        424 AGCTGGTACAGGGACTGGTTCGAGCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 483


RESULT 2
AL551886
LOCUS       AL551886                735 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL551886 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI061YP03 5
            prime, mRNA sequence.
ACCESSION   AL551886
VERSION     AL551886.1  GI:12890261
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      161 a    206 c    223 g    140 t      5 others
ORIGIN

  Query Match             72.9%;  Score 261;  DB 9;  Length 735;
  Best Local Similarity   86.6%;  Pred. No. 2e-61;
  Matches  311;  Conservative    2;  Mismatches   37;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        108 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 167

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db        168 TGTGCAGCCTCTGGATTCAMCTTTAGTAGCCATTGGATGAGCTGGGTCCGCCAGGCTCCA 227

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
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Db        228 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATAMTATGTG 287

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        288 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 347

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| |||||||||||||||||| |  | ||
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Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                  |  | |||   ||||||||||||||||||| ||||||||||||||||||||||
Db        408 --------GGCTGGTACGCGGACTACTGGGGCCAGGGAACTCTGGTCACCGTCTCCTCA 458


RESULT 3
BG756291
LOCUS       BG756291                848 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602713609F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853667 5',
            mRNA sequence.
ACCESSION   BG756291
VERSION     BG756291.1  GI:14066944
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 848)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1700  row: b  column: 04
            High quality sequence stop: 778.
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                     /clone="IMAGE:4853667"
                     /clone_lib="NIH_MGC_48"
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                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      187 a    252 c    236 g    173 t
ORIGIN

  Query Match             69.6%;  Score 249;  DB 12;  Length 848;
  Best Local Similarity   85.0%;  Pred. No. 4.4e-58;
  Matches  305;  Conservative    0;  Mismatches   45;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db        124 GTGCAGCTGGTGGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 183

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||| |||| ||    ||    | || |||||| ||||||||||||
Db        184 TGTGCAGCCTCTGGATTCACTTTTAGTATCTATTGGATGACCTGGGTCCGCCAGGCTCCA 243

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||  |||||||||||||||||  ||||||| || ||  |||| |||    |||||||| |
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Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        304 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 363

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||| | ||||||||||||||||  |  ||
Db        364 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCATCTATTACTGTGCGAGAGTAAGTTGG 423

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                |  |    |  | || |          ||||||||||||||||||||||||||||||||
Db        424 ATGGTTCAGGGAGTTAGT--------TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 474


RESULT 4
BQ709359
LOCUS       BQ709359                904 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7983019 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215641
            5', mRNA sequence.
ACCESSION   BQ709359
VERSION     BQ709359.1  GI:21848258
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 904)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2384  row: o  column: 02
            High quality sequence stop: 667.

FEATURES             Location/Qualifiers
     source          1. .904
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215641"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      200 a    265 c    254 g    185 t
ORIGIN

  Query Match             69.3%;  Score 248.2;  DB 14;  Length 904;
  Best Local Similarity   84.4%;  Pred. No. 7.6e-58;
  Matches  303;  Conservative    0;  Mismatches   53;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||| |||||||||||||||||||||||||||| ||||||| |||||||| |||||||||
Db        128 GTGCGGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTAAGACTCTCC 187

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| |||||| |||||||| |||| | |  ||    | || |||||| ||||||||||||
Db        188 TGTGAAGCCTCTGGATTCACGTTTAGTGGCCATTGGATGACCTGGGTCCGCCAGGCTCCA 247

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||| ||||||||||||||||  || |||| ||  |  |||| |||   || |||||||
Db        248 GGGAGGGGGCTGGAGTGGGTGGCCAACATAAAGGACGATGGAAGTGACAAATTCTATGCG 307

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        308 GACTCACTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTA 367

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Db        368 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTTCTGTGGGAGA--CATCTGC 425

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                |  |    | |||||||||| ||||||||||||||||||||||||||||||||
Db        426 TAGGGGGTAACAACGACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 484


RESULT 5
BG756386
LOCUS       BG756386                831 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602715711F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855682 5',
            mRNA sequence.
ACCESSION   BG756386
VERSION     BG756386.1  GI:14067039
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 831)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1705  row: f  column: 03
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           High quality sequence stop: 790.
FEATURES             Location/Qualifiers
     source          1. .831
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4855682"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      182 a    244 c    237 g    168 t
ORIGIN

  Query Match             69.1%;  Score 247.4;  DB 12;  Length 831;
  Best Local Similarity   84.7%;  Pred. No. 1.2e-57;
  Matches  304;  Conservative    0;  Mismatches   46;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||| |||||||||||||||||| ||||||| ||||||||||||||||||
Db        123 GTGCAGCTGGTGGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 182

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||| |||| ||    ||    | || |||||| ||||||||||
Db        183 TGTGCAGCCTCTGGATTCACTTTTAGTATCTATTGGATGACCTGGGTCCGCCAGGCTCCA 242

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||| ||||||||||||||||  ||||||| || ||  |||| |||   |||||||| |
Db        243 GGGAAAGGGCTGGAGTGGGTGGCCAATATAAAGGAAGATGGAAGTGACAAATACTATGTG 302

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        303 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 362

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| | ||||||||||||||   |  ||
Db        363 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCATCTATTACTGTGCGAGAGTAAGTTGG 422

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |  |    |   || |        ||||||||||||||||||||||||||||||||
Db        423 ATGGTTCAGGGACTTAGT--------TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 473


RESULT 6
BG755960
LOCUS       BG755960                 853 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602716437F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856553 5',
            mRNA sequence.
ACCESSION   BG755960
VERSION     BG755960.1  GI:14066613
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1707  row: j  column: 10
            High quality sequence stop: 793.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4856553"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      183 a    254 c    239 g    177 t
ORIGIN

  Query Match             69.1%;  Score 247.4;  DB 12;  Length 853;
  Best Local Similarity   84.7%;  Pred. No. 1.2e-57;
  Matches  304;  Conservative    0;  Mismatches   46;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||| |||||||||||||||||| ||||||| ||||||||||||||||||
Db        129 GTGCAGCTGGTGGAATCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 188

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| | |||||| |||| ||    ||    | || |||||| ||||||||||
Db        189 TGTGCAGCCTCTGTATTCACTTTTAGTATCTATTGGATGACCTGGGTCCGCCAGGCTCCA 248

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||| ||||||||||||||||  ||||||| || ||  |||| |||   |||||||| |
Db        249 GGGAAAGGGCTGGAGTGGGTGGCCAATATAAAGGAAGATGGAAGTGACAAATACTATGTG 308

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        309 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 368

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| | ||||||||||||||   |  ||
Db        369 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCATCTATTACTGTGCGAGAGTAAGTTGG 428

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |  |    |  | || |        ||||||||||||||||||||||||||||||||
Db        429 ATGGTTCAGGGAGTTAGT--------TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 479


RESULT 7
BQ706683
LOCUS       BQ706683                 888 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7976366 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214494
            5', mRNA sequence.
ACCESSION   BQ706683
VERSION     BQ706683.1  GI:21845582
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 888)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
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            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2381  row: o  column: 07
           High quality sequence stop: 653.
FEATURES             Location/Qualifiers
     source          1. .888
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6214494"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC_Library."
BASE COUNT      188 a    259 c    248 g    192 t      1 others
ORIGIN

  Query Match             68.4%;  Score 245;  DB 14;  Length 888;
  Best Local Similarity   83.8%;  Pred. No. 5.8e-57;
  Matches  301;  Conservative    0;  Mismatches   55;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        113 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 172

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
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Db        173 TGTGCAGCCTCTGGATTCGCCTTTAGTAGTTTTTGGATGAGTTGGGTCCGCCAGGCTCCA 232

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||||  ||  ||||    ||  ||||  |||   ||||||||  |
Db        233 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAACCAAGATGGAAGTGAGAAATACTATGTG 292

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        293 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCTCTGTTTCTG 352

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
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Db        353 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTCTATTATTGTGCGAGA--GTTTATG 410

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                ||  |  ||          |||| ||||||||||||||| | ||||||||||||||||||
Db        411 GTTCGGGGAGCTATCCAGATGACCACTGGGGCCAGGGAGCGCTGGTCACCGTCTCCTCA 469


RESULT 8
BQ711129
LOCUS       BQ711129                950 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7977239 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215821
            5', mRNA sequence.
ACCESSION   BQ711129
VERSION     BQ711129.1  GI:21850028
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 950)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM2385  row: f  column: 14
           High quality sequence stop: 398.
FEATURES             Location/Qualifiers
     source          1. .950
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215821"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      192 a    259 c    297 g    200 t      2 others
ORIGIN

  Query Match             68.2%;  Score 244;  DB 14;  Length 950;
  Best Local Similarity   83.2%;  Pred. No. 1.1e-56;
  Matches  302;  Conservative    0;  Mismatches   56;  Indels    5;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
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Db        131 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 190

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||  |||||||||||||  |||  ||    | |||||||||  ||||||||||||
Db        191 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 250

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||||  || |||| |  ||  |||| |||   ||||||||  |
Db        251 NGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 310

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        311 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 370

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
              |||||||||||||||||||||||||||||||||| ||||||||||||||||  |  |  |
Db        371 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGTGTGTGGGG 430

Qy        299 ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
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Db        431 GGCTGGTACATCACCTACGGTATGGACGTCTGGGGCCACGGGACCACTGTCAATATCTCC 490

Qy        356 TCA 358
              |||
Db        491 TCA 493


RESULT 9
BG758713
LOCUS       BG758713                770 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602712981F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852916 5',
            mRNA sequence.
ACCESSION   BG758713
VERSION     BG758713.1  GI:14069379
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
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  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1698  row: b  column: 21
            High quality sequence stop: 718.
FEATURES             Location/Qualifiers
     source          1. .770
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4852916"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      168 a    221 c    225 g    156 t
ORIGIN

  Query Match             68.1%;  Score 243.8;  DB 12;  Length 770;
  Best Local Similarity   84.4%;  Pred. No. 1.1e-56;
  Matches  303;  Conservative    0;  Mismatches   42;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| |||| || ||||||||||||||||||
Db        125 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCGGGGGGGTCCCTGAGACTCTCC 184

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||| ||| ||   | ||||||||| ||||||||||||
Db        185 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 244

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  || | |||   |||||||| |
Db        245 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCCAGATGGCAGTGAGAAATACTATGTG 304

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||| |||||||||  ||||
Db        305 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAAAACTCACTGTCTCTG 364

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |  | |
Db        365 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGACGAGATGATCT 424

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                        | | ||| ||||||||||||||||||||||||||||||||||||
Db        425 ------------GGCCCTCGACCACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 470


RESULT 10
BQ710073
LOCUS       BQ710073                 895 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7983184 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215340
            5', mRNA sequence.
ACCESSION   BQ710073
VERSION     BQ710073.1  GI:21848972
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2384  row: b  column: 13
            High quality sequence stop: 654.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6215340"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      193 a    273 c    235 g    194 t
ORIGIN

  Query Match             68.0%;  Score 243.6;  DB 14;  Length 895;
  Best Local Similarity   83.1%;  Pred. No. 1.4e-56;
  Matches  304;  Conservative    0;  Mismatches   54;  Indels    8;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||| |||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        106 GTGCGGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 165

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| || ||| |||||||||||||| ||| ||   | ||||||||| |||||||  |||
Db        166 TGTGTAGTCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGACCCA 225

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              | |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        226 GTGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 285

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| |||||||||| |||||||  ||||
Db        286 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAGCTCACTGTTTCTG 345

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGA-------GAGG 292
              ||||| |||||||||||||||||||||||||| ||||| ||||||||||        ||
Db        346 CAAATCAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAAAACTAGTAGC 405

Qy        293 GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 352
              ||      |   |  |     |||||||||||||||||||||||||||  ||||||||||
Db        406 GACTATCCACCTATCCATTACTACTTTGACTACTGGGGCCAGGGAACTTTGGTCACCGTC 465

Qy        353 TCCTCA 358
              ||||||
Db        466 TCCTCA 471


RESULT 11
BQ708566
LOCUS       BQ708566                 934 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_7975980 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214806
            5', mRNA sequence.
ACCESSION   BQ708566
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VERSION     BQ708566.1  GI:21847465
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 934)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2382  row: l  column: 07
            High quality sequence start: 6
            High quality sequence stop: 653.
FEATURES             Location/Qualifiers
     source          1. .934
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6214806"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      203 a    271 c    257 g    200 t      3 others
ORIGIN

  Query Match             68.0%;  Score 243.6;  DB 14;  Length 934;
  Best Local Similarity   83.1%;  Pred. No. 1.4e-56;
  Matches  304;  Conservative    0;  Mismatches   54;  Indels    8;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||| |||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        108 GTGCGGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 167

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| || ||| |||||||||||| ||| ||   | ||||||||| |||||||  |||
Db        168 TGTGTAGTCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGACCCA 227

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              | |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        228 GTGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 287

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||| |||||||||| |||||||| ||||
Db        288 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAGCTCACTGTTTCTG 347

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGA-------GAGG 292
              ||||| |||||||||||||||||||||||||| ||||| ||||||||||          ||
Db        348 CAAATCAACAGCCTGAGAGCCGAGGACACGGCTGTGTACTACTGTGCGAAAACTAGTAGC 407

Qy        293 GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC 352
              ||     |  | |     |||||||||||||||||||||||||  ||||||||||
Db        408 GACTATCCACCTATCCATTACTACTTTGACTACTGGGGCCAGGGAACTTTGGTCACCGTC 467

Qy        353 TCCTCA 358
              ||||||
Db        468 TCCTCA 473
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RESULT 12
BQ708029
LOCUS       BQ708029                979 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8352453 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277625
            5', mRNA sequence.
ACCESSION   BQ708029
VERSION     BQ708029.1  GI:21846928
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 979)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464  row: e  column: 18
            High quality sequence stop: 626.
FEATURES             Location/Qualifiers
     source          1. .979
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6277625"
                     /clone_lib="NIH_MGC_113"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
BASE COUNT      257 a    262 c    279 g    180 t      1 others
ORIGIN

  Query Match             68.0%;  Score 243.4;  DB 14;  Length 979;
  Best Local Similarity   88.2%;  Pred. No. 1.7e-56;
  Matches  276;  Conservative    0;  Mismatches   36;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        130 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 189

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||   | ||||||||| |||||||||||
Db        190 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 249

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        250 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 309

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        310 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 369

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||| |||||||||||||||||| |||
Db        370 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGTGATTATG 429

Qy        300 CTTATGACAGAGG 312
              ||| |   | ||
Db        430 ATTACGTTTGGGG 442
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RESULT 13
BF974771
LOCUS       BF974771               1164 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602245420F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336541 5',
            mRNA sequence.
ACCESSION   BF974771
VERSION     BF974771.1  GI:12341986
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1164)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1209  row: g  column: 06
            High quality sequence stop: 696.
FEATURES             Location/Qualifiers
     source          1. .1164
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4336541"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      284 a    313 c    330 g    236 t      1 others
ORIGIN

  Query Match           67.9%;  Score 243.2;  DB 12;  Length 1164;
  Best Local Similarity   83.3%;  Pred. No. 2.1e-56;
  Matches  300;  Conservative    0;  Mismatches   58;  Indels    2;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 183

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||| | |    |    | ||||||| | ||||||||||||
Db        184 TGTGCAGCCTCTGGATTCACCTTCAGTGACTACTACATGAGCTGGATCCGCCAGGCTCCA 243

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||      | || |          | | | |   ||  ||| ||
Db        244 GGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTTACACAAGCTACGCA 303

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        304 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 363

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG-GGATCTG 298
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |    |
Db        364 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGATCAGAGG 423

Qy        299 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |  ||  |   | ||||||||||||||||||||||||||||||||||||||||||||
Db        424 AACAACCAGCTGGTAGATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 483


RESULT 14
AW401428
LOCUS       AW401428               443 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aad-b-02-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3053139 5', mRNA sequence.
ACCESSION   AW401428
VERSION     AW401428.1  GI:6920011
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 443)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .443
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3053139"
                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D.  and M. Bento Soares, Ph.D."
BASE COUNT       93 a    116 c    131 g    103 t
ORIGIN

  Query Match           67.5%;  Score 241.8;  DB 10;  Length 443;
  Best Local Similarity   83.3%;  Pred. No. 2.9e-56;
  Matches  299;  Conservative    0;  Mismatches   57;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| |||||||||||| |||||||||| |||||
Db         85 GTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGAGTCTCC 144

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||| ||||    || | | || |||||| ||||||||||||
Db        145 TGTGCAGCCTCTGGATTCACCTTCACTACCTATACCATGAACTGGGTCCGCCAGGCTCCA 204

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||        || |         || | | |   |||||| ||
Db        205 GGGAAGGGGCTGGAGTGGGTCTCATCCATGAGTAGTACTGGTACTTACATATACTACGCA 264

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        265 GACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 324

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              || |||||||||||||||||||||||||| || || |||||||||||||||||    |
Db        325 CAGATGAACAGCCTGAGAGCCGAGGACACCGCTGTCTATTACTGTGCGAGAGG--AGTTC 382
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Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |    |       ||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 CCATGGTTCAGTTCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 441


RESULT 15
AW402648
LOCUS       AW402648                 540 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aav-b-10-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3055051 5', mRNA sequence.
ACCESSION   AW402648
VERSION     AW402648.1  GI:6921355
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3055051"
                     /clone_lib="NIH_MGC_36"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D.  and M. Bento Soares, Ph.D."
BASE COUNT      120 a    133 c    161 g    126 t
ORIGIN

  Query Match            67.5%;  Score 241.8;  DB 10;  Length 540;
  Best Local Similarity  82.9%;  Pred. No. 3.3e-56;
  Matches  301;  Conservative    0;  Mismatches   57;  Indels    5;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Db        130 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 189

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||   |  ||   | ||| ||||| |||||| |||||
Db        190 TGTGCAGCCTCTGGATTCACCTTTAGCAACTATTGGATGAGTTGGGTCCGCCAGTCTCCA 249

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||  || |||| || ||  |||| |||   |||||||| |
Db        250 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGGAAGATGGAAGTGAGAAATACTATGTG 309

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| |||||||||||||||| ||||||
Db        310 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTATATCTG 369

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||| |||||||||||| || |||||||||| |||||       |
Db        370 CAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTATATTACTGTGTGAGAGACCATGAT 429
```

```
Qy        300 CTTATGACAGAGGCTA----CTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
              ||  |    |  ||      | |  ||||||||||||||||||||| |||||||
Db        430 ACTAGCAGCTGGTATAAACTGGTCGGACCCTGGGGCCAGGGAACCCTGGTCATCGTCTCC 489

Qy        356 TCA 358
              |||
Db        490 TCA 492


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Job time : 622.38 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 04:14:58 ; Search time 92.8077 Seconds
(without alignments)
8686.944 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 1 gtgcagctggtggagtctgg.....ccctggtcaccgtctcctca 358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	256.6	71.7	375	22	AAF29077	Human HIV-1 monocl
2	254.6	71.1	814	20	AAV74274	Human clone A6 fus
3	243	67.9	675	22	AAH41661	Human interleukin
4	243	67.9	675	22	AAH30007	Anti-IL8 monoclona
5	241	67.3	402	24	AAK98398	Human anti-FAPalph
6	241	67.3	788	24	AAK98407	Anti-FAPalpha anti
7	240	67.0	792	24	ABK32988	Affinity matured c
8	240	67.0	794	24	ABK32986	Affinity matured c
9	240	67.0	795	24	ABK32983	DNA sequence of hu
10	240	67.0	877	16	AAQ78945	Human immunoglobul
11	240	67.0	939	20	AAV72533	Single chain Apo-2
12	240	67.0	939	24	ABL41734	Nucleotide sequenc
13	239	66.8	294	16	AAQ89332	DP54 VH gene. Hom
14	238.6	66.6	366	22	AAF75589	Human anti-HER2/ne
15	238.6	66.6	366	24	ABK14254	AAV293 anti-(MCP)-
16	238.2	66.5	366	22	AAS03534	DNA encoding anti-
17	237.4	66.3	1395	21	AAA46866	DNA encoding the h
18	237.4	66.3	1395	21	AAA46894	DNA encoding the h
19	237	66.2	348	24	ABA94334	MAb 27A1 heavy cha
20	236.8	66.1	1736	22	AAS22532	Human cDNA encodin
21	235.8	65.9	681	22	AAH30055	TRO005 heavy chain
22	235.8	65.9	738	21	AAZ55614	Internalising anti
23	233.6	65.3	659	14	AAQ36131	IN2A8 MAb heavy ch
24	233.6	65.3	1741	22	AAS22531	Human cDNA encodin
25	233	65.1	1392	21	AAA46864	DNA encoding the h
26	233	65.1	1392	21	AAA46870	DNA encoding the h
27	233	65.1	1392	21	AAA46890	cDNA encoding the
28	233	65.1	1392	21	AAA46892	DNA encoding the h
29	233	65.1	1392	21	AAA46896	DNA encoding the h
30	233	65.1	1999	21	AAA46891	DNA encoding the h
31	233	65.1	5924	21	AAZ38921	hCAT1 binding huma
32	233	65.1	5925	21	AAZ38770	HCAT1 clone 25 ant
33	232.6	65.0	681	22	AAH30056	TRO005 heavy chain
34	232.6	65.0	681	22	AAH30057	TRO005 heavy chain
35	232.2	64.9	366	22	AAF75587	Human anti-HER2/ne
36	232.2	64.9	458	22	AAH41153	Human coding seque
37	232	64.8	363	20	AAV72235	Human anti-GPIIb/I
38	231.8	64.7	375	22	AAF29079	Human HIV-1 monocl
39	231.6	64.7	410	24	ABL55674	ACZ885 antibody he
40	231.6	64.7	519	20	AAZ20407	IgG antibody 2.1.1
41	231.4	64.6	354	24	ABK88453	Human anti-CD40 mo
42	231.4	64.6	354	24	ABA94330	MAb 6-2 heavy chai
43	231.4	64.6	355	22	AAF55226	Nucleotide sequenc
44	231.4	64.6	355	22	AAF55240	DNA sequence of he
45	231	64.5	462	24	ABK48972	DNA encoding heavy

ALIGNMENTS

RESULT 1
AAF29077
ID AAF29077 standard; DNA; 375 BP.
XX
AC AAF29077;
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody coding sequence SEQ ID NO: 33.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gp120; diagnosis; ds.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US17327.
XX
PR 30-JUN-1999; 99US-0141701.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR P-PSDB; AAB62776.
XX
PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1

PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal -
XX
PS Claim 4; Page 46; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection.
XX
SQ Sequence 375 BP; 81 A; 90 C; 116 G; 88 T; 0 other;

Query Match 71.7%; Score 256.6; DB 22; Length 375;
Best Local Similarity 85.1%; Pred. No. 1.7e-61;
Matches 314; Conservative 0; Mismatches 44; Indels 11; Gaps 2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          7 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 66

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| ||| ||   | ||||||||| ||||||||||||
Db         67 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 126

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        127 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 186

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||| ||||  ||||||||||||||||||||||||
Db        187 GACTCTGTGAAGGGCCGATTCACCATCTTCAGAAACAACGCCAAGAACTCACTGTATCTG 246

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCT-- 297
              |||||||||||||||||||||||||||||||| ||||||||||||||||  |   ||
Db        247 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGTTGCTACTAT 306

Qy        298 --------GTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACC 349
                      |  |||| |       |  ||||| ||||||||||||||||||||||||||
Db        307 GGTTCGGGGAGTTATTATTTCTACCCCTTTGCCTACTGGGGCCAGGGAACCCTGGTCACC 366

Qy        350 GTCTCCTCA 358
              |||||||||
Db        367 GTCTCCTCA 375
```

RESULT 2
AAV74274
ID AAV74274 standard; DNA; 814 BP.
XX
AC AAV74274;
XX
DT 10-MAY-1999 (first entry)
XX
DE Human clone A6 fusion protein antibody DNA.
XX
KW Antibody; human; clone A6; hAb; fusion protein; polyhistidine tag;
KW Western blot; enzyme-linked immunosorbent assay; ELISA; therapy;
KW immunofluorescence; immunoprecipitation assay; affinity purification;
KW diagnosis; vaccine; serum; immune response; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3..814
FT /*tag= a
FT /note= "Partial sequence, no stop codon given"
XX
PN WO9901475-A2.
XX
PD 14-JAN-1999.
XX
PF 03-JUL-1998; 98WO-DE01882.
XX
PR 04-JUL-1997; 97DE-1028697.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Braunagel M, Doersam H, Kipriyanov S, Kuerschner T;
PI Little M, Welschof M;
XX
DR WPI; 1999-106000/09.
DR P-PSDB; AAW90180.
XX
PT Human antibody against fusion protein with polyhistidine tag -
PT useful as standard in immunoassays, for affinity purification,
PT diagnosis and therapy and for preparing vaccines
XX
PS Claim 2; Fig 4; 20pp; German.
XX
CC This invention describes a human antibody (hAb) against a fusion
CC (poly)peptide or protein that includes a segment of at least 6
CC consecutive His residues. This antibody is useful in Western blots,
CC enzyme-linked immunosorbent assay (ELISA), immunofluorescence or
CC immunoprecipitation assays. Also hAb can be used for affinity
CC purification of the protein, for in vivo diagnosis or therapy, and
CC in production of vaccines. hAb are universally applicable
CC alternatives to human serum. They are specific for the polyhistidine
CC tag, regardless of the nature of the rest of the protein. Since hAb
CC are not produced in an animal, they contain no components that can
CC induce an immune response in humans.
XX
SQ Sequence 814 BP; 181 A; 228 C; 232 G; 173 T; 0 other;

Query Match 71.1%; Score 254.6; DB 20; Length 814;
Best Local Similarity 85.1%; Pred. No. 6.9e-61;
Matches 309; Conservative 0; Mismatches 49; Indels 5; Gaps 2;

```
Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db         12 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 71

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| ||| ||   | ||||||||| ||||||||||||
Db         72 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 131

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        132 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 191

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        192 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 251

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
              |||||||||||||||||||||||||||||||| ||||||||||||||||||  | | |
Db        252 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAAGCAGC 311

Qy        299 ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
                  |  |||    | |     |||||   |||||||| || ||  ||||||||||||
Db        312 AGCTGGTATCTTGGGGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCT 371

Qy        356 TCA 358
              |||
Db        372 TCA 374
```

RESULT 3
AAH41661
ID AAH41661 standard; DNA; 675 BP.
XX
AC AAH41661;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody nucleotide sequence M1-23H.
XX

```
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US33042.
XX
PR   06-DEC-1999;   99US-0456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding
PT   to nonhuman-antibodies, involves contacting sample with human antibody
PT   which binds to antibodies from nonhuman species and detecting binding
PT   -
XX
PS   Example 22; Page 88; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the
CC   amount of target antigen in a sample in a semi-quantitative or relative
CC   sense. Quantification of one or more target antigens in a sample can
CC   also be carried out using (I). AAH41612 to AAH41686, and AAB99361 to
CC   AAB99399, represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;

  Query Match             67.9%;  Score 243;  DB 22;  Length 675;
  Best Local Similarity   84.1%;  Pred. No. 1.1e-57;
  Matches  302;  Conservative    0;  Mismatches   45;  Indels   12;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||| ||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||| | ||   ||    | |  |||||| ||||||||||||
Db         64 TGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || ||||||||||||||||||    |||| |   |  |||| | || ||||| ||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||||| |||  |||||||| | |||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------- 295

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                  |||  | |||||||||||||||||||||||||||||||||||||||||||||||
Db        296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351


RESULT 4
AAH30007
ID   AAH30007 standard; DNA; 675 BP.
XX
AC   AAH30007;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody nucleotide fragment M1-23H.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US27237.
XX
PR   02-OCT-1999;   99US-0157415.
PR   01-DEC-1999;   99US-0453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells -
XX
PS   Example 22; Page 92; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention.
XX
SQ   Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 other;

  Query Match             67.9%;  Score 243;  DB 22;  Length 675;
  Best Local Similarity   84.1%;  Pred. No. 1.1e-57;
```

```
  Matches  302;  Conservative    0;  Mismatches   45;  Indels   12;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||| |||||||||||||| ||||| |||||||  ||||||||||||||||||
Db          4 GTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||||| | ||   ||   | |  |||||| ||||||||||||
Db         64 TGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || ||||||||||||||||||    |||| |   |  |||| | || ||||| ||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||| |||  |||||||| | |||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------- 295

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                 |||  | ||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351


RESULT 5
AAK98398
ID   AAK98398 standard; DNA; 402 BP.
XX
AC   AAK98398;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human anti-FAPalpha antibody fragment VH50 DNA.
XX
KW   Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;
KW   gene therapy; cancer; wound healing; inflammation; cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200168708-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-EP04716.
XX
PR   17-MAR-2000; 2000DE-1013286.
PR   11-SEP-2000; 2000GB-0022216.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI   Park J,  Garin-Chesa P,  Pfizenmaier K,  Moosmayer D,  Mersmann M;
PI   Schmidt A;
XX
DR   WPI; 2002-041180/05.
DR   P-PSDB; AAO14049.
XX
PT   New human humanized antibody that specifically binds to fibroblasts
PT   activating protein alpha, useful for treating cancer or tumor, and for
PT   imaging tumors associated with activated stromal fibroblasts, e.g. lung
PT   or breast cancer  -
XX
PS   Claim 20; Page 43; 109pp; English.
XX
CC   The present invention relates to a human or humanised antibody (Ab) which
CC   specifically binds to fibroblast activating protein alpha (FAPalpha). The
CC   antibodies are useful for preparing a composition for the treatment of
CC   cancer, and for imaging tumours associated with activated stromal
CC   fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
CC   breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
CC   cancer, pancreatic cancer and metastatic brain cancer, and diseases
CC   associated with the same, such as inflammation and wound healing. The
CC   present sequence is a coding sequence described in the exemplification of
CC   the invention.
XX
SQ   Sequence 402 BP; 92 A; 105 C; 124 G; 81 T; 0 other;

  Query Match             67.3%;  Score 241;  DB 24;  Length 402;
  Best Local Similarity   82.1%;  Pred. No. 3.5e-57;
  Matches  308;  Conservative    0;  Mismatches   50;  Indels   17;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              || |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| ||    ||   | ||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGG------- 292
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTTCACTC 303

Qy        293 ---------GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTG 343
                      | |   |    || |||     ||||||||||||||||||||
Db        304 TGTACTGATGGTAGCTGCCCCACCATAGGGCCTGGGCCAAACTGGGGCCAGGGAACCCTG 363

Qy        344 GTCACCGTCTCCTCA 358
              |||||||||||||||
Db        364 GTCACCGTCTCCTCA 378


RESULT 6
AAK98407
ID   AAK98407 standard; DNA; 788 BP.
XX
AC   AAK98407;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Anti-FAPalpha antibody fragment VH50YOLVLIII25 DNA.
XX
KW   Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;
KW   gene therapy; cancer; wound healing; inflammation; cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200168708-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-EP04716.
XX
PR   17-MAR-2000; 2000DE-1013286.
PR   11-SEP-2000; 2000GB-0022216.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI   Park J,  Garin-Chesa P,  Pfizenmaier K,  Moosmayer D,  Mersmann M;
PI   Schmidt A;
XX
DR   WPI; 2002-041180/05.
DR   P-PSDB; AAO14058.
XX
PT   New human humanized antibody that specifically binds to fibroblasts
PT   activating protein alpha, useful for treating cancer or tumor, and for
```

PT imaging tumors associated with activated stromal fibroblasts, e.g. lung
PT or breast cancer -
XX
PS Claim 90; Page 46-47; 109pp; English.
XX
CC The present invention relates to a human or humanised antibody (Ab) which
CC specifically binds to fibroblast activating protein alpha (FAPalpha). The
CC antibodies are useful for preparing a composition for the treatment of
CC cancer, and for imaging tumours associated with activated stromal
CC fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
CC breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
CC cancer, pancreatic cancer and metastatic brain cancer, and diseases
CC associated with the same, such as inflammation and wound healing. The
CC present sequence is a coding sequence described in the exemplification of
CC the invention.
XX
SQ Sequence 788 BP; 191 A; 212 C; 212 G; 173 T; 0 other;

Query Match 67.3%; Score 241; DB 24; Length 788;
Best Local Similarity 82.1%; Pred. No. 4e-57;
Matches 308; Conservative 0; Mismatches 50; Indels 17; Gaps 2;

```
Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              || |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| ||    ||    | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   ||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGG------- 292
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTTCACTC 303

Qy        293 ---------GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTG 343
                      | |   |       || |||          ||||||||||||||||||||
Db        304 TGTACTGATGGTAGCTGCCCCACCATAGGGCCTGGGCCAAACTGGGGCCAGGGAACCCTG 363

Qy        344 GTCACCGTCTCCTCA 358
              |||||||||||||||
Db        364 GTCACCGTCTCCTCA 378
```

RESULT 7
ABK32988
ID ABK32988 standard; DNA; 792 BP.
XX
AC ABK32988;
XX
DT 23-APR-2002 (first entry)
XX
DE Affinity matured clone M36-12 DNA from anti-IL8 scFv clone 123-36.
XX
KW Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
KW variable light-chain; VL; anti-IL8; interleukin-8; scFV clone; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200200729-A2.
XX
PD 03-JAN-2002.
XX
PF 25-JUN-2001; 2001WO-US20542.
XX
PR 23-JUN-2000; 2000US-0602373.
PR 23-JUN-2000; 2000US-0602972.
PR 23-JUN-2000; 2000US-0603658.
PR 23-JUN-2000; 2000US-0603663.
XX
PA (GENE-) GENETASTIX CORP.
XX
PI Zhu L, Hua SB;
XX
DR WPI; 2002-090521/12.
DR P-PSDB; AAU75154.
XX
PT Screening libraries of tester proteins against protein, peptide or
PT nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT generating recombinant human antibodies and screening for their
PT affinity binding with target antigens -
XX
PS Example 8; Fig 20; 251pp; English.
XX
CC The present invention relates to compositions and methods for high
CC throughput generation and screening of a human antibody or immunoglobulin
CC (Ig) library in yeast. The method comprises expressing a library of
CC tester fusion proteins in yeast cells, each tester fusion protein
CC comprising either an activation domain or a DNA binding domain of a
CC transcription activator and a tester protein having a large diversity
CC within the library. The tester protein comprises a first polypeptide
CC subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC within the library, a second polypeptide subunit (e.g. human variable
CC light-chain, VL) whose sequence varies within the library independently
CC of the first polypeptide, and a linker peptide which links the first and
CC second polypeptide subunits. The method is useful for generating
CC recombinant human antibodies and screening for their affinity binding
CC with target antigens. The present DNA sequence represents an anti-IL8
CC scFv clone as described in the methods of the present invention.
XX
SQ Sequence 792 BP; 166 A; 210 C; 247 G; 169 T; 0 other;

Query Match 67.0%; Score 240; DB 24; Length 792;
Best Local Similarity 81.5%; Pred. No. 7.5e-57;
Matches 313; Conservative 0; Mismatches 45; Indels 26; Gaps 2;

```
Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||| |||||||||||||| |||| || ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCCGGGGGAGGCTTGGTCCAGCCCGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||   | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||    | |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCTACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCATTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |  ||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAAGAGT 303

Qy        300 -------------------------CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG 334
                                       |  ||       ||||  ||||||||||||||||
Db        304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGCCAG 363

Qy        335 GGAACCCTGGTCACCGTCTCCTCA 358
              |||||||||||||||||||||||
Db        364 GGAACCCTGGTCACCGTCTCCTCA 387
```

RESULT 8
ABK32986
ID ABK32986 standard; DNA; 794 BP.

```
XX
AC   ABK32986;
XX
DT   23-APR-2002  (first entry)
XX
DE   Affinity matured clone M36-8 DNA from anti-IL8 scFv clone 123-36.
XX
KW   Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
KW   variable light-chain; VL; anti-IL8; interleukin-8; scFV clone; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200200729-A2.
XX
PD   03-JAN-2002.
XX
PF   25-JUN-2001; 2001WO-US20542.
XX
PR   23-JUN-2000; 2000US-0602373.
PR   23-JUN-2000; 2000US-0602972.
PR   23-JUN-2000; 2000US-0603658.
PR   23-JUN-2000; 2000US-0603663.
XX
PA   (GENE-) GENETASTIX CORP.
XX
PI   Zhu L,  Hua SB;
XX
DR   WPI; 2002-090521/12.
DR   P-PSDB; AAU75152.
XX
PT   Screening libraries of tester proteins against protein, peptide or
PT   nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT   generating recombinant human antibodies and screening for their
PT   affinity binding with target antigens -
XX
PS   Example 8; Fig 20; 251pp; English.
XX
CC   The present invention relates to compositions and methods for high
CC   throughput generation and screening of a human antibody or immunoglobulin
CC   (Ig) library in yeast. The method comprises expressing a library of
CC   tester fusion proteins in yeast cells, each tester fusion protein
CC   comprising either an activation domain or a DNA binding domain of a
CC   transcription activator and a tester protein having a large diversity
CC   within the library. The tester protein comprises a first polypeptide
CC   subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC   within the library, a second polypeptide subunit (e.g. human variable
CC   light-chain, VL) whose sequence varies within the library independently
CC   of the first polypeptide, and a linker peptide which links the first and
CC   second polypeptide subunits. The method is useful for generating
CC   recombinant human antibodies and screening for their affinity binding
CC   with target antigens. The present DNA sequence represents an anti-IL8
CC   scFv clone as described in the methods of the present invention.
XX
SQ   Sequence 794 BP; 166 A; 213 C; 247 G; 168 T; 0 other;

  Query Match           67.0%;  Score 240;  DB 24;  Length 794;
  Best Local Similarity  81.5%;  Pred. No. 7.5e-57;
  Matches  313;  Conservative    0;  Mismatches   45;  Indels   26;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||| |||||||||||||||| |||| || ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCCGGGGGAGGCTTGGTCCAGCCCGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| ||| ||    | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||    | |||| |  || |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCTACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||||||| |||||||||||||||| ||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCATTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |  ||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAAGAGT 303

Qy        300 -------------------------CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG 334
                                       |  ||      ||||  ||||||||||||||||
Db        304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGCCAG 363

Qy        335 GGAACCCTGGTCACCGTCTCCTCA 358
              ||||||||||||||||||||||||
Db        364 GGAACCCTGGTCACCGTCTCCTCA 387


RESULT 9
ABK32983
ID   ABK32983 standard; DNA; 795 BP.
XX
AC   ABK32983;
XX
DT   23-APR-2002  (first entry)
XX
DE   DNA sequence of human anti-IL8 scFv clone 123-36.
XX
KW   Human antibody; immunoglobulin; Ig; variable heavy-chain; VH;
KW   variable light-chain; VL; anti-IL8; interleukin-8; scFV clone; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200200729-A2.
XX
PD   03-JAN-2002.
XX
PF   25-JUN-2001; 2001WO-US20542.
XX
PR   23-JUN-2000; 2000US-0602373.
PR   23-JUN-2000; 2000US-0602972.
PR   23-JUN-2000; 2000US-0603658.
PR   23-JUN-2000; 2000US-0603663.
XX
PA   (GENE-) GENETASTIX CORP.
XX
PI   Zhu L,  Hua SB;
XX
DR   WPI; 2002-090521/12.
DR   P-PSDB; AAU75149.
XX
PT   Screening libraries of tester proteins against protein, peptide or
PT   nucleic acid target(s) using a two-hybrid method in yeast, useful for
PT   generating recombinant human antibodies and screening for their
PT   affinity binding with target antigens -
XX
PS   Example 8; Fig 16; 251pp; English.
XX
CC   The present invention relates to compositions and methods for high
CC   throughput generation and screening of a human antibody or immunoglobulin
CC   (Ig) library in yeast. The method comprises expressing a library of
CC   tester fusion proteins in yeast cells, each tester fusion protein
CC   comprising either an activation domain or a DNA binding domain of a
CC   transcription activator and a tester protein having a large diversity
CC   within the library. The tester protein comprises a first polypeptide
CC   subunit (e.g. human variable heavy-chain, VH) whose sequence varies
CC   within the library, a second polypeptide subunit (e.g. human variable
CC   light-chain, VL) whose sequence varies within the library independently
CC   of the first polypeptide, and a linker peptide which links the first and
CC   second polypeptide subunits. The method is useful for generating
CC   recombinant human antibodies and screening for their affinity binding
CC   with target antigens. The present DNA sequence represents an anti-IL8
CC   scFv clone as described in the methods of the present invention.
XX
```

```
SQ   Sequence 795 BP; 166 A; 211 C; 247 G; 171 T; 0 other;

  Query Match           67.0%;  Score 240;  DB 24;  Length 795;
  Best Local Similarity  81.5%;  Pred. No. 7.5e-57;
  Matches  313;  Conservative    0;  Mismatches   45;  Indels   26;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||| |||||||||||||| |||| || ||||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCCGGGGGAGGCTTGGTCCAGCCCGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||   | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||    | |||| | ||  |||| |||    |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCTACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCATTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||||||||||||||||||||  |   ||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGTAAAGAGT 303

Qy        300 ------------------------CTTATGACAGAGGCTACTTTGACTACTGGGGCCAG 334
                                       |  ||       ||||  ||||||||||||||||
Db        304 AGCAGTAGCTGGTCTTACTATGATAGTAGTGGTTATTACTACCCTGACTACTGGGGCCAG 363

Qy        335 GGAACCCTGGTCACCGTCTCCTCA 358
              ||||||||||||||||||||||||
Db        364 GGAACCCTGGTCACCGTCTCCTCA 387


RESULT 10
AAQ78945
ID   AAQ78945 standard; DNA; 877 BP.
XX
AC   AAQ78945;
XX
DT   01-AUG-1995  (first entry)
XX
DE   Human immunoglobulin Vh gene #7.
XX
KW   Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW   cosmid; placenta; vector; pJB81; E.coli; mammalian; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             184..638
FT                   /*tag=  a
FT                   /product= Human immunoglobulin Variable heavy chain
FT   intron          229..331
FT                   /*tag=  b
FT   misc_signal     638..640
FT                   /*tag=  c
FT                   /note=  "miscellaneous signal, does not conform to
FT                           terminator or splice site sequence"
XX
PN   WO9426895-A.
XX
PD   24-NOV-1994.
XX
PF   10-MAY-1993;   93WO-JP00603.
XX
PR   10-MAY-1993;   93WO-JP00603.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
PI   Honjo T,  Matsuda F;
XX
DR   WPI; 1995-006791/01.
DR   P-PSDB; AAR66301.
XX
PT   DNA fragment comprising human immunoglobulin Vh genes - for the
PT   production of human immunoglobulin in mammalian hosts
XX
PS   Claim 16; Page 39-40; 130pp; Japanese.
XX
CC   A series of genes (AAQ78939-79002) encoding human immunoglobulin
CC   variable heavy chains. The genes were isolated and cloned from a series
CC   of cosmid constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131,
CC   by PCR amplification using primers AAQ78917-38. The genes are subdivided
CC   into 5 families of Vh genes. The fragments cover a region of 800 kb.
CC   The DNA fragments were isolated from high molecular weight DNA from
CC   human placenta. The DNA was partially digested with TaqI restriction
CC   enzyme. The fragments were separated by gel elecrophoresis and 35-45 kb
CC   fractions were collected. The fragments were ligated with ClaI-digested
CC   cosmid vector pJB81. The ligation products were in vitro packed and
CC   infected into E.coli 490A. The fragments were then subcloned by colony
CC   hybridisation. The Vh genes and the DNA fragments encoding them are
CC   useful in producing human immunoglobulin in mammalian hosts.
XX
SQ   Sequence 877 BP; 198 A; 207 C; 258 G; 214 T; 0 other;

  Query Match           67.0%;  Score 240;  DB 16;  Length 877;
  Best Local Similarity  91.1%;  Pred. No. 7.6e-57;
  Matches  266;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        347 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 406

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||   | ||||||||| ||||||||||||
Db        407 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 466

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        467 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 526

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        527 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 586

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        587 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 638


RESULT 11
AAV72533
ID   AAV72533 standard; cDNA; 939 BP.
XX
AC   AAV72533;
XX
DT   16-MAR-1999  (first entry)
XX
DE   Single chain Apo-2 antibody 20E6 encoding cDNA.
XX
KW   Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
KW   tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
KW   TNF cytokine; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..939
FT                   /*tag=  a
XX
PN   WO9851793-A1.
XX
PD   19-NOV-1998.
XX
```

```
PF   14-MAY-1998;   98WO-US09704.
XX
PR   09-FEB-1998;   98US-0020746.
PR   15-MAY-1997;   97US-0857216.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Adams CW,  Ashkenazi AJ,  Chuntharapai A,  Kim KJ;
XX
DR   WPI; 1999-045228/04.
DR   P-PSDB; AAW83323.
XX
PT   Human Apo-2 polypeptide inducing apoptosis - useful to treat
PT   conditions linked with decreased apoptosis e.g. cancer, and produce
PT   antibodies to increase or decrease apoptosis
XX
PS   Example 14; Fig 15B; 134pp; English.
XX
CC   The present invention describes human Apo-2. Apo-2 can be used
CC   therapeutically to induce apoptosis in mammalian cells, and so is useful
CC   to treat conditions associated with decreased apoptosis e.g. cancer.
CC   Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor
CC   (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC   binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
CC   can be used to identify agents activating Apo-2, useful to treat
CC   mammalian cancer cells, and to produce Apo-2 chimeras useful
CC   therapeutically (e.g. those containing immunoglobulin sequences can be
CC   inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC   tag polypeptide allow Apo-2 detection and purification using anti-tag
CC   antibodies). It can be used to produce antibodies which can be combined
CC   with a (particularly pharmaceutically acceptable) carrier in compositions
CC   or used to produce dimeric molecules (especially homodimeric molecules
CC   comprising first and second Apo-2 antibodies). Agonistic (especially
CC   single-chain) antibodies can be administered to induce apoptosis in
CC   mammalian cancer cells, and antagonistic antibodies used to block
CC   excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC   antibodies may also be used diagnostically e.g. to detect Apo-2
CC   expression in cells/tissues and in Apo-2 purification. The present
CC   sequence encodes a single chain Apo-2 antibody, designated 20E6.
XX
SQ   Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;

  Query Match             67.0%;  Score 240;  DB 20;  Length 939;
  Best Local Similarity   91.1%;  Pred. No. 7.7e-57;
  Matches  266;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        121 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 180

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| |||  ||    | ||||||||| ||||||||||
Db        181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412


RESULT 12
ABL41734
ID   ABL41734 standard; DNA; 939 BP.
XX
AC   ABL41734;
XX
DT   29-MAY-2002  (first entry)
XX
DE   Nucleotide sequence of single-chain Apo-2 antibody 20E6.
XX
KW   Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
KW   caspase; apoptosis; cancer; antibody; ss.
XX
OS   Bacteriophage.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..939
FT                   /*tag=  a
FT                   /product= "single-chain Apo-2 antibody 20E6"
XX
PN   US6342369-B1.
XX
PD   29-JAN-2002.
XX
PF   14-MAY-1998;   98US-0079029.
XX
PR   15-MAY-1997;   97US-046615P.
PR   09-FEB-1998;   98US-074119P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ;
XX
DR   WPI; 2002-224941/28.
DR   P-PSDB; ABB09604.
XX
PT   New nucleic acids encoding an Apo-2 ligand, useful for activating or
PT   stimulating apoptosis in cancer cells, thus especially useful in the
PT   treatment of cancer, or in enhancing immune-mediated cell death  -
XX
PS   Example 14; Fig 15B; 68pp; English.
XX
CC   The present sequence encodes a single-chain Apo-2 antibody, designated
CC   20E6, which is isolated from a phage library. It is believed that
CC   Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
CC   family. Apo-2 polypeptide is capable of triggering caspase-dependent
CC   apoptosis and activating nuclear factor-kappa B. A soluble
CC   extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2
CC   antibodies may be used to activate or stimulate apoptosis in cancer
CC   cells. They are therefore especially useful in the treatment of cancer,
CC   to enhance immune-mediated cell death in cells expressing Apo-2, to
CC   detect expression of Apo-2 in specific cells, tissues or serum, and in
CC   affinity purification of Apo-2 from recombinant cell culture or natural
CC   sources.
XX
SQ   Sequence 939 BP; 218 A; 232 C; 287 G; 202 T; 0 other;

  Query Match             67.0%;  Score 240;  DB 24;  Length 939;
  Best Local Similarity   91.1%;  Pred. No. 7.7e-57;
  Matches  266;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        121 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 180

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| |||  ||    | ||||||||| ||||||||||
Db        181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
```

```
Db        361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412


RESULT 13
AAQ89332
ID   AAQ89332 standard; DNA; 294 BP.
XX
AC   AAQ89332;
XX
DT   26-SEP-1995  (first entry)
XX
DE   DP54 VH gene.
XX
KW   Graves ophthalmopathy associated immunoglobulin protein;
KW   orbital antigen; monoclonal antibody; heavy chain; H chain;
KW   variable region; autoimmunity; ss.
XX
OS   Homo sapiens.
XX
PN   WO9508336-A.
XX
PD   30-MAR-1995.
XX
PF   22-SEP-1994;   94WO-US10756.
XX
PR   22-SEP-1993;   93US-0124469.
XX
PA   (NICH-) NICHOLS INST DIAGNOSTICS.
XX
PI   Mclachlan SM,  Rapoport B;
XX
DR   WPI; 1995-139383/18.
DR   P-PSDB; AAR72074.
XX
PT   Graves' ophthalmopathy-associated monoclonal antibody - produced
PT   by molecular cloning of immunoglobulin genes by PCR
XX
PS   Disclosure; Page 72; 94pp; English.
XX
CC   L- and H-chain DNA was amplified by PCR from Graves' orbital
CC   tissue and clones encoding autoimmune-associated immunoglobulin
CC   fragments were obtained.  2/15 clones of H chain (IgG1) genes
CC   showed homology to the germline gene DP54 (AAQ89332).  The DNA
CC   (AAQ89333) and corresp. amino acid (AAR72075) sequences of the VH
CC   region of a representative clone, OF7H1.19, are provided.
XX
SQ   Sequence 294 BP; 69 A; 66 C; 98 G; 61 T; 0 other;

  Query Match             66.8%;  Score 239;  DB 16;  Length 294;
  Best Local Similarity   91.1%;  Pred. No. 1.2e-56;
  Matches  265;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||| |||  ||   | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||| || |||| |  ||  |||| |||   ||||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA 290
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294


RESULT 14
AAF75589
ID   AAF75589 standard; DNA; 366 BP.
XX
AC   AAF75589;
XX
DT   10-MAY-2001  (first entry)
XX
DE   Human anti-HER2/neu antibody 2-E8 heavy chain coding sequence.
XX
KW   Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy;
KW   3-F2; 1-D2; 2-E8; growth factor receptor; ds.
XX
OS   Homo sapiens.
XX
PN   WO200109187-A2.
XX
PD   08-FEB-2001.
XX
PF   25-JUL-2000; 2000WO-US20272.
XX
PR   29-JUL-1999;   99US-0146313.
PR   10-MAR-2000; 2000US-0188539.
XX
PA   (MEDA-) MEDAREX INC.
XX
PI   Keler T,  Deo Y;
XX
DR   WPI; 2001-168698/17.
DR   P-PSDB; AAB72883.
XX
PT   New human monoclonal antibody that specifically binds to growth factor
PT   receptor HER2/neu, for  treating, preventing or diagnosing diseases
PT   characterized by aberrant HER2/neu expression e.g. cancers  -
XX
PS   Disclosure; Page 108; 113pp; English.
XX
CC   The present invention provides the protein and coding sequences for human
CC   monoclonal antibodies which bind specifically to the HER2/neu growth
CC   factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
CC   and 2-E8. They can be used in the immunotherapy-based treatment and
CC   prognosis of cancers, particularly adenocarcinomas such as salivary
CC   gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
CC   and ovarian cancer. The present sequence is a coding sequence of an
CC   antibody of the invention.
XX
SQ   Sequence 366 BP; 80 A; 87 C; 114 G; 85 T; 0 other;

  Query Match             66.6%;  Score 238.6;  DB 22;  Length 366;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-56;
  Matches  299;  Conservative    0;  Mismatches   59;  Indels    5;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||| | |||  ||   | |  |||||| ||||||||||||
Db         64 TGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGTCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||    ||||  |   |  ||||  | |   |||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||  |||||||||||||||||||||||||||  |||  |||||||  | |||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTG- 298
              |||||||||||||||||||||||||||||||| ||||||||||||||     | |  |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCTTATGGTTCGG 303

Qy        299 ---TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
```

```
                    |  |   |  || ||||||||||||||||||||||||||||||||||||||||||||
Db        304 GGACTTATTATAACGGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 363

Qy        356 TCA 358
              |||
Db        364 TCA 366


RESULT 15
ABK14254
ID   ABK14254 standard; cDNA; 366 BP.
XX
AC   ABK14254;
XX
DT   08-MAY-2002  (first entry)
XX
DE   AAV293 anti-(MCP)-1 antibody heavy chain cDNA sequence.
XX
KW   Human; antibody; MCP; monocyte chemoattractant; antiasthmatic;
KW   antiallergic; antiinflammatory; idiopathic thrombocytopaenia;
KW   immunosuppressive; cytostatic; vasotropic; antiarteriosclerotic;
KW   antirheumatic; antiarthritic; osteopathic; antigen-binding site;
KW   immunoglobulin heavy chain; monocyte migration; T cell migration;
KW   CC-type chemokine; eotaxin; allergy; allergic rhinitis; cancer;
KW   hypersensitivity response; allergic contact dermatitis; gene;
KW   inflammatory disease; asthma; psoriasis; COPD; osteoporosis;
KW   inflammatory bowel disease; multiple sclerosis; autoimmune disease;
KW   rheumatoid arthritis; diabetes; systemic lupus erythematosus;
KW   bone disease; osteoporosis; osteoarthritis; periodontal disease;
KW   haematological disorder; haemolytic anaemia; graft rejection;
KW   leucocyte infiltration; restenosis; arteriosclerosis; AAV293; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "AAV293 heavy chain protein"
FT                   /transl_except= (pos:142..144, aa:Val)
FT                   /partial
FT                   /note= "No start or stop codon shown"
XX
PN   WO200202640-A2.
XX
PD   10-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-EP07468.
XX
PR   30-JUN-2000; 2000GB-0016138.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Hiestand P,  Hofstetter H,  Payne TG,  Urfer R,  Di Padova FE;
XX
DR   WPI; 2002-164525/21.
DR   P-PSDB; AAU75737.
XX
PT   New compound that binds human monocyte chemoattractant protein-1,
PT   useful e.g. for treating inflammation, comprises immunoglobulin chains
PT   with specific hypervariable regions  -
XX
PS   Example 1; Page 21; 42pp; English.
XX
CC   This invention relates to a molecule that binds MCP-1 (human monocyte
CC   chemoattractant protein-1). The molecule has at least one antigen
CC   -binding site comprising at least one immunoglobulin (Ig) heavy and/or
CC   light chain variable domain (Vh, Vl). The antibody of the invention
CC   inhibits binding of MCP-1 (and also eotaxin) to specific receptors, so
CC   preventing migration of monocytes and T cells. These are human
CC   antibodies with very high affinity for MCP-1, but no significant
CC   reaction with other human CC-type chemokines or MCP-1 from other
CC   species. The MCP-1 binding molecules, specifically antibodies that cross
CC   -react with eotaxin, are used to prevent or treat MCP-1 or eotaxin-
CC   mediated disorders, particularly those that involve migration or
CC   activation of monocytes and T cells, e.g. allergies (allergic rhinitis,
CC   hypersensitivity responses, allergic contact dermatitis), inflammatory
CC   diseases (asthma, psoriasis, COPD, inflammatory bowel disease,
CC   multiple sclerosis) autoimmune disease (rheumatoid arthritis; diabetes,
CC   systemic lupus erythematosus), diseases of bone and cartilage
CC   (osteoporosis, osteoarthritis, periodontal disease) haematological
CC   disorders (haemolytic anaemia, idiopathic thrombocytopaenia) graft
CC   rejection, cancers that include leucocyte infiltration, (re)stenosis,
CC   arteriosclerosis, osteoporosis and many other diseases listed in the
CC   specification. The present sequence represents the human AAV293
CC   anti-(MCP) antibody heavy chain cDNA sequence of the invention.
XX
SQ   Sequence 366 BP; 78 A; 87 C; 118 G; 83 T; 0 other;

  Query Match             66.6%;  Score 238.6;  DB 24;  Length 366;
  Best Local Similarity   82.4%;  Pred. No. 1.6e-56;
  Matches  299;  Conservative    0;  Mismatches   59;  Indels    5;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||| |||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGCAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||||||||||| |    |    | ||||||||| ||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTCACTACTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||| |||||||||||| |||  || |||  |  ||  |||| |||   |||||||| |
Db        124 GGGAAAGGGCTGGAGTGGCTGGCCAACATAGAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAATTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG----GGAT 295
              |||||||||||| |||||||||||||||||||| ||||||| ||||||||  |     ||
Db        244 CAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTGTATTTCTGTGCGAGGGATCTTGAA 303

Qy        296 CTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCC 355
                  |||      || ||||| ||    |||||||  || ||||||||||||||||||
Db        304 GGTCTACATGGGGATGGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACCGTCTCT 363

Qy        356 TCA 358
              |||
Db        364 TCA 366


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Listing first 45 summaries

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SUMMARIES

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2	241	67.3	402	10	US-09-811-737-7	Sequence 7, Appli
3	241	67.3	788	10	US-09-811-737-24	Sequence 24, Appl
4	240	67.0	939	15	US-10-052-798-7	Sequence 7, Appli
5	239	66.8	294	12	US-09-995-529-7	Sequence 7, Appli
6	237.6	66.4	672	12	US-09-972-656-67	Sequence 67, Appl
7	237.4	66.3	1395	15	US-10-153-382-8	Sequence 8, Appli
8	237	66.2	348	15	US-10-324-493-15	Sequence 15, Appl
9	236	65.9	375	15	US-10-172-317-1	Sequence 1, Appli
10	233	65.1	1392	15	US-10-153-382-1	Sequence 1, Appli
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12	233	65.1	1392	15	US-10-153-382-12	Sequence 12, Appl
13	233	65.1	1999	15	US-10-153-382-2	Sequence 2, Appli
14	231.4	64.6	354	15	US-10-324-493-7	Sequence 7, Appli
15	231	64.5	357	15	US-10-073-644C-1	Sequence 1, Appli
16	231	64.5	630	11	US-09-844-684-14	Sequence 14, Appl
17	231	64.5	630	15	US-10-040-244-14	Sequence 14, Appl
c 18	230.6	64.4	9182	12	US-09-927-122-41	Sequence 41, Appl
c 19	230.6	64.4	9182	12	US-09-927-121B-89	Sequence 89, Appl
20	230.2	64.3	675	12	US-09-453-234-59	Sequence 59, Appl
21	230.2	64.3	675	12	US-09-453-234-91	Sequence 91, Appl
22	230.2	64.3	677	12	US-09-453-234-55	Sequence 55, Appl
23	230	64.2	1798	10	US-09-925-299-230	Sequence 230, App
24	230	64.2	1798	12	US-09-925-299-230	Sequence 230, App
25	229.4	64.1	580	11	US-09-844-684-12	Sequence 12, Appl
26	229.4	64.1	580	15	US-10-040-244-12	Sequence 12, Appl
27	228.2	63.7	669	12	US-09-972-656-85	Sequence 85, Appl
28	228	63.7	375	12	US-09-848-798-89	Sequence 89, Appl
29	226.6	63.3	411	11	US-09-423-800-58	Sequence 58, Appl
30	226.6	63.3	411	15	US-10-182-018-58	Sequence 58, Appl
31	226.6	63.3	411	15	US-10-169-003-58	Sequence 58, Appl
32	226.4	63.2	375	12	US-09-848-798-90	Sequence 90, Appl
33	225.4	63.0	351	15	US-10-324-493-23	Sequence 23, Appl
34	225.4	63.0	375	12	US-09-848-798-91	Sequence 91, Appl
35	225.4	63.0	675	12	US-09-453-234-107	Sequence 107, App
36	224.8	62.8	375	12	US-09-848-798-77	Sequence 77, Appl
37	223.8	62.5	675	12	US-09-453-234-105	Sequence 105, App
38	223.6	62.5	381	12	US-09-848-798-88	Sequence 88, Appl
39	223.4	62.4	660	12	US-09-791-153A-56	Sequence 56, Appl
40	223.2	62.3	363	11	US-09-822-698A-4	Sequence 4, Appli
41	223.2	62.3	1143	11	US-09-822-698A-6	Sequence 6, Appli
42	223.2	62.3	1356	11	US-09-822-698A-27	Sequence 27, Appl
43	222.2	62.1	675	12	US-09-453-234-61	Sequence 61, Appl
44	222.2	62.1	675	12	US-09-453-234-69	Sequence 69, Appl
45	222.2	62.1	675	12	US-09-453-234-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-09-453-234-67
; Sequence 67, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-23H
; NAME/KEY: CDS
; LOCATION: (1)..(675)
US-09-453-234-67

Query Match 67.9%; Score 243; DB 12; Length 675;
Best Local Similarity 84.1%; Pred. No. 3.3e-73;
Matches 302; Conservative 0; Mismatches 45; Indels 12; Gaps 2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||| |||||||||||||| ||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||| | ||   ||   | |  |||||| ||||||||||||
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Db          64 TGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy         120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
               || |||||||||||||||||||     |||| |   |  |||| | || ||||| ||||
Db         124 GGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATGCA 183

Qy         180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
               ||||| |||||||||||||||||||||||||||| |||  |||||||| | |||||||||
Db         184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy         240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
               |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG--------- 295

Qy         300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                   |||  | ||||||||||||||||||||||||||||||||||||||||||||||||
Db         296 ---ATGGGATAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 351


RESULT 2
US-09-811-737-7
; Sequence 7, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Human FAP-alpha-specific antibodies
;  FILE REFERENCE: 1-1129
;  CURRENT APPLICATION NUMBER: US/09/811,737
;  CURRENT FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 402
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-811-737-7

  Query Match           67.3%;  Score 241;  DB 10;  Length 402;
  Best Local Similarity  82.1%;  Pred. No. 1.4e-72;
  Matches  308;  Conservative    0;  Mismatches   50;  Indels   17;  Gaps    2;

Qy           1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
               || |||||||||||||||||||||||||||||||| |||||| |||||||||||||||||
Db           4 GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy          61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
               |||||||||| |||||||||||| ||   ||   | ||||||||| ||||||||||||
Db          64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy         120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
               |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db         124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy         180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy         240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGG------- 292
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTTCACTC 303

Qy         293 ---------GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTG 343
                        | |   |      || |||           ||||||||||||||||||||
Db         304 TGTACTGATGGTAGCTGCCCCACCATAGGGCCTGGGCCAAACTGGGGCCAGGGAACCCTG 363

Qy         344 GTCACCGTCTCCTCA 358
               |||||||||||||||
Db         364 GTCACCGTCTCCTCA 378


RESULT 3
US-09-811-737-24
; Sequence 24, Application US/09811737
; Patent No. US20020099180A1
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Human FAP-alpha-specific antibodies
;  FILE REFERENCE: 1-1129
;  CURRENT APPLICATION NUMBER: US/09/811,737
;  CURRENT FILING DATE: 2001-03-19
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 788
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-811-737-24

  Query Match           67.3%;  Score 241;  DB 10;  Length 788;
  Best Local Similarity  82.1%;  Pred. No. 1.7e-72;
  Matches  308;  Conservative    0;  Mismatches   50;  Indels   17;  Gaps    2;

Qy           1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
               || |||||||||||||||||||||||||||||||| |||||| |||||||||||||||||
Db           4 GTACAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy          61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
               |||||||||| |||||||||||| ||   ||   | ||||||||| ||||||||||||
Db          64 TGTGCAGCCTCTGGATTCACCTTTAGTAACTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy         120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
               |||||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db         124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy         180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
               |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db         184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy         240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGG------- 292
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGTTCACTC 303

Qy         293 ---------GATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTG 343
                        | |   |      || |||           ||||||||||||||||||||
Db         304 TGTACTGATGGTAGCTGCCCCACCATAGGGCCTGGGCCAAACTGGGGCCAGGGAACCCTG 363

Qy         344 GTCACCGTCTCCTCA 358
               |||||||||||||||
Db         364 GTCACCGTCTCCTCA 378


RESULT 4
US-10-052-798-7
; Sequence 7, Application US/10052798
; Publication No. US20020150985A1
;   GENERAL INFORMATION:
;        APPLICANT: Adams, Camilia W.
;                   Ashkenazi, Avi J.
;                   Chuntharapai, Anan
;                   Kim, Kyung J.
;        TITLE OF INVENTION: Apo-2 Receptor
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/052,798
```

```
;             FILING DATE: 02-No. US20020150985A1-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/079,029
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Marschang, Diane L.
;             REGISTRATION NUMBER: 35,600
;             REFERENCE/DOCKET NUMBER: P1101R2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-5416
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 939 base pairs
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-052-798-7

  Query Match             67.0%;  Score 240;  DB 15;  Length 939;
  Best Local Similarity   91.1%;  Pred. No. 4e-72;
  Matches  266;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        121 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 180

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| ||||||||||||| ||| ||   | ||||||||| ||||||||||||
Db        181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412


RESULT 5
US-09-995-529-7
; Sequence 7, Application US/09995529
; Publication No. US20030099655A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Huse, William D.
;  APPLICANT:  Tang, Ying
;  TITLE OF INVENTION: Humanized Collagen Antibodies and
;  TITLE OF INVENTION:  Related Methods
;  FILE REFERENCE: P-IX 4976
;  CURRENT APPLICATION NUMBER: US/09/995,529
;  CURRENT FILING DATE:  2001-11-26
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 294
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-995-529-7

  Query Match             66.8%;  Score 239;  DB 12;  Length 294;
  Best Local Similarity   91.1%;  Pred. No. 6e-72;
  Matches  265;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||

Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| ||||||||||||| ||| ||   | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||  || |||| |  ||  |||| |||   |||||||| |
Db        124 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        184 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA 290
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA 294


RESULT 6
US-09-972-656-67
; Sequence 67, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
;  APPLICANT: Deshpande, Rajendra
;  APPLICANT:  Tsai, Mei-Mei
;  TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
;  TITLE OF INVENTION:  Neutralizing Activity
;  FILE REFERENCE: A-799
;  CURRENT APPLICATION NUMBER: US/09/972,656
;  CURRENT FILING DATE:  2001-10-05
;  NUMBER OF SEQ ID NOS: 135
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
;   LENGTH: 672
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(672)
US-09-972-656-67

  Query Match             66.4%;  Score 237.6;  DB 12;  Length 672;
  Best Local Similarity   82.9%;  Pred. No. 2.4e-71;
  Matches  295;  Conservative    0;  Mismatches   59;  Indels    2;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| ||||||||||||| ||  || | | ||||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||  ||| |  |   ||  |   ||||||| ||
Db        124 GGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||  |||||||||||  |||||||||||||||||  |||  ||||||||  | |||||||||
Db        184 GACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG-GGATCTG 298
              |||||||||||||||||||||||||||||||| ||||||||||||  ||      ||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGATCGGGTG 303

Qy        299 TCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 354
                |||  |||  ||     |||||||||||||||||||||||||||||||||||||
Db        304 GGGTATAGCAGCAGCCTTCTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 359


RESULT 7
US-10-153-382-8
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; Sequence 8, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-8

  Query Match             66.3%;  Score 237.4;  DB 15;  Length 1395;
  Best Local Similarity   82.7%;  Pred. No. 3.5e-71;
  Matches  297;  Conservative    0;  Mismatches   56;  Indels    6;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              ||| |||| || |||||||||| | ||   ||    | |  ||||||||||||||||||
Db        121 TGTACAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || ||||||||||||||||||    |||| |  |  |||| | |   | ||||||
Db        181 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAACACTATGGA 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||| | |||  |||||||| | |||||||||
Db        241 GACTCCGTGAAGGGCCGATTCACCATCTCCAGTGACAATTCCAAGAACACGCTGTATCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||| ||||||||||||||||||     |
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGAGAGA 360

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              ||  | |     ||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGGGGTC-----CTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 414


RESULT 8
US-10-324-493-15
; Sequence 15, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
;  APPLICANT: Pluenneke, John
;  TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 3005-C
;  CURRENT APPLICATION NUMBER: US/10/324,493
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/847,816
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: 09/579,808
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/665,343
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/785,934
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
;   LENGTH: 348
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(348)
US-10-324-493-15

  Query Match             66.2%;  Score 237;  DB 15;  Length 348;
  Best Local Similarity   83.3%;  Pred. No. 3.1e-71;
  Matches  299;  Conservative    0;  Mismatches   45;  Indels   15;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              ||| |||| || |||||||||| | |||  ||    | |  ||||||||||||||||||
Db         64 TGTTCAGCGTCTGGATTCACCTTCAGTAGATATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || | |||||||||||||||||  | ||||  | | |  |||| | | | |||||||||
Db        124 GGCAGGGGGCTGGAGTGGGTGGCAATTATATGGTTTGAAGGAAATAATCAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||| ||||||||| |||  |||||||| | |||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||| ||||||||||||||||||     |
Db        244 GAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGAAGT-- 301

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                          ||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ------------ACTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 348


RESULT 9
US-10-172-317-1
; Sequence 1, Application US/10172317
; Publication No. US20030091561A1
; GENERAL INFORMATION:
;  APPLICANT: van de Winkel, Jan G.J.
;  APPLICANT:  van Dijk, Marcus A.
;  APPLICANT:  Halk, Edward
;  APPLICANT:  Gerritsen, Arnout F.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO
;  TITLE OF INVENTION:  EPIDERMAL GROWTH FACTOR RECEPTOR (EGFR)
;  FILE REFERENCE: GMI-020
;  CURRENT APPLICATION NUMBER: US/10/172,317
;  CURRENT FILING DATE:  2002-06-13
;  PRIOR APPLICATION NUMBER: US 60/298,172
;  PRIOR FILING DATE: 2001-06-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-172-317-1

  Query Match             65.9%;  Score 236;  DB 15;  Length 375;
  Best Local Similarity   81.5%;  Pred. No. 6.9e-71;
  Matches  303;  Conservative    0;  Mismatches   55;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||| | ||   ||    | |  |||||| ||||||||||||
Db         64 TGTGCAGCGTCTGGATTCACCTTCAGTACCTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||     |||| ||  |  |||| | |   ||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGGATGATGGAAGTTATAAATACTATGGA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
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Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG-------- 291
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGTATT 303

Qy        292 -----GGATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                  || || |      |   |  | ||||||||||||||||||||||||||||||||||
Db        304 ACTATGGTTCGGGGAGTTATGAAGGACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363

Qy        347 ACCGTCTCCTCA 358
              ||||||||||||
Db        364 ACCGTCTCCTCA 375


RESULT 10
US-10-153-382-1
; Sequence 1, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-1

  Query Match            65.1%;  Score 233;  DB 15;  Length 1392;
  Best Local Similarity  82.2%;  Pred. No. 1.1e-69;
  Matches  295;  Conservative    0;  Mismatches   55;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||| || |||||||||||| | |||  ||    | |  ||||||  ||||||||||||
Db        121 TGTGTAGCGTCTGGATTCACCTTCAGTAGCCATGGCATGCACTGGGTCCGCCAGGCTCCA 180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||    ||||  |   |  ||||   |   |||||||||
Db        181 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGAAATAAATACTATGCA 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||| |||  |||||||| | |||| ||||
Db        241 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGG------- 353

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                | ||   ||    |||||||||||||||||||||||||||||||||||||||||||
Db        354 -AGGTCACTTCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 411


RESULT 11
US-10-153-382-4
; Sequence 4, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-4

  Query Match            65.1%;  Score 233;  DB 15;  Length 1392;
  Best Local Similarity  82.2%;  Pred. No. 1.1e-69;
  Matches  295;  Conservative    0;  Mismatches   55;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||| || |||||||||||| | |||  ||    | |  ||||||  ||||||||||||
Db        121 TGTGTAGCGTCTGGATTCACCTTCAGTAGCCATGGCATGCACTGGGTCCGCCAGGCTCCA 180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||    ||||  |   |  ||||   |   |||||||||
Db        181 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGAAATAAATACTATGCA 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||| |||  |||||||| | |||| ||||
Db        241 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGG------- 353

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                | ||   ||    |||||||||||||||||||||||||||||||||||||||||||
Db        354 -AGGTCACTTCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 411


RESULT 12
US-10-153-382-12
; Sequence 12, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-12

  Query Match            65.1%;  Score 233;  DB 15;  Length 1392;
  Best Local Similarity  82.2%;  Pred. No. 1.1e-69;
  Matches  295;  Conservative    0;  Mismatches   55;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              ||| |||| || |||||||||||| | |||  ||    | |  ||||||  ||||||||||||
Db        121 TGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTCCA 180
```

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Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||||     |||| |    | ||||    |    | |||||||
Db        181 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATGCA 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| | |||||||||||||||||||||||||| |||  ||||||||  | |||||||||
Db        241 GACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGACTG 360

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              ||         || ||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CT--------GGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 411


RESULT 13
US-10-153-382-2
; Sequence 2, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1999
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-2

  Query Match             65.1%;  Score 233;  DB 15;  Length 1999;
  Best Local Similarity   82.2%;  Pred. No. 1.3e-69;
  Matches  295;  Conservative    0;  Mismatches   55;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||
Db         61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||| || |||||||||| | |||  ||   | |  |||||| ||||||||||||
Db        121 TGTGTAGCGTCTGGATTCACCTTCAGTAGCCATGGCATGCACTGGGTCCGCCAGGCTCCA 180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||||     |||| |    | ||||    |   |||||||||
Db        181 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGAAATAAATACTATGCA 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||| |||  ||||||||  | |||| ||||
Db        241 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGG------- 353

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                  | ||   ||   |||||||||||||||||||||||||||||||||||||||||||
Db        354 -AGGTCACTTCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 411


RESULT 14
US-10-324-493-7
; Sequence 7, Application US/10324493
; Publication No. US20030124121A1
; GENERAL INFORMATION:
;  APPLICANT: Pluenneke, John
;  TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 3005-C
;  CURRENT APPLICATION NUMBER: US/10/324,493
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/847,816
;  PRIOR FILING DATE: 2001-05-01
;  PRIOR APPLICATION NUMBER: 09/579,808
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 09/665,343
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/785,934
;  PRIOR FILING DATE: 2001-02-15
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 354
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(354)
US-10-324-493-7

  Query Match             64.6%;  Score 231.4;  DB 15;  Length 354;
  Best Local Similarity   81.9%;  Pred. No. 2.6e-69;
  Matches  294;  Conservative    0;  Mismatches   56;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||| |||||| |||| | |||  || |||     ||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCGCCTTCAGTAGCTATGCTATTCAGTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||||     |||| |    | ||||    |   |||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAAGAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||| |||  ||||||||  | |||||| ||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAATACGCTGTATTTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||| |||||||||| |||||||||||||||||||    |
Db        244 CAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGGGAGA 303

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |       | || |  ||||||||||||||||||||||||||||||||||||||||||||
Db        304 C--------GTGGGTCGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 354


RESULT 15
US-10-073-644C-1
; Sequence 1, Application US/10073644C
; Publication No. US20030082643A1
; GENERAL INFORMATION:
;  APPLICANT: Hudson, Debra
;  APPLICANT:  van de Winkel, Jan
;  APPLICANT:  van Dijk, Marc
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO FC ALPHA
;  TITLE OF INVENTION:  RECEPTOR (CD89)
;  FILE REFERENCE: MXI-211
;  CURRENT APPLICATION NUMBER: US/10/073,644C
;  CURRENT FILING DATE:  2002-02-11
;  PRIOR APPLICATION NUMBER: US 60/338,956
;  PRIOR FILING DATE: 2001-11-05
;  PRIOR APPLICATION NUMBER: US 60/268,075
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 357
;   TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-073-644C-1

Query Match 64.5%; Score 231; DB 15; Length 357;
Best Local Similarity 81.6%; Pred. No. 3.6e-69;
Matches 293; Conservative 0; Mismatches 60; Indels 6; Gaps 2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||| |||||||||||||||||||| ||||| ||||||| |||||||||||||||||
Db          4 GTGCAACTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||| | |||  ||  |  |  |||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTCAGTAGTTATGTTCTGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||| |||||||     |||   |  |  ||||   |   |||||  ||
Db        124 GGCAAGGGGCTGGATTGGGTGGCAGTGATATCAGATGATGGAAGGAATAAATACTTCGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||||| |||  |||||||| | |||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||| |||||||||| |||||||||||| |||||
Db        244 CAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGTGAGAG-----AAG 298

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                |||  | |  |||  ||||||||||||||||||||||||||||||||||||||||
Db        299 GGTATAGCGGCAGCTGGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 357
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OM nucleic - nucleic search, using sw model

Run on: July 18, 2003, 09:26:19 ; Search time 18.9834 Seconds
(without alignments)
5783.490 Million cell updates/sec

Title: US-09-627-896B-30
Perfect score: 358
Sequence: 1 gtgcagctggtggagtctgg.....ccctggtcaccgtctcctca 358

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	240	67.0	877	3	US-08-545-809A-7	Sequence 7, Appli
2	240	67.0	939	4	US-09-079-029-7	Sequence 7, Appli
3	228	63.7	375	4	US-09-240-274-89	Sequence 89, Appl
4	226.4	63.2	375	4	US-09-240-274-90	Sequence 90, Appl
5	225.8	63.1	1350	1	US-08-157-101A-9	Sequence 9, Appli
6	225.8	63.1	1576	1	US-08-157-101A-6	Sequence 6, Appli
7	225.4	63.0	375	4	US-09-240-274-91	Sequence 91, Appl
8	224.8	62.8	375	4	US-09-240-274-77	Sequence 77, Appl
9	223.6	62.5	381	4	US-09-240-274-88	Sequence 88, Appl
10	223.4	62.4	354	2	US-08-652-816A-22	Sequence 22, Appl
11	223	62.3	363	4	US-09-202-181-3	Sequence 3, Appli
12	222.6	62.2	432	1	US-08-026-320A-1	Sequence 1, Appli
13	222.2	62.1	892	4	US-09-273-839A-11	Sequence 11, Appl
14	221.6	61.9	375	4	US-09-240-274-92	Sequence 92, Appl
15	220.4	61.6	381	4	US-09-240-274-87	Sequence 87, Appl
16	219.4	61.3	360	2	US-08-428-197-21	Sequence 21, Appl
17	219.4	61.3	360	5	PCT-US93-10555-21	Sequence 21, Appl
18	218.4	61.0	363	3	US-08-599-226-37	Sequence 37, Appl
19	218.4	61.0	363	4	US-09-125-098-37	Sequence 37, Appl
20	217.8	60.8	360	2	US-08-428-197-19	Sequence 19, Appl
21	217.8	60.8	360	2	US-08-958-201-7	Sequence 7, Appli
22	217.8	60.8	360	2	US-08-958-201-9	Sequence 9, Appli
23	217.8	60.8	360	5	PCT-US93-10555-19	Sequence 19, Appl
24	217.6	60.8	715	3	US-08-545-809A-11	Sequence 11, Appl
25	216.8	60.6	375	4	US-09-240-274-78	Sequence 78, Appl
26	216.8	60.6	375	4	US-09-240-274-93	Sequence 93, Appl
27	216.2	60.4	360	2	US-08-428-197-23	Sequence 23, Appl
28	216.2	60.4	360	2	US-08-428-197-25	Sequence 25, Appl
29	216.2	60.4	360	2	US-08-428-197-27	Sequence 27, Appl
30	216.2	60.4	360	5	PCT-US93-10555-23	Sequence 23, Appl
31	216.2	60.4	360	5	PCT-US93-10555-25	Sequence 25, Appl
32	216.2	60.4	360	5	PCT-US93-10555-27	Sequence 27, Appl
33	215.4	60.2	417	4	US-08-134-346A-49	Sequence 49, Appl
34	215.2	60.1	908	4	US-09-273-839A-9	Sequence 9, Appli
35	214.8	60.0	360	2	US-08-428-197-29	Sequence 29, Appl
36	214.8	60.0	360	2	US-08-428-197-31	Sequence 31, Appl
37	214.8	60.0	360	5	PCT-US93-10555-29	Sequence 29, Appl
38	214.8	60.0	360	5	PCT-US93-10555-31	Sequence 31, Appl
39	214.8	60.0	378	4	US-09-240-274-192	Sequence 192, App
40	214.6	59.9	389	5	PCT-US93-08435-11	Sequence 11, Appl
41	214.6	59.9	423	1	US-08-259-372A-1	Sequence 1, Appli
42	214.6	59.9	423	1	US-08-468-671-1	Sequence 1, Appli
43	214.4	59.9	519	3	US-08-545-809A-21	Sequence 21, Appl
44	214.4	59.9	743	3	US-08-545-809A-48	Sequence 48, Appl
45	214.2	59.8	351	4	US-09-240-274-184	Sequence 184, App

ALIGNMENTS

RESULT 1
US-08-545-809A-7
; Sequence 7, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 877 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL TYPE: human lymphoblast
; CELL LINE: CGM1
US-08-545-809A-7

Query Match 67.0%; Score 240; DB 3; Length 877;

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  Best Local Similarity   91.1%;  Pred. No. 1.4e-63;
  Matches  266;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        347 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 406

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||| |||   ||    | |||||||| ||||||||||||
Db        407 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 466

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||||   || |||| |   ||  |||| |||    |||||||| |
Db        467 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 526

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        527 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 586

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        587 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 638


RESULT 2
US-09-079-029-7
; Sequence 7, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Camilia W.
;    APPLICANT:  Ashkenazi, Avi J.
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Kim, Kyung J.
;    TITLE OF INVENTION:  Apo-2 Receptor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,029
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P1101R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  939 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-09-079-029-7

  Query Match             67.0%;  Score 240;  DB 4;  Length 939;
  Best Local Similarity   91.1%;  Pred. No. 1.4e-63;
  Matches  266;  Conservative    0;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||
Db        121 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 180

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||| |||   ||    | |||||||| ||||||||||||
Db        181 TGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCA 240

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              |||||||||||||||||||||||   || |||| |   ||  |||| |||    |||||||| |
Db        241 GGGAAGGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTG 300

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        301 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTG 360

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAG 291
              |||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        361 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG 412


RESULT 3
US-09-240-274-89
; Sequence 89, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-89

  Query Match             63.7%;  Score 228;  DB 4;  Length 375;
  Best Local Similarity   80.1%;  Pred. No. 4.6e-60;
  Matches  298;  Conservative    0;  Mismatches   60;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||| | |||||||||||||| ||||| |||||||  ||||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||  || |||||||||||| | ||   ||    | |  |||||| ||||||||||||
Db         64 TGTGTAGTGTCTGGATTCACCTTCAATAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||    |||   | | |  |||| | |   |||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATTTGGTTTGATGGAAGTAATAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||| |||  |||||||| ||||||| |||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC--- 296
              |||||||||||||||||||||||||||||| || ||||||||||||||||| || |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGAGAACCAG 303

Qy        297 ----------TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                       |||      ||     ||||||||||||||||||||||||||||||||||
Db        304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363

Qy        347 ACCGTCTCCTCA 358
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Db        364 ACCGTCTCCTCA 375


RESULT 4
US-09-240-274-90
; Sequence 90, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 90
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-90

  Query Match           63.2%;  Score 226.4;  DB 4;  Length 375;
  Best Local Similarity  79.8%;  Pred. No. 1.4e-59;
  Matches  297;  Conservative    0;  Mismatches   61;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | ||||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||  || || |||||||| | ||   ||   | |  |||||| ||||||||||||
Db         64 TGTGTAGTGTCTGGTTTCACCTTCAATAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||||    |||   | | |  |||| | |   |||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATTTGGTTTGATGGAAGTAATAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||||| |||  |||||||| ||||||| |||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC--- 296
              |||||||||||||||||||||||||||||||| || |||||||||||||||| || |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGAGAACCAG 303

Qy        297 ----------TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                     |||     ||     ||||||||||||||||||||||||||||||||||||
Db        304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363

Qy        347 ACCGTCTCCTCA 358
              ||||||||||||
Db        364 ACCGTCTCCTCA 375


RESULT 5
US-08-157-101A-9
; Sequence 9, Application US/08157101A
; Patent No. 5808032
;  GENERAL INFORMATION:
;    APPLICANT:  KURIHARA, TATSUYA
;    APPLICANT:  MATSUKURA, SHIGEKAZU
;    APPLICANT:  TSURUOKA, NOBUO
;    APPLICANT:  ARIMA, KENJI
;    APPLICANT:  NISHIHARA, TATSURO
;    TITLE OF INVENTION:  ANTI-HBs ANTIBODY GENES AND EXPRESSION
;    TITLE OF INVENTION:  PLASMIDS THEREFOR
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/157,101A
;      FILING DATE:  05-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TITUS, MARLANA K
;      REGISTRATION NUMBER:  35843
;      REFERENCE/DOCKET NUMBER:  9437/204199
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3711
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUCH
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1350 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-157-101A-9

  Query Match           63.1%;  Score 225.8;  DB 1;  Length 1350;
  Best Local Similarity  80.5%;  Pred. No. 3.1e-59;
  Matches  289;  Conservative    0;  Mismatches   67;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||||  |||||||||||  | |||  |||  |||  |  ||||||  ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTCAGTAGCAATTCTATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || ||||||  ||||||||||||     ||||  |     |  ||||  | |    || ||| ||
Db        124 GGCAAGGGGTTGGAGTGGGTGGCAGTTATATTATATGATGGAAATCATAAATTCTACGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||  ||||||| |||  |||||||| ||||||||||
Db        184 GACTCCGTGAAGGGCCGATTCACCATTTCCAGAGACAATTCCAAGAACACACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              || |||| ||||||  | | ||||||||||  || |||||||||   |||  ||||
Db        244 GAAGTGAAGAGCCTGCAAACTGAGGACACGGGTGTCTATTACTGTATAAGA--GATCAAA 301

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |||| |       |  ||||||| ||||||||||||||||||||||||||||||||||||
Db        302 CTTACGGAGTCCACAGATTTGACTCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 360


RESULT 6
US-08-157-101A-6
; Sequence 6, Application US/08157101A
; Patent No. 5808032
;  GENERAL INFORMATION:
;    APPLICANT:  KURIHARA, TATSUYA
;    APPLICANT:  MATSUKURA, SHIGEKAZU
;    APPLICANT:  TSURUOKA, NOBUO
;    APPLICANT:  ARIMA, KENJI
;    APPLICANT:  NISHIHARA, TATSURO
```

```
;    TITLE OF INVENTION:  ANTI-HBs ANTIBODY GENES AND EXPRESSION
;    TITLE OF INVENTION:  PLASMIDS THEREFOR
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PILLSBURY, MADISON & SUTRO
;      STREET:  1100 NEW YORK AVENUE, N.W.
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/157,101A
;      FILING DATE:  05-APR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TITUS, MARLANA K
;      REGISTRATION NUMBER:  35843
;      REFERENCE/DOCKET NUMBER:  9437/204199
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-861-3711
;      TELEFAX:  202-822-0944
;      TELEX:  6714627 CUCH
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1576 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-157-101A-6

  Query Match             63.1%;  Score 225.8;  DB 1;  Length 1576;
  Best Local Similarity   80.5%;  Pred. No. 3.2e-59;
  Matches  289;  Conservative    0;  Mismatches   67;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||
Db         45 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 104

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||| | ||| ||| ||| |  |||||| ||||||||||||
Db        105 TGTGCAGCCTCTGGATTCACCTTCAGTAGCAATTCTATGCACTGGGTCCGCCAGGCTCCA 164

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||| ||||||||||||    |||| |    | |||| | |   || ||| ||
Db        165 GGCAAGGGGTTGGAGTGGGTGGCAGTTATATTATATGATGGAAATCATAAATTCTACGCA 224

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||| ||||||| |||  |||||||| ||||||||||
Db        225 GACTCCGTGAAGGGCCGATTCACCATTTCCAGAGACAATTCCAAGAACACACTGTATCTG 284

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              || |||| ||||||  | | ||||||||||  || |||||||||   |||  ||||
Db        285 GAAGTGAAGAGCCTGCAAACTGAGGACACGGGTGTCTATTACTGTATAAGA--GATCAAA 342

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |||| |       |   ||||||| ||||||||||||||||||||||||||||||||
Db        343 CTTACGGAGTCCACAGATTTGACTCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 401


RESULT 7
US-09-240-274-91
; Sequence 91, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-91

  Query Match             63.0%;  Score 225.4;  DB 4;  Length 375;
  Best Local Similarity   79.8%;  Pred. No. 2.8e-59;
  Matches  296;  Conservative    0;  Mismatches   61;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | |||||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||  || || |||||||| | ||   ||   | |  |||||| ||||||||||||
Db         64 TGTGTAGTGTCTGGTTTCACCTTCAATAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || ||||||||||||||||||||    |||   | | |  |||| | |   |||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATTTGGTTTGATGGAAGTAATAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||||||| |||  |||||||| ||||||| |||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC--- 296
              |||||||||||||||||||||||||||||||| || ||||||||||||||| || |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGAGAACCAG 303

Qy        297 ----------TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                         |||     ||     ||||||||||||||||||||||||||||||||||
Db        304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363

Qy        347 ACCGTCTCCTC 357
              |||||||||||
Db        364 ACCGTCTCCTC 374


RESULT 8
US-09-240-274-77
; Sequence 77, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D01
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US-09-240-274-77

Query Match 62.8%; Score 224.8; DB 4; Length 375;
Best Local Similarity 79.6%; Pred. No. 4.3e-59;
Matches 296; Conservative 0; Mismatches 62; Indels 14; Gaps 2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | |||||||||||||||| ||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||  || || |||||||| | ||   ||   | |  |||||| ||||||||||||
Db         64 TGTGTAGTGTCTGGTTTCACCTTCAATAACTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || ||||||||||||||||||    |||   | | |  |||| | |   |||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATTTGGTTTGATGGAAGTAATAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||  |||||||||||||||||||||||||||||| |||  |||||||| ||||||| |||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC--- 296
              |||||||||||||||||||||||||||||| || ||||||||||||||| || |
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGAGAACCAG 303

Qy        297 ----------TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                       |||      ||     ||||||||| ||||||||||||||||||||||||
Db        304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGATTACTGGGGCCAGGGAACCCTGGTC 363

Qy        347 ACCGTCTCCTCA 358
              ||||||||||||
Db        364 ACCGTCTCCTCA 375
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RESULT 9
US-09-240-274-88
; Sequence 88, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D14
US-09-240-274-88

Query Match 62.5%; Score 223.6; DB 4; Length 381;
Best Local Similarity 79.1%; Pred. No. 1e-58;
Matches 299; Conservative 0; Mismatches 59; Indels 20; Gaps 2;

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Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | ||||| ||||||||||||||  ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCGGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||| | ||   ||   | |  |||||| ||||||||||||
Db         64 TGTGCAGCGTCTGGATTCACCTTCAGTACTTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTTTGATGGAAGTAAGAGAGACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              || || ||||||||||||||||||||||||||||||| |||| |||||||| ||||||||||
Db        184 GAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA--------- 290
              |||||||||||||||||||||||||||||| |||| |||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAGAAAATGTG 303

Qy        291 ----------GGGATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACC 340
                         |||         |     |||     |||||||||||||||||||||||||||||
Db        304 GCTCGTGGGGGGGGGGGGCATTCGATACAAGTACTACTTTGACTACTGGGGCCAGGGAACC 363

Qy        341 CTGGTCACCGTCTCCTCA 358
              ||||||||||||||||||
Db        364 CTGGTCACCGTCTCCTCA 381
```

RESULT 10
US-08-652-816A-22
; Sequence 22, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308

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;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-474-6300
;  INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  354 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
US-08-652-816A-22

  Query Match             62.4%;  Score 223.4;  DB 2;  Length 354;
  Best Local Similarity   80.5%;  Pred. No. 1.1e-58;
  Matches  289;  Conservative    0;  Mismatches   61;  Indels    9;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              || || ||||||||||||||| ||| ||||||  ||||||| ||||||||||||||||||
Db          4 GTACACCTGGTGGAGTCTGGGAGAGCCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||  ||  || | | |||||||| ||||||||||||
Db         64 TGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||||       ||| |  |      ||    |     |||||||  ||
Db        124 GGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||| ||||||||||||||| |||  |||||||| | |||||||||
Db        184 GACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAG-------- 295

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
              |||  |   | ||     |  |  ||||||||||||||||||||||||||||||||||
Db        296 CTTTGGTTCGGGGAGTTATAAAGGACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 354


RESULT 11
US-09-202-181-3
; Sequence 3, Application US/09202181
; Patent No. 6254867
; GENERAL INFORMATION:
;  APPLICANT:  REISNER, Yair  et al.
;  TITLE OF INVENTION:  HUMAN MONOCLONAL ANTIBODIES TO THE HEPATITIS B SURFACE
;  TITLE OF INVENTION:  ANTIGEN
;  FILE REFERENCE:  REISNER=5
;  CURRENT APPLICATION NUMBER: US/09/202,181
;  CURRENT FILING DATE:  1998-12-10
;  PRIOR APPLICATION NUMBER:  118625
;  PRIOR FILING DATE:  1996-06-11
;  PRIOR APPLICATION NUMBER:  IL97/00184
;  PRIOR FILING DATE:  1997-06-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 363
;   TYPE: DNA
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(363)
US-09-202-181-3

  Query Match             62.3%;  Score 223;  DB 4;  Length 363;
  Best Local Similarity   79.9%;  Pred. No. 1.5e-58;
  Matches  287;  Conservative    0;  Mismatches   70;  Indels    2;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||||||||||||||||||| ||||| ||||||| ||||||||||||||||||
Db          4 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||| | || |||||||  ||| |  ||  ||    | |  |||||| |||||| |||||
Db         64 TGTGCACCGTCTGGATTCGTCTTCAGGAGTTATGGCATGCACTGGGTCCGCCAGACTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||| |||||||||      ||||  |   |  |||| | |   || ||||||
Db        124 GGCAAGGGGCTTGAGTGGGTGTCACTTATATGGCATGATGGAAGTAATAGATTCTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||||||||||||||||||||| |||  |||||||| || ||||| ||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACATTGTATTTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||| |||||||  |||| | ||||||||||| ||
Db        244 CAAATGAACAGCCTGAGAGCCGAAGACACGGCTATGTACTTCTGTGCGAGAGAGGCTG 303

Qy        300 CTTATGACAGAGGCT-ACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC 357
              ||     ||  |||  |||||||  ||||||||||||||||||||||||||||||| .
Db        304 ATTGCAGCACCTGCTGCCTTTGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTC 362


RESULT 12
US-08-026-320A-1
; Sequence 1, Application US/08026320A
; Patent No. 5419904
;  GENERAL INFORMATION:
;    APPLICANT:  Irie, Reiko F
;    TITLE OF INVENTION:  HUMAN B-LYMPHOBLASTOID CELL LINE
;    TITLE OF INVENTION:  SECRETING ANTI-GANGLIOSIDE ANTIBODY
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Poms, Smith, Lande & Rose
;      STREET:  2029 Century Park East, Suite 3800
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  90067
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/026,320A
;      FILING DATE:  26-FEB-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/609803
;      FILING DATE:  05-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oldenkamp, David J
;      REGISTRATION NUMBER:  29421
;      REFERENCE/DOCKET NUMBER:  94268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  3107885046
;      TELEFAX:  3102771297
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  432 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Epstein Barr Virus Transformed B cell
;      CELL LINE:  L612
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..432
;      OTHER INFORMATION:  /function= "Heavy Chain"
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;       OTHER INFORMATION:  /product= "Immunoglobulin Variable Region"
;       OTHER INFORMATION:  /standard_name= "HuMab L612 Heavy Chain Variable
;       OTHER INFORMATION:  Region Sequence"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  148..162
;       OTHER INFORMATION:  /function= "Complementary
;       OTHER INFORMATION:  determining region 1 (CDR1)"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  271..300
;       OTHER INFORMATION:  /function= "Complementary
;       OTHER INFORMATION:  determining region 2 (CDR2)"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  397..429
;       OTHER INFORMATION:  /function= "Complementary determining
;       OTHER INFORMATION:  region 3 (CDR3)"
US-08-026-320A-1

  Query Match             62.2%;  Score 222.6;  DB 1;  Length 432;
  Best Local Similarity   79.9%;  Pred. No. 2.1e-58;
  Matches  287;  Conservative    0;  Mismatches   69;  Indels    3;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| |||| ||||||||||||||||  ||||||| |||| ||||||||||||
Db         61 GTGCAGCTGTTGGATTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTGCCTGAGACTCTCC 120

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||||||  ||    | | | ||||||||| ||||||||||||
Db        121 TGTGCAGCCTCTGGATTCACCTTTAGCAGCTGTGCCATGAGCTGGGTCCGCCAGGCTCCA 180

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              ||||||||||||||||||       ||| |  |      ||    |     ||||||| ||
Db        181 GGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA 240

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              ||||| |||||||||||  |||||||||||||||| |||   ||||||||  |  ||||||||
Db        241 GACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAAATCCAAGAACACGTTGTATCTG 300

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              |||||||||||||||||||||||||||||||| |||||||||||| |||    |
Db        301 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGGTGGCAAC 360

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                |||       | |  ||   ||  ||||||||||||||||||||||||||||||
Db        361 GATATTTTGACTGGTTATTATGCT--TGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 417


RESULT 13
US-09-273-839A-11
; Sequence 11, Application US/09273839A
; Patent No. 6329156
; GENERAL INFORMATION:
;  APPLICANT:  Cirino, Nick M
;  APPLICANT:  Jackson, Paul J
;  APPLICANT:  Lehnert, Bruce E
;  TITLE OF INVENTION:  Disruption of Anthrax Toxin Binding to Cell Surface
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE:  S-89,662
;  CURRENT APPLICATION NUMBER: US/09/273,839A
;  CURRENT FILING DATE:  1999-03-22
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 892
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-273-839A-11

  Query Match             62.1%;  Score 222.2;  DB 4;  Length 892;
  Best Local Similarity   80.5%;  Pred. No. 3.4e-58;
  Matches  289;  Conservative    0;  Mismatches   58;  Indels   12;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              |||||||||||||||||||||||||||||| ||||| |||||||  ||||||||||||||||
Db        106 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 165

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||||| |||||||||| | ||    || ||| |    ||||| ||||||||||||
Db        166 TGTGCAGCCTCTGGATTCACCTTCAATAACCATGCTATGGAATGGGTCCGCCAGGCTCCA 225

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||    |  ||| |     |  ||   |    ||   |||||
Db        226 GGCAAGGGGCTGGAGTGGGTCTCTGGTATTAATTGGGATGGTGGTAGCACAGGTTATGCA 285

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||||||||||||||||| || ||||||||| ||||||||||||||| |||||||||
Db        286 GACTCTGTGAAGGGCCGATTCGCCGTCTCCAGAGACAACGCCAAGAACTCCCTGTATCTG 345

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATCTGT 299
              ||||| ||||| ||||||| |||||||||||| ||||||||||||||| ||||
Db        346 CAAATAAACAGTCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCCAGAG-------- 397

Qy        300 CTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 358
                | || | ||   | |||||||||||||||||| ||||||||||||||||||||
Db        398 ---CTAACTGGGGACGCATTGACTACTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCA 453


RESULT 14
US-09-240-274-92
; Sequence 92, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D18
US-09-240-274-92

  Query Match             61.9%;  Score 221.6;  DB 4;  Length 375;
  Best Local Similarity   79.0%;  Pred. No. 4e-58;
  Matches  294;  Conservative    0;  Mismatches   64;  Indels   14;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | |||||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||| ||  || || ||||||| | ||   ||   | |  |||||| ||||||||| ||
Db         64 TGTGTAGTGTCTGGTTTCACCTTCAATAACTATGGCATGCACTGGGTCCGCCAGGCTTCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||| ||||||||||||    |||   | | |  |||| | |   |||||||||
Db        124 GGCAAGGGGTTGGAGTGGGTGGCAGTTATTTGGTTTGATGGAAGTAATAAATACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              |||||  |||||||||||||||||||||||||||| |||  |||||||| ||||||| |||
Db        184 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACACTGTACCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGAGGGATC--- 296
              |||||||||||||||||||||||||||||||| || ||||||||||||||| || |
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Db        244 CAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTATATTACTGTGCGAGAGAGAACCAG 303

Qy        297 ----------TGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 346
                         |||      ||      ||||||||||||||||||||||||||||||||||
Db        304 ATAAAGCTATGGTCCCGATACCTTTACTACTTTGACTACTGGGGCCAGGGAACCCTGGTC 363

Qy        347 ACCGTCTCCTCA 358
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Db        364 ACCGTGTCCTCA 375


RESULT 15
US-09-240-274-87
; Sequence 87, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D13
US-09-240-274-87

  Query Match             61.6%;  Score 220.4;  DB 4;  Length 381;
  Best Local Similarity   78.6%;  Pred. No. 9.3e-58;
  Matches  297;  Conservative    0;  Mismatches   61;  Indels   20;  Gaps    2;

Qy          1 GTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCAAGCCTGGAGGGTCCCTGAGACTCTCC 60
              ||||||||| | |||||||||||||| ||||| |||||||  ||||||||||||||||
Db          4 GTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCC 63

Qy         61 TGTGCAGCCTC-GGATTCACCTTTACTAGGAATCCTACGAGCTGGGTACGCCAGGCTCCA 119
              |||||||| || |||||||||||| | ||    ||    | | ||||||| ||||||||||||
Db         64 TGTGCAGCGTCTGGATTCACCTTCAGTACTTATGGCATGCACTGGGTCCGCCAGGCTCCA 123

Qy        120 GGGAAGGGGCTGGAGTGGGTGGTTAATATAATGGTAGTCGGAATTGAACCATACTATGCG 179
              || |||||||||||||||||||     ||||  | | | |||| | |    | |||||||
Db        124 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTTTGATGGAAGTAACAGAGACTATGCA 183

Qy        180 GACTCTGTGAAGGGCCGATTCACCATCTCCAGAGGCAACGCCAAGAACTCACTGTATCTG 239
              || || |||||||||||||||||||||||||||| |||  |||||||| ||||||||||
Db        184 GAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAGTCCAAGAACACACTGTATCTG 243

Qy        240 CAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTGTATTACTGTGCGAGA--------- 290
              |||||||||||||||||||||||||| |||| |||||||| |||||||||
Db        244 CAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTATTGTGCGAGAGAAAATGTG 303

Qy        291 ----------GGGATCTGTCTTATGACAGAGGCTACTTTGACTACTGGGGCCAGGGAACC 340
                         |||       |    |||  . ||||||||||||||||||||||||||||
Db        304 GCTCGTGGGGGGGGGGGCGTTCGATACAAGTACTACTTTGACTACTGGGGCCAGGGAACC 363

Qy        341 CTGGTCACCGTCTCCTCA 358
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Db        364 CTGGTCACCGTCTCCTCA 381


Search completed: July 18, 2003, 19:59:09
Job time : 19.9834 secs
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